OM protein - protein search, using sw model

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          GenCore version 5.1.6
          Copyright (c) 1993 - 2004  Compugen Ltd.
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Run on: February 14, 2004, 22:43:11 ; Search time 27 Seconds
                   (without alignments)
                   1919.386 Million cell updates/sec

Title: US-09-974-573-1
Perfect score: 5790
Sequence: 1 MELENYEQPVVLREDNRRRR..........QFNWFLHLVLGIKQGEKHSA 1102

Scoring table: BLOSUM62
          Gapop 10.0 , Gapext 0:5

Searched: 127863 segs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query/Length	DB	ID	Description
1	5785	99.9	1102	1	P11G_PIG	O02697 sus scrofa
2	5523.5	95.4	1101	1	P11G_HUMAN	P48736 homo sapien
3	5506	95.1	1102	1	P11G_MOUSE	Q9jhg7 mus musculu
4	1465.5	25.3	1068	1	P11A_BOVIN	P32871 bos taurus
5	1460.5	25.2	1068	1	P11A_HUMAN	P42336 homo sapien
6	1450.5	25.1	1068	1	P11A_MOUSE	P42337 mus musculu
7	1362	23.5	1070	1	P11B_RAT	Q92il0 rattus norv
8	1354.5	23.4	1070	1	P11B_HUMAN	P42338 homo sapien
9	1349.5	23.3	1044	1	P11D_HUMAN	O00329 homo sapien
10	1319	22.8	1043	1	P11D_MOUSE	O35904 mus musculu
11	1297	22.4	1570	1	P3K1_DICDI	P54673 dictyosteli
12	1233	21.3	1858	1	P3K2_DICDI	P54674 dictyosteli
13	1136.5	19.6	1585	1	P3K3_DICDI	P54675 dictyosteli
14	1041	18.0	1146	1	AGE1_CAEEL	Q94125 caenorhabdi
15	1021	17.6	1634	1	PK3B_HUMAN	O00750 homo sapien
16	922	15.9	1505	1	PK3G_RAT	O70173 rattus norv
17	881	15.2	1506	1	PK3G_MOUSE	O70167 mus musculu
18	856.5	14.8	1448	1	PK3G_HUMAN	O75747 homo sapien
19	720.5	12.4	816	1	P3K4_DICDI	P54676 dictyosteli
20	714.5	12.3	801	1	VP34_SCHPO	P50520 schizosacch
21	672	11.6	814	1	P3K1_SOYBN	P42347 glycine max
22	669	11.6	812	1	P3K2_SOYBN	P42348 glycine max
23	657.5	11.4	814	1	PI3K_ARATH	P42339 arabidopsis
24	649.5	11.2	875	1	VP34_YEAST	P22543 saccharomyc
25	562	9.7	1020	1	VP34_CANAL	Q92213 candida alb
26	402	6.9	854	1	PI4K_HUMAN	P42356 homo sapien
27	380	6.6	1900	1	STT4_YEAST	P37297 saccharomyc
28	314.5	5.4	1093	1	PI4K_DICDI	P54677 dictyosteli
29	277	4.8	1066	1	PIK1_YBAST	P39104 saccharomyc
30	248	4.3	851	1	YDBG_SCHPO	Q10366 schizosacch
31	239	4.1	4128	1	PRKD_HUMAN	P78527 homo sapien
32	232	4.0	4128	1	PRKD_MOUSE	P97313 mus musculu
33	225	3.9	2787	1	TEL1_YEAST	P38110 saccharomyc
34	215.5	3.7	2337	1	TOR2_SCHPO	Q9y7k2 schizosacch
35	215.5	3.7	2470	1	TOR1_YEAST	P35169 saccharomyc
36	210.5	3.6	2368	1	ESR1_YEAST	P38111 saccharomyc
37	200.5	3.5	2386	1	RAD3_SCHPO	Q02099 schizosacch
38	191	3.3	2473	1	TOR2_YEAST	P32600 saccharomyc
39	191	3.3	3056	1	ATM_HUMAN	Q13315 homo sapien
40	178.5	3.1	2549	1	FRAP_MOUSE	Q9jln9 mus musculu
41	178	3.1	3066	1	ATM_MOUSE	Q62388 mus musculu
42	177.5	3.1	2549	1	FRAP_HUMAN	P42345 homo sapien
43	174.5	3.0	2549	1	FRAP_RAT	P42346 rattus norv
44	172	3.0	2335	1	TOR1_SCHPO	O14356 schizosacch
45	143	2.5	6885	1	SNE2_HUMAN	Q8wxh0 homo sapien

ALIGNMENTS

```
RESULT 1
P11G_PIG
ID   P11G_PIG     STANDARD;      PRT;   1102 AA.
AC   O02697;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit,
DE   gamma isoform (p110) (PI3K) (PI3-kinase p110 subunit gamma) (Ptdins-
DE   3-kinase p110) (PI3K) (P120-PI3K).
GN   PIK3CG.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC   TISSUE=Neutrophils;
RX   MEDLINE=97248491; PubMed=9094719;
RA   Stephens L.R., Eguinoa A., Erdjument-Bromage H., Lui M., Cooke F.,
RA   Coadwell J., Smrcka A.S., Thelen M., Cadwallader K., Tempst P.,
RA   Hawkins P.T.;
RT   "The G beta gamma sensitivity of a PI3K is dependent upon a tightly
RT   associated adaptor,p101.";
RL   Cell 89:105-114(1997).;
RN   [2]
RP   REVISIONS.
RA   Stephens L.R.;
RL   Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: 3-PHOSPHORYLATES THE CELLULAR PHOSPHOINOSITIDE
CC       PTDINS-4,5-BIPHOSPHATE (PTDINS(4,5)P2).
CC   -!- CATALYTIC ACTIVITY: ATP + 1-phosphatidyl-1D-myo-inositol 4,5-
CC       bisphosphate = ADP + 1-phosphatidyl-1D-myo-inositol 3,4,5-
CC       trisphosphate.
CC   -!- ENZYME REGULATION: WHEN BOUND TO P101 THE PI3K ACTIVITY OF P120
CC       COULD BE ACTIVATED GREATER THAN 100-FOLD BY THE BETA-GAMMA G
CC       PROTEINS.
CC   -!- PATHWAY: SIGNALING PATHWAYS REGULATING CELL GROWTH.
CC   -!- SUBUNIT: HETERODIMER OF A 101 kDa SUBUNIT AND A 120 kDa CATALYTIC
CC       SUBUNIT.
CC   -!- SIMILARITY: BELONGS TO THE PI3/PI4-KINASES FAMILY.
CC   -----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----------------------------------------------------------------------
DR   EMBL; Y10743; CAA71731.1; -.
DR   PDB; 1B7U; 01-OCT-00.
DR   PDB; 1B8X; 01-OCT-02.
DR   InterPro; IPR000403; PI3_PI4_kinase.
DR   InterPro; IPR002420; PI3K_C2.
DR   InterPro; IPR000341; PI3K_ras_bind.
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[handwritten annotation: Payne]

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DR   InterPro; IPR001263; PI3Ka.
DR   Pfam; PF00454; PI3_PI4_kinase; 1.
DR   Pfam; PF00792; PI3K_C2; 1.
DR   Pfam; PF00794; PI3K_rbd; 1.
DR   Pfam; PF00613; PI3Ka; 1.
DR   SMART; SM00142; PI3K_C2; 1.
DR   SMART; SM00144; PI3K_rbd; 1.
DR   SMART; SM00145; PI3Ka; 1.
DR   SMART; SM00146; PI3Kc; 1.
DR   PROSITE; PS00915; PI3_4_KINASE_1; 1.
DR   PROSITE; PS00916; PI3_4_KINASE_2; 1.
DR   PROSITE; PS00290; PI3_4_KINASE_3; 1.
KW   Transferase; Kinase; Multigene family; 3D-structure.
FT   DOMAIN      17     22    POLY-ARG.
FT   DOMAIN     828   1073    PI3K/PI4K.
SQ   SEQUENCE   1102 AA;  126657 MW;  9E7D4211FD626DFC CRC64;

Query Match             99.9%;  Score 5785;  DB 1;  Length 1102;
Best Local Similarity   99.9%;  Pred. No. 0;  Indels  1;  Gaps  0;
Matches 1101;  Conservative  0;  Mismatches  1;

Qy     1 MELENYEQPVVLREDNRRRRRMKPRSTAASLSSMELIPIEFVLPTSQRNTKTPETALLH 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MELENYEQPVVLREDNRRRRRMKPRSTAASLSSMELIPIEFVLPTSQRNTKTPETALLH 60

Qy    61 VAGHGNVEQMKAQVWLRALETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLD 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 VAGHGNVEQMKAQVWLRALETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLD 120

Qy   121 CLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRL 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRL 180

Qy   181 VTPRMAEVAGRDPKLYAMHPWVTSKPLPEYLLKKITNNCVFIVIHRSTTSQTIKVSADDT 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 VTPRMAEVAGRDPKLYAMHPWVTSKPLPEYLLKKITNNCVFIVIHRSTTSQTIKVSADDT 240

Qy   241 PGTILQSFFTKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 PGTILQSFFTKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG 300

Qy   301 EEIHLVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK 360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 EEIHLVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK 360

Qy   361 FRVKIRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTSPKPFTEEVLWNVWLEFSIKI 420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 FRVKIRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTSPKPFTEEVLWNVWLEFSIKI 420

Qy   421 KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYVNLLLIDHRFLLRHGEY 480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYVNLLLIDHRFLLRHGEY 480

Qy   481 VLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKIRPTDPDEG 540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 VLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKIRPTDPDEG 540

Qy   541 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQ 600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQ 600

Qy   601 QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 660

Qy   661 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY 720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY 720

Qy   721 LRGCGTAMLHDFTQQVQVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLP 780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 LRGCGTAMLHDFTQQVQVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLP 780

Qy   781 QSFRVPYDPGLKAGALVIEKCKVMASKKKPLWLBFKCADPTALSNETIGIIFKHGDDLRQ 840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 QSFRVPYDPGLKAGALVIEKCKVMASKKKPLWLBFKCADPTALSNETIGIIFKHGDDLRQ 840

Qy   841 DMLLIQILRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG 900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 DMLLIQILRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG 900

Qy   901 AFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL 960
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 AFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL 960

Qy   961 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLAL 1020
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLAL 1020

Qy  1021 RHHTNLLILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYPLDQIEVCRDKGW 1080
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 RHHTNLLILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYPLDQIEVCRDKGW 1080

Qy  1081 TVQFNWFLHLVLGIKQGEKHSA 1102
         ||||||||||||||||||||||
Db  1081 TVQFNWFLHLVLGIKQGEKHSA 1102


RESULT 2
P11G_HUMAN
ID   P11G_HUMAN    STANDARD;    PRT;   1101 AA.
AC   P48736;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   ...phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit,
```

OM protein - protein search, using sw model

```
                GenCore version 5.1.6
          Copyright (c) 1993 - 2004 Compugen Ltd.

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ALIGNMENTS

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P11G_PIG
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AC   O02697;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit,
DE   gamma isoform (EC 2.7.1.153) (PI3-kinase p110 subunit gamma) (PtdIns-
DE   3-kinase p110) (PI3K) (P120-PI3K).
GN   PIK3CG.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
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RC   TISSUE=Neutrophils;
RX   MEDLINE=97248491; PubMed=9094719;
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RL   Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
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CC       PTDINS-4,5-BIPHOSPHATE (PTDINS(4,5)P2).
CC   -!- CATALYTIC ACTIVITY: ATP + 1-phosphatidyl-1D-myo-inositol 4,5-
CC       bisphosphate = ADP + 1-phosphatidyl-1D-myo-inositol 3,4,5-
CC       trisphosphate.
CC   -!- ENZYME REGULATION: WHEN BOUND TO P101 THE PI3K ACTIVITY OF P120
CC       COULD BE ACTIVATED GREATER THAN 100-FOLD BY THE BETA-GAMMA G
CC       PROTEINS.
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CC       SUBUNIT.
CC   -!- SIMILARITY: BELONGS TO THE PI3/PI4-KINASES FAMILY.
```

```
DR   EMBL; Y10743; CAA71731.1; -.
DR   PDB; 1ETU; 01-DEC-00.
DR   PDB; 1E8X; 01-OCT-02.
DR   InterPro; IPR000403; PI3 PI4 kinase.
DR   InterPro; IPR002420; PI3K_C2.
DR   InterPro; IPR000341; PI3K_ras_bind.
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provide

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DR   InterPro; IPR001263; PI3Ka.
DR   Pfam; PF00454; PI3_PI4_kinase; 1.
DR   Pfam; PF00792; PI3K_C2; 1.
DR   Pfam; PF00794; PI3K_rbd; 1.
DR   Pfam; PF00613; PI3Ka; 1.
DR   SMART; SM00142; PI3K_C2; 1.
DR   SMART; SM00144; PI3K_rbd; 1.
DR   SMART; SM00145; PI3Ka; 1.
DR   SMART; SM00146; PI3Kc; 1.
DR   PROSITE; PS00915; PI3_4_KINASE_1; 1.
DR   PROSITE; PS00916; PI3_4_KINASE_2; 1.
DR   PROSITE; PS50290; PI3_4_KINASE_3; 1.
KW   Transferase; Kinase; Multigene family; 3D-structure.
FT   DOMAIN     17     22       POLY-ARG.
FT   DOMAIN    828   1073       PI3K/PI4K.
SQ   SEQUENCE   1102 AA;  126657 MW;  9E7D4211FD626DFC CRC64;
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Query Match           99.9%;  Score 5785;  DB 1;  Length 1102;
Best Local Similarity 99.9%;  Pred. No. 0;
Matches 1101;  Conservative 0;  Mismatches 0;  Indels 1;  Gaps 0;

Qy     1 MELENYEQPVVLREDNRRRRRRMKPRSTAASLSSMELIPIEFVLPTSQRNTKTPETALLH 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MELENYEQPVVLREDNRRRRRRMKPRSTAASLSSMELIPIEFVLPTSQRNTKTPETALLH 60

Qy    61 VAGHGNVEQMKAQVWLRALETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLD 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 VAGHGNVEQMKAQVWLRALETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLD 120

Qy   121 CLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRL 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRL 180

Qy   181 VTPRMAEVAGRDPKLYAMHPWVTSKPLPEYLLKKITNNCVFIVIHRSTTSQTIKVSADDT 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 VTPRMAEVAGRDPKLYAMHPWVTSKPLPEYLLKKITNNCVFIVIHRSTTSQTIKVSADDT 240

Qy   241 PGTILQSFFTKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 PGTILQSFFTKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG 300

Qy   301 EEIHLVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 EEIHLVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK 360

Qy   361 FRVKIRGIDIPVLPRTADLTVFVEANIQYGGQVLCQRRTSPKPFTEEVLWNVWLEFSIKI 420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 FRVKIRGIDIPVLPRTADLTVFVEANIQYGGQVLCQRRTSPKPFTEEVLWNVWLEFSIKI 420

Qy   421 KDLPKGALLNLQIYCGKAPALSGKTSAEMPESKGKGAQLLYYVNLLLIDHRPLLRHGEY 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 KDLPKGALLNLQIYCGKAPALSGKTSAEMPESKGKGAQLLYYVNLLLIDHRPLLRHGEY 480

Qy   481 VLHWQLSGKGEDQGSFNADKLTSATNFDKENSMSISILLDNYCHPIALPGHRPTPDPEG 540
           |||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db   481 VLHWQLSGKGEDQGSFNADKLTSRTNPDKENSMSISILLDNYCHPIALPGHRPTPDPEG 540

Qy   541 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQ 600
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQ 600

Qy   601 QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 660
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 660

Qy   661 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY 720
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY 720

Qy   721 LRGCGTAMLHDFTQQVVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQLENLQNLNLP 780
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 LRGCGTAMLHDFTQQVVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQLENLQNLNLP 780
```

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Qy   781 QSFRVPYDPGLKAGALVIEKCKVMASKKKPLWLEFKCADPTALSNETGIIFKHGDDLRQ 840
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 QSFRVPYDPGLKAGALVIEKCKVMASKKKPLWLEFKCADPTALSNETGIIFKHGDDLRQ 840

Qy   841 DMLIQLRIMESIWETESLDLCLLPYGCISTGDKIGMEIVKDATTIAKIQQSTVGNTG 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 DMLIQLRIMESIWETESLDLCLLPYGCISTGDKIGMEIVKDATTIAKIQQSTVGNTG 900

Qy   901 AFKDEVLSHWLKEKCPIEBKFQAAVERFVYSCAGYCVATPVLGIGDRHNDNIMISETGNL 960
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 AFKDEVLSHWLKEKCPIEBKFQAAVERFVYSCAGYCVATPVLGIGDRHNDNIMISETGNL 960

Qy   961 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLAL 1020
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLAL 1020

Qy  1021 RHHTNLLIIFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW 1080
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 RHHTNLLIIFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW 1080

Qy  1081 TVQFNWFLHIVLGIKQGEKHSA 1102
           ||||||||||||||||||||||
Db  1081 TVQFNWFLHIVLGIKQGEKHSA 1102
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RESULT 2
P11G_HUMAN
ID   P11G_HUMAN    STANDARD;     PRT;  1101 AA.
AC   P48736;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit,
DE   gamma isoform (EC 2.7.1.153) (PI3-kinase p110 subunit gamma) (PtdIns-
DE   3-kinase p110) (PI3Kgamma).
GN   PIK3CG.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95356661; PubMed=7624799;
RA   Stoyanov B., Volinia S., Hanck T., Rubio I., Loubtchenkov M.,
RA   Malek D., Stoyanova S., Vanhaesebroeck B., Dhand R., Nuernberg B.,
RA   Gierschik P., Seedorf K., Hsuan J.J., Waterfield M.D., Wetzker R.;
RT   "Cloning and characterization of a G protein-activated human
RT   phosphoinositide-3 kinase.";
RL   Science 269:690-693(1995).
RN   [2]
RP   REVISIONS.
RA   Waterfield M.D.;
RL   Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: 3-PHOSPHORYLATES THE CELLULAR PHOSPHOINOSITIDE
CC       PTDINS-4,5-BIPHOSPHATE (PTDINS(4,5)P2).
CC   -!- CATALYTIC ACTIVITY: ATP + 1-phosphatidyl-1D-myo-inositol 4,5-
CC       bisphosphate = ADP + 1-phosphatidyl-1D-myo-inositol 3,4,5-
CC       trisphosphate.
CC   -!- ENZYME REGULATION: ACTIVATED BY BOTH THE ALPHA AND THE BETA-GAMMA
CC       G PROTEINS.
CC   -!- PATHWAY: SIGNALING PATHWAYS REGULATING CELL GROWTH.
CC   -!- SUBUNIT: HETERODIMER OF A 101 kDa SUBUNIT AND A 120 kDa CATALYTIC
CC       SUBUNIT (BY SIMILARITY)
CC   -!- TISSUE SPECIFICITY: PANCREAS, SKELETAL MUSCLE, LIVER, AND HEART.
CC   -!- SIMILARITY: BELONGS TO THE PI3/PI4-KINASES FAMILY.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
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Db   600 QEIVAKTYQLLARREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLSLEDDDVLHYL 659
         |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Qy   661 LQLVQAVKFPYHDSALARFLLKRGLRNCRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY 720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   660 LQLVQAVKFPYHDSALARFLLKRGLRNCRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY 719
Qy   721 LRGGCTAMLHDFTQCVQVIDMLQKVTIDKSLSAEKYDVSSQVISQLKQKLENLQNLNLP 780
         ||||||||||||||| |||| ||||||| |||||||||||||||||||||||||||| |
Db   720 LRGGCTAMLHDFTQQVQVIEMLQKVTLDIKSLSAEKYDVSSQVISQLKQKLENLQNSQLP 779
Qy   781 QSFRVPYDPGLKAGALVIEBCKVMASKKKPLWLBFKCADPTALSNETIGIIFKHGDDLRQ 840
         |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db   780 ESFRVPYDPGLKAGALAIEBCKVMASKKKPLWLBFKCADPTALSNETIGIIFKHGDDLRQ 839
Qy   841 DMLIQILRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG 900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   840 DMLIQILRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG 899
Qy   901 AFKDEVLSHWLKEKCPIEKFQAAVERFYYSCAGYCVATFVLGIGDRHNDNIMITETGNL 960
         ||||||| | ||| | |||||||||||| |||||||||||||||||||||||||||||
Db   900 AFKDEVLNHVLKEKSPTEBKFQAAVERFVSCAGYCVATFVLGIGDRHNDNIMITETGNL 959
Qy   961 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFWMGTSGKKTSLHFKPQDVCKAYIAL 1020
         ||||||||||||||||||||||||||||||||||||||||||||| || ||| |||||
Db   960 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFWMGTSGKKTSPHFQKPQDICVKAYIAL 1019
Qy  1021 RHHTNLLILIFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW 1080
         |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db  1020 RHHTNLLILIFSMMLMTGMPQLTSKEDIEYIRDALTVGKNEEDAKKYFLDQIEVCRDKGW 1079
Qy  1081 TVQFNWFLHIVLGIKQGEKHSA 1102
         ||||||||||||||||||||||
Db  1080 TVQFNWFLHIVLGIKQGEKHSA 1101
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RESULT 3
P11G_MOUSE
ID   P11G_MOUSE       STANDARD;       PRT;   1102 AA.
AC   Q9JHG7;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit,
DE   gamma isoform (p110) (PI3K) (PI-kinase p110 subunit gamma) (Ptdins-
DE   3-kinase p110) (PI3Kgamma).
GN   PI3CG OR PI3KG1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Hirsch E.;
RT   "Murine PI3kgamma: cDNA cloning and gene structure description.";
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Wymann M.P., Hirsch E.;
RT   "Murine G protein-coupled phosphoinositide 3-kinase gamma cDNA and
RT   genomic organisation.";
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: 3-PHOSPHORYLATES THE CELLULAR PHOSPHOINOSITIDE
CC       PTDINS-4,5-BIPHOSPHATE (PTDINS(4,5)P2) (BY SIMILARITY).
CC   -!- CATALYTIC ACTIVITY: ATP + 1-phosphatidyl-1D-myo-inositol 4,5-
CC       bisphosphate = ADP + 1-phosphatidyl-1D-myo-inositol 3,4,5-
CC       trisphosphate.
CC   -!- ENZYME REGULATION: ACTIVATED BY BOTH THE ALPHA AND THE BETA-GAMMA
CC       G PROTEINS (BY SIMILARITY). WORTMANNIN SENSITIVE IN NM RANGE.
CC   -!- PATHWAY: SIGNALING PATHWAYS REGULATING CELL GROWTH.
CC   -!- SUBUNIT: HETERODIMER OF A 101 kDa SUBUNIT AND A 120 kDa CATALYTIC
CC       SUBUNIT (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE PI3/PI4-KINASES FAMILY.
CC
DR   EMBL; X83368; CAA58284.1; -.
DR   PDB; 1E8Y; 17-NOV-00.
DR   PDB; 1E8Z; 17-NOV-00.
DR   Genew; HGNC:8978; PIK3CG.
MIM; 601232;
DR   GO; GO:0004429; F:1-phosphatidylinositol 3-kinase; TAS.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
DR   InterPro; IPR000403; PI3_PI4_kinase.
DR   InterPro; IPR000420; PI3K_C2.
DR   InterPro; IPR000341; PI3K_rbd_bind.
DR   InterPro; IPR001263; PI3Ka.
DR   Pfam; PF00454; PI3_PI4_kinase; 1.
DR   Pfam; PF00792; PI3K_C2; 1.
DR   Pfam; PF00794; PI3K_rbd; 1.
DR   Pfam; PF00613; PI3Ka; 1.
DR   SMART; SM00142; PI3K_C2; 1.
DR   SMART; SM00144; PI3K_rbd; 1.
DR   SMART; SM00145; PI3Ka; 1.
DR   SMART; SM00146; PI3Kc; 1.
DR   PROSITE; PS00915; PI3_4_KINASE_1; 1.
DR   PROSITE; PS00916; PI3_4_KINASE_2; 1.
DR   PROSITE; PS50290; PI3_4_KINASE_3; 1.
KW   Transferase; Kinase; Multigene family; 3D-structure.
FT   DOMAIN     18    22       POLY-ARG.
FT   DOMAIN    827  1072       PI3K/PI4K.
SQ   SEQUENCE 1101 AA;   126410 MW;  266BAA6495C8AE9E CRC64;
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Query Match             95.4%;  Score 5523.5;  DB 1;  Length 1101;
Best Local Similarity   95.2%;  Pred. No. 0;
Matches 1049;  Conservative 21;  Mismatches 31;  Indels 1;  Gaps 1;

Qy    1 MELENYEQPVVLREDNRRRRRRMKPRSTAASLSSMELIPIEFVLPTSQRNKTPETALLH 60
        ||||| |||||||||| |||||||||| ||||||||||||||||||||||| ||||||||
Db    1 MELENYKQPVVLREDNCRRRRRMKPRS-AASLSSMELIPIEFVLPTSQRKCKSPETALLH 59
Qy   61 VAGHGNVEQMKAQVWLRALETSVSADFYHRLGPDHFLLLYQKKGGWYEIYDKYQVVQTLD 120
        ||||||||||||||||||||||| ||||||||| |||||||||||||||||||||||||
Db   60 VAGHGNVEQMKAQVWLRALETSVAADFYHRLGPHHFLLLYQKKGGWYEIYDKYQVVQTLD 119
Qy  121 CLRYWKVLHRSPGQIHVVQRHAPSEETLAFORQLNALIGYDVTDVSNVHDDELEFTRRRL 180
        |||||| ||||||||| |||| ||||| |||||| ||||||||||||||||||||||| |
Db  120 CLRYWKATHRSPGQIHLVQRHPPSEESQAFORQLTALIGYDVTDVSNVHDDELEFTRRGL 179
Qy  181 VTPRMAEVAGRDPKLYAMHPWTSKPLPEYLLKKITNNCVFIVIHRSTTSQTIKVSADDT 240
        |||||||| ||||||||||||||||||||| |||| ||| |||||||||||||||| |||
Db  180 VTPRMAEVASRDPKLYAMHPWTSKPLPEYLWKKIANNCIFIVIHRSTTSQTIKVSPDDT 239
Qy  241 PGTILQSFFTKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG 300
        || |||||||||||||||||||||| | |||||||||||||||||||||||||| |||||
Db  240 PGAILQSFFTKMAKKKSLMDIPESQSEQDFVLRVCGRDEYLVGETPIKNFQWVRHCLKNG 299
Qy  301 EEIHLVLDTPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLMDCDRK 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  300 EEIHLVLDTPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLMDCDRK 359
Qy  361 FRVKIRGIDIPVLPRTADLTVFVEANIQYGGQVLCQRRTSPKPFTEEVLMNVWLEFSIKI 420
        |||||||||||||| | |||||||||| ||||||||||||||||||||||||||||||||
Db  360 FRVKIRGIDIPVLPRNTDLTVFVEANIQHGGQVLCQRRTSPKPFTEEVLMNVWLEFSIKI 419
Qy  421 KDLPKGALLNLQIYCCGKAPALSGKTSAEMSPESKGKAQLLYYVNLLLIDHRFLLRHGEY 480
        ||||||||||||||| ||||||| |  || ||| |||| |||||||||||||||||| ||
Db  420 KDLPKGALLNLQIYCGKAPALSSKASAESPSSESKGKVRLLYYVNLLLIDHRFLLRRGEY 479
Qy  481 VLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKHRPTPDPEG 540
        ||||||| |||||||||||||||||||||||||||||||||||||||||||| ||||||
Db  480 VLHMWQISGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKHQPTPDPEG 539
Qy  541 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKNGQ 600
        ||||||||||||||||||||||||||||||||||||||||||||| |||||||||| |||
Db  540 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKHPKAYPKLFSSVKWGQ 599
Qy  601 QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLSLEDDDVLHYL 660
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Db    421 KDLPKGALLNLQIYCCKTPSLSSKASAETPGSESKGKAQLLYVNLLLIDHRFLLRHGDY 480

Qy    481 VLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKGHRPTPDPEG 540
              ||||||||||:||||||| |||||||||||||||||||||||||||||||||||||||||
Db    481 VLHMWQISGKAEQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKGHRPTPDPEG 540

Qy    541 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKPDKAYPKLFSSVKWGQ 600
              ||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||
Db    541 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKPKAYPKLFSSVKWGQ 600

Qy    601 QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 660
              ||||||||||||| |:||||||||||||||||||||||||||||||||||||||||||
Db    601 QEIVAKTYQLLARREIWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 660

Qy    661 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY 720
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY 720

Qy    721 LRGCGTAMLHDFTQQVVQIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLP 780
              |||||||||||||||||||||||||||||||||||||||||||||||:||||||||||
Db    721 LRGCGTAMLQDFTQQVVIEMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLESLQNSNLP 780

Qy    781 QSPRVPYDPGLKAGALVIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ 840
              :|:|||||||||||||||||||||||:||||||||||||||||||||||||||||||||
Db    781 ESFRVPYDPGLKAGTLVIEKCKVMASKKKPLWLEFKCADPTVLSNETIGIIFKHGDDLRQ 840

Qy    841 DMLILQIIRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG 900
              ||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db    841 DMIILQIIRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAQIQQSTVGNTG 900

Qy    901 AFKDEVLSHWLKEKCPIBEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL 960
              |||||:|:||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AFKDEVLNHWLKEKCPIBEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL 960

Qy    961 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLAL 1020
              ||||||||||||||||||||||||||||||||||||:|||||||||||||||||:||||
Db    961 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGGSGKKTSPHFQKFQDVCVRAYLAL 1020

Qy   1021 RHHTNLLIILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW 1080
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 RHHTNLLIILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW 1080

Qy   1081 TVQPNWFLHLVLGIKQGEKGHSA 1102
              |||||||||||||||||||||||
Db   1081 TVQPNWFLHLVLGIKQGEKGHSA 1102
```

RESULT 4

```
P11A_BOVIN
ID   P11A_BOVIN    STANDARD;     PRT;    1068 AA.
AC   P32871;
DT   01-OCT-1993 (Rel. 27, Created)
DT   01-OCT-1993 (Rel. 27, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit,
DE   alpha isoform (EC 2.7.1.153) (PI3-kinase p110 subunit alpha) (PtdIns-
DE   3-kinase p110) (PI3K).
GN   PIK3CA.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC   TISSUE=Brain;
RX   MEDLINE=92354059; PubMed=1322797;
RA   Hiles I.D., Otsu M., Volinia S., Fry M.J., Gout I., Dhand R.,
RA   Panayotou G., Ruiz-Larrea F., Thompson A., Totty N.F., Hsuan J.J.,
RA   Courtneidge S.A., Parker P.J., Waterfield M.D.;
RT   "Phosphatidylinositol 3-kinase: structure and expression of the 110
RT   kd catalytic subunit.";
RL   Cell 70:419-429(1992).
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DR   EMBL; AJ249413; CAB89851.1; -.
DR   EMBL; AJ249414; CAB89851.1; JOINED.
DR   EMBL; AJ249415; CAB89851.1; JOINED.
DR   EMBL; AJ249416; CAB89851.1; JOINED.
DR   EMBL; AJ249417; CAB89851.1; JOINED.
DR   EMBL; AJ249418; CAB89851.1; JOINED.
DR   EMBL; AJ249419; CAB89851.1; JOINED.
DR   EMBL; AJ249420; CAB89851.1; JOINED.
DR   EMBL; AJ249280; CAB89686.1; -.
DR   MGD; MGI:1353576; Pik3cg.
DR   InterPro; IPR000403; PI3_PI4_kinase.
DR   InterPro; IPR002420; PI3K_C2.
DR   InterPro; IPR001263; PI3K_ras_bind.
DR   InterPro; IPR000341; PI3Ka.
DR   Pfam; PF00454; PI3_PI4_kinase; 1.
DR   Pfam; PF00792; PI3K_C2; 1.
DR   Pfam; PF00794; PI3K_rbd; 1.
DR   Pfam; PF00613; PI3Ka; 1.
DR   SMART; SM00142; PI3K_C2; 1.
DR   SMART; SM00144; PI3K_rbd; 1.
DR   SMART; SM00145; PI3Ka; 1.
DR   SMART; SM00146; PI3Kc; 1.
DR   PROSITE; PS00915; PI3_4_KINASE_1; 1.
DR   PROSITE; PS00916; PI3_4_KINASE_2; 1.
DR   PROSITE; PS50290; PI3_4_KINASE_3; 1.
KW   Transferase; Kinase; Multigene family.
FT   DOMAIN     18     22      POLY-ARG.
FT   DOMAIN    828   1073      PI3K/PI4K.
SQ   SEQUENCE  1102 AA;  126361 MW;  B9E94CFDD0C21D57 CRC64;
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Query Match            95.1%;  Score 5506;  DB 1;  Length 1102;
Best Local Similarity  94.3%;  Pred. No. 0;
Matches 1039;  Conservative 31;  Mismatches 32;  Indels 0;  Gaps 0;

Qy      1 MELENYEQPVVLREDNRRRRRMKPRSTAASLSSMELIPIEFVLPTSQRNTKTPETALLH 60
            |||||||||||||||||||||||||||:|||:|||||||||||||||:||:|||||||||
Db      1 MELENYEQPVVLREDNLRRRRRMKPRSAAGSLSSMELIPIEFVLPTSQRISKTPETALLH 60

Qy     61 VAGHGNVEQMKAQVWLRALETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLD 120
            ||||||||||||||||||||||||:|||:||||||:||||||||||||:|||:||||||||
Db     61 VAGHGNVEQMKAQVWLRALETSVAAEFYHRLGPDQFLLLYQKKGQWYEIYDRYQVVQTLD 120

Qy    121 CLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRLNALIGYDVTDVSNVHDDELEFTRRRL 180
            ||:||||:||||||||||||||||||||||||:|||||||||||||||||||||||||||
Db    121 CLHYWKLMHKSPGQIHVVQRHVPSEETLAFQKQLTSLIGYDVTDISNVHDDELEFTRRRL 180

Qy    181 VTPRMAEVAGRDPKLYAMHPWVTSKPLPEYLLKKITNNCVPIVIHRSTTSQTIKVSADDT 240
            |||||||||||||||||||||||||||||||||||:|||||||||||||||||||||||||
Db    181 VTPRMAEVAGRDAKLYAMHPWVTSKPLPDYLSKKIANNCIFIVIHRGTTSQTIKVSADDT 240

Qy    241 PGTILQSFFTKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG 300
            ||||||||||||||||||||||||:||||||||||||||||||||||||||||||||||||
Db    241 PGTILQSFFTKMAKKKSLMNIPESQSQDFVLRVCGRDEYLVGETPLKNFQWVRQCLKNG 300

Qy    301 EEIHLVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK 360
            :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 DEIHLVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVVTVSLWDCDRK 360

Qy    361 FRVKIRGIDIPVLPRTADLTVPVEANIQYGGQVLCQRRTSPKPFTEVLMNVWLEFSIKI 420
            ||||||||||:|||||:||||||||:|||||||||||||||||||:|:|||||||||||||
Db    361 FRVKIRGIDIPVLPRNTDLTVPVEANIQHGGQVLCQRRTSPKPFAEEVLMNVWLEFGIKI 420

Qy    421 KDLPKGALLNLQIYCGKCAPALSGKTSAEMPSPESKGKAQLLYVNLLLIDHRFLLRHGEY 480
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CC   -!- FUNCTION: PHOSPHORYLATES PTDINS, PTDINS4P AND PTDINS(4,5)P2 WITH A
CC       PREFERENCE FOR PTDINS(4,5)P2.
CC   -!- CATALYTIC ACTIVITY: ATP + 1-phosphatidyl-1D-myo-inositol 4,5-
CC       bisphosphate = ADP + 1-phosphatidyl-1D-myo-inositol 3,4,5-
CC       trisphosphate.
CC   -!- SUBUNIT: HETERODIMER OF A P110 (CATALYTIC) AND A P85 (REGULATORY)
CC       SUBUNIT.
CC   -!- SIMILARITY: BELONGS TO THE PI3/PI4-KINASES FAMILY.
CC   -!- SIMILARITY: Contains 1 C2 domain.
CC   --------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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DR   EMBL; M93252; AAA30698.1; -.
DR   PIR; A43322; A43322.
DR   InterPro; IPR000008; C2.
DR   InterPro; IPR000403; PI3_PI4_kinase.
DR   InterPro; IPR002420; PI3K_C2.
DR   InterPro; IPR003113; PI3K_p85B.
DR   InterPro; IPR000341; PI3K_rbd.
DR   InterPro; IPR001263; PI3Ka.
DR   Pfam; PF00454; PI3_PI4_kinase; 1.
DR   Pfam; PF00792; PI3K_C2; 1.
DR   Pfam; PF02192; PI3K_p85B; 1.
DR   Pfam; PF00794; PI3K_rbd; 1.
DR   Pfam; PF00613; PI3Ka; 1.
DR   SMART; SM00239; C2; 1.
DR   SMART; SM00142; PI3K_C2; 1.
DR   SMART; SM00143; PI3K_p85B; 1.
DR   SMART; SM00144; PI3K_rbd; 1.
DR   SMART; SM00145; PI3Ka; 1.
DR   SMART; SM00146; PI3Kc; 1.
DR   PROSITE; PS50004; C2_DOMAIN_2; FALSE_NEG.
DR   PROSITE; PS00915; PI3_4_KINASE_1; 1.
DR   PROSITE; PS00916; PI3_4_KINASE_2; 1.
DR   PROSITE; PS50290; PI3_4_KINASE_3; 1.
KW   Transferase; Kinase; Multigene family.
FT   DOMAIN    319    428    C2 DOMAIN.
FT   DOMAIN    797   1068    PI3K/PI4K.
SQ   SEQUENCE 1068 AA; 124327 MW; C753DCC2F39FDDF0 CRC64;

Query Match        25.3%;    Score 1465.5; DB 1; Length 1068;
Best Local Similarity 33.5%;  Pred. No. 1.5e-89;
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Qy   23  MKPRSTAASLSSMELIP---IEFVLPTSQQRNTKTPETALLHVAGHGNVEQMKAQVWLRA   78
                        :::  ||| :|::||||
Db    1  MPPRPSSGELWGIHLMPPRRLIVECLLPNGMIVT------LECLREATLITIKHELFKEA   53

Qy   79  LETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTIDCLRYWKVLHRSPGQIHVV  138
Db   54  RKYPL----HQLLQDESSYIFVSVTQEAEREEFFDETRRLCDLRLFQPF-------LKVI  102

Qy  139  QRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRLVTPRMAEVAGRD------  192
Db  103  EPVGNREEKI-LNREIGFAIGMPVCEFDMVKDPEVQDFRRNILNVCKEAVDLRDLNSPHS  161

Qy  193  PKLYAVHPWVTSKP-LPEYLLKKITNNCVFIVI-----HRSTTSQTIKVSADDTPGTIL  245
Db  162  RAMYVYPNVESSPELPKHIYNKLDKGQIIVIWVIVSPNNDKQKYTLKINHDCVPEQVI  221

Qy  246  QSFFTKMAKKKSLMDIPES------QNERDFVLRVCGRDBYLVGETPIKNFQWVRQCLKN  299
Db  222  AEAIRK--KTRSMLLSSEQLKLCVLEYQGKYILKVCGCDEYFLEKYPLSQYKYIRSCIML  279

Qy  300  GEEIHLVLDTPDDPALDEVRKEEWPLVDDCTGVTGYHEQLT-----IHGKDHESVFTVSL  354
Db  280  GRMPNLML------MAKESLLYSQLPM--DCFTMPSYSRRISTATPYMNGE----TSTKSL  327

Qy  355  WDCDRKFRVK--------IRGIDIPVLPRTADLTVFEANIQGQVLCQRRTSPKPF  404
Db  328  WVINSALRIKILCATVVNVNIRDID-----------KIYYRTGIYHGGEPLCDNVNTQRVP  377

Qy  405  TEEVLMNVWLEFSIKIKDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYYV  464
Db  378  CSNPRWNEWLNYDIYIPDLPRAARLCLSI-C-----KEEHCPLAWG  425

Qy  465  NLLLIDHRFLRHGEYVLHMWQLSGKGEDGSFNADKLTSATNPDKENSMISILLDNYC  524
Db  426  NINLFDYTDTLVSGKVALNWMPVPHGLED-LLNPIGVT-GSNPNKE-TPCLELBFDWFS  481

Qy  525  HPIALPKHRPTPDFEGDRV-----------RAEMPNQLR----KQLEAIIATDPLN  565
Db  482  SVVKFPDMSVIEEHANWSVSREAGFSYSHAGLSNRLARDNELRENDKEQLRAICTRDPLS  541

Qy  566  PLTAEDKELLWHFRVESLKDPKAYPKLFSVKWGQQQBIVAKTYQLLAKREVWDQSALDVG  625
Db  542  EITEQEKDFLWSHRHYCVTIPEILPKLLLSVKNNSRDEVAQMYCL-----VKDWPPIKPE  596

Qy  626  LTMQLLDCNFSDENVRAIAVQKLES-LEDDDVLHYLLQLVQAVKFEPYHDSALARFLLKR  684
Db  597  QAMELLDCNYPDPMVRGFAVRCLEKYLTDDKLSQYLIQLVQVLKYEQYLDNLLVRFLLKK  656

Qy  685  GLRNKRIGHFLFWFLRSEIAQSRHYQQRPAVILEAYLRGCGTAMLHDFTQQVQVIDMLQK  744
Db  657  ALTNQRIGHFFFWHLKSEM-HNKTVSQRFGLLLESYCRACGMYLKH-LNRQVEAMEKLIN  714

Qy  745  VTIDIKSLSAEKYDVSSQVISQLKQKLENLQN--LNLPQSFRVPYDPGLKAGALVIEKC  801
Db  715  LT-DI--LKQEKKDETQKV--QMKFLVEQMRRPDFMDALQGFLSPLNPAHQLGNLRLEBC  769

Qy  802  KVMASKKKPlWLEFKCADPTALS-------NETIGIIFKGDDLRQDMLILQILRIMEGIW  855
Db  770  RIMSSAKRPLWLNWE--NPDIMSELLFQNNE---IIFKNGDDLRQDMTLIQIIRIMENIW  824

Qy  856  ETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTGA-FKDEVLSHWLKE  913
Db  825  QNQGLDLRMLPYGCLSIGDCVGLIEVVRNSHTIMQI-QCKGGLKGALQFNSHTLHQWLKD  883

Qy  914  KCPIEKFQAAVERFVYSCAGYCVATFVLGIGDHNDNIMISETGNLFHIDFGHILGNYK  973
Db  884  KNK-GEIYDAAIDLFTRSCAGYCVATFIIGIGDHNSNIMVKDDGQLFHIDFGHFLDHKK  942

Qy  974  SFLGINKERVPFVLTPDFLFVMGTSGKK--TSLHFQKFQDVCVKAYLALRHHTNLLILF  1031
Db  943  KKFGVKRERVPFVLTQDFLIVISKGAQECTKTREFERFQEMCYKAYLAIRQHANLFINLF  1002

Qy 1032  SMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGWTVQFNWFLHLV  1091
Db 1003  SMMLGSGMPELQSFDDIAYIRKTLALDKTEQEALEYFMKQMNDAHHGGWTTKMDWIFHTI  1062
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RESULT 5

P11A_HUMAN

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AC   P42336; Q99762;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit,
DE   alpha isoform (EC 2.7.1.153) (PI3-kinase p110 subunit alpha) (Ptdins-
DE   3-kinase p110) (PI3K).
GN   PIK3CA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95229146; PubMed=7713498;
RA   Volinia S., Hiles I., Ormondroyd E., Nizetic D., Antonacci R.,
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RA   Rocchi M., Waterfield M.;
RT   "Molecular cloning, cDNA sequence, and chromosomal localization of
RT   the human phosphatidylinositol 3-kinase p110 alpha (PIK3CA) gene.";
RL   Genomics 24:472-477(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=9196568; PubMed=9043658;
RA   Stirdivant S.M., Ahern J., Conroy R.R., Barnett S.F., Ledder L.M.,
RA   Oliff A., Heimbrook D.C.;
RT   "Cloning and mutagenesis of the p110 alpha subunit of human
RT   phosphoinositide 3'-hydroxykinase.";
RL   Bioorg. Med. Chem. 5:65-74(1997).
CC   -!- FUNCTION. PHOSPHORYLATES PTDINS, PTDINS4P AND PTDINS(4,5)P2 WITH A
CC       PREFERENCE FOR PTDINS(4,5)P2.
CC   -!- CATALYTIC ACTIVITY: ATP + 1-phosphatidyl-1D-myo-inositol 4,5-
CC       bisphosphate = ADP + 1-phosphatidyl-1D-myo-inositol 3,4,5-
CC       triphosphate.
CC   -!- SUBUNIT: HETERODIMER OF A P110 (CATALYTIC) AND A P85 (REGULATORY)
CC       SUBUNIT.
CC   -!- SIMILARITY: BELONGS TO THE PI3/PI4-KINASES FAMILY.
CC   -!- SIMILARITY: Contains 1 C2 domain.
CC   ------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ------------------------------------------------------------------
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DR   Genew; HGNC:8975; PIK3CA.
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DR   GO; GO:0007048; P:oncogenesis; TAS.
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DR   InterPro; IPR000403; PI3_PI4_kinase.
DR   InterPro; IPR002420; PI3K_C2.
DR   InterPro; IPR003113; PI3K_p85B.
DR   InterPro; IPR000341; PI3K_ras_bind.
DR   InterPro; IPR001263; PI3Ka.
DR   Pfam; PF00454; PI3_PI4_kinase; 1.
DR   Pfam; PF00792; PI3K_C2; 1.
DR   Pfam; PF02192; PI3K_p85B; 1.
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DR   SMART; SM00144; PI3K_rbd; 1.
DR   SMART; SM00145; PI3Ka; 1.
DR   SMART; SM00146; PI3Kc; 1.
KW   Transferase; Kinase; Multigene family.
FT   DOMAIN      319    428       C2 DOMAIN.
FT   DOMAIN      797   1068       PI3K/PI4K.
FT   CONFLICT     43     43       V -> I (IN REF. 2).
FT   CONFLICT    170    170       H -> N (IN REF. 2).
FT   CONFLICT    187    187       R -> K (IN REF. 2).
FT   CONFLICT    286    287       KM -> ML (IN REF. 2).
FT   CONFLICT    332    332       R -> S (IN REF. 2).
FT   CONFLICT    346    346       L -> V (IN REF. 2).
FT   CONFLICT    723    723       R -> K (IN REF. 2).
FT   CONFLICT    751    751       L -> F (IN REF. 2).
FT   CONFLICT    767    767       K -> E (IN REF. 2).
SQ   SEQUENCE  1068 AA;  124412 MW;  9E16BA7401A87B57 CRC64;
DR   PROSITE; PS50004; C2_DOMAIN_2; FALSE_NEG.
DR   PROSITE; PS00915; PI3_4_KINASE_1; 1.
DR   PROSITE; PS00916; PI3_4_KINASE_2; 1.
DR   PROSITE; PS50290; PI3_4_KINASE_3; 1.

Query Match             25.2%;  Score 1460.5;  DB 1;  Length 1068;
Best Local Similarity   33.3%;  Pred. No. 3.3e-89;
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Qy    23 MKPRSTAASLSMELIP----IEFVLFTSQRNTKTPETALLHVAGHGNVEQMKAQVWLRA 78
                                                         |:|
Db     1 MPPRPSSGELWGIHLMPPRILVECLLPNGMIVT------LECLREATLVTIKGHELFKEA 53

Qy    79 LETSVSADFYHRLGPDHFLLLYCKKGQWYEIYDKYQVYQTLDCLRYWKVLHRSPGQIHVV 138
                            |:|             |:|          |:|
Db    54 RKYPL-----HQLLQDESSYIFVSVTQEAEREEFFDETRRLCDLRLFQPF-----LKVI 102

Qy   139 QRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRLVTPRMAEVAGRD------ 192
                   |:|          |:|              |:|
Db   103 EPVGNREEKI-LNREIGFAIGMPVCEFDMVKDPEVQDFRRNILNVCKEAVDLRDLNSPHS 161

Qy   193 PKLYAMHPWTSKP-LPEYLLKKITNNCVFIVI--------HRSTTSQTIKVSADDTPGTIL 245
                  |:|         |:|            |:|
Db   162 RAMVYFPHVESSPELPKIHYNKLDRGQIIVIWIVSPNNDKQKYTLKINHDCVPEQVI 221

Qy   246 QSFFTKMAKKKSLMDIPES----------QNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKN 299
                  |:|                      |:|
Db   222 AEAIRK--KTRSWLLSSEQLKLCVLBYQGKYILKVCGCDEYPLEKYPLSQYYIRSCIML 279

Qy   300 GEEIHLVLDTPPPALDEVRKE---EWPLVDDCTGVTGYHQLT-----IHGKDHESVF 350
                        |:|                  |:|
Db   280 GRM-----------PNLKWMAKESLYSQLPM-DCFTMPSYSRRISTATPYMNGE----TS 323

Qy   351 TVSLWDCDRKFRVK-----------IRGIDIPVLPRTADLTVVEANIQYGQQVLCQRRTS 400
              |||          |:|              |:|
Db   324 TKSLWVINRALRIKILCATYVNLNIRDID--------KIVRTGIYHGGEPLCDNVNT 373

Qy   401 PKPFTEEVLMNVWLEFSIKIKDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQL 460
              |:|             |||                |:|
Db   374 QRVPCSNPRWNEWLNYDIYIPDLPRAARLCLSI-C------SVKGRKGA-------KEEHCP 421

Qy   461 LYYVNLLLIDHRFLLRHGEYVLHMWQLSGKGEDQGSFNADKLTSAATNPDKENSMSISILL 520
              |:|        |:|             |:|
Db   422 LAWGNINLFDYTDTLVSGKMALNLWPVPHGLED---LLNPIGVT-GSNPNKS-TPCLEBEF 477

Qy   521 DNYCHPIALPKHRPTPDPEGDRV-----------RAEMPNQLR---KQLEAIIAT 561
              |:|              |:|              |||
Db   478 DWFSSVVKFPDMSVIEEHANWSVSREAGFSYSHAGLSNRLARDNELRENDKEQLKAISTR 537

Qy   562 DPLNPLTABDKELLWHFRYESLKDPKAYPKLFSSVKNGQQEIVAKTYQLLAKREVWDQSA 621
              |||:||||||||  |||:||  |:|    |||||:|   |||  :|         |||
Db   538 DPLSEITEQEKDFIWSHRHYCVTIPEILPKLLLSVKWNSRDEVAQMYCL-----VKDWPP 592

Qy   622 LDVGLTMQLLDCNFSDENVRAIAVQKLES-LEDDDVLHYLLQLVQAVKFEPYHDSALARF 680
              |:| |||||||||  |:| ||||  |||   |:||  |||:|||  |||   |||:|
Db   593 IKPEQAMELLDCNYPDEMVRGFAVRCLEKYLTDDKLSQYLIQLVQVLKYEQYLDNLLVRF 652

Qy   681 LLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQPRAVILEAYLRGCGTAMLHDFTQQVQID 740
              |||:||  |||||| || |:|||    |||  |:|    |||||| :|        |:|
Db   653 LLKKALTNQRIGHFFFWHLKSEM-HNKTVSQRFGLLLSYCRACGMYLKGI-LNRQVEAME 710

Qy   741 MLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQN--LNLPQSFRVPYDPGLKAGALV 797
              |:|     |||      |:|         |:|      |:|
Db   711 KLINLT-DI--LKQERKDETQKV--QMKFLVEQMRRPDFMDALQGLLSPLNPAHQLGNLR 765

Qy   798 IEKCKVMASKKKPLWLEFKCADPTALS-----NETIGIIFKHGDDLRQDMLLIQILRIM 851
              |:|          |:|    |:|       :|||| |||:||||||||  ||:|||||||
Db   766 LKECRIMSSAKRPLWLNWE---NPDIMSELLFQNNE---IIFKNGDDLRQDMLTLQIIRIM 820

Qy   852 ESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTGA--FKDEVLSH 909
              |:| |||||:||||||| |:|| |||:|:|    |:|        |:|    |:|
Db   821 ENIKQNQGLDLRMLPYGCLSIGDCVGLIEVVRNSHTIMQI-QCKGGLKGALQPNSHTIHQ 879

Qy   910 WLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNLFHIDFGHIL 969
              |||:|   |:|    |:|||||||||||||| :||||||||:|||      :|||||||||:|
Db   880 WLKDKNK-GEIYDAAIDLFTRSCAGYCVATFLIGIGDRHNSNIMVKDDGQLFHIDFGHFL 938

Qy   970 GNYKSFLGINKERVPFVLTPDFLFVMGTSGKK--TSLHFQKFQDVCVKAYLALRHHTNLL 1027
              |||  |:||||||||||| |:||    |:|       |:|     |:|||||||:|
Db   939 DHKKKFKFGYKRERVPFVLTQDFLVISKGAQECTKTREFERFQEMCYKAYLAIRQHANLF 998
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Qy  1028  IILFSMLMTGMPQLTSKEDIEYIRDALTVGCKSEEDAKKYFLDQIEVCRDKGWTVQFNWF  1087
          |||||||  |||:| ||:.|||:|::||| | |: :|::|| |:  ||:|||||:|:
Db   999  INLFSWMLGSGMPELQSFDDIAYIRKTLALDKTEQEALEYFMKQMNDAHHGGWTTKMDWI  1058

Qy  1088  LHLV  1091
          |||:
Db  1059  FHTI  1062
```

RESULT 6
P11A_MOUSE

```
ID   P11A_MOUSE     STANDARD;     PRT;   1068 AA.
AC   P42337;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit,
DE   alpha isoform (EC 2.7.1.153) (PI3-kinase p110 subunit alpha) (PtdIns-
DE   3-kinase p110) (PI3K).
GN   PIK3CA.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RX   MEDLINE=94187738; PubMed=8139567;
RA   Klippel A., Escobedo J.A., Hirano M., Williams L.T.;
RT   "The interaction of small domains between the subunits of
RT   phosphatidylinositol 3-kinase determine enzyme activity.";
RL   Mol. Cell. Biol. 14:2675-2685(1994).
CC   -!- FUNCTION: PHOSPHORYLATES PTDINS, PTDINS4P AND PTDINS(4,5)P2 WITH A
CC       PREFERENCE FOR PTDINS(4,5)P2.
CC   -!- CATALYTIC ACTIVITY: ATP + 1-phosphatidyl-1D-myo-inositol 4,5-
CC       bisphosphate = ADP + 1-phosphatidyl-1D-myo-inositol 3,4,5-
CC       trisphosphate.
CC   -!- SUBUNIT: HETERODIMER OF A P110 (CATALYTIC) AND A P85 (REGULATORY)
CC       SUBUNIT.
CC   -!- SIMILARITY: BELONGS TO THE PI3/PI4-KINASES FAMILY.
CC   -!- SIMILARITY: Contains 1 C2 domain.
CC   -------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -------------------------------------------------------------
DR   EMBL; U03279; AAA18334.1; -.
DR   MGD; MGI:1206581; Pik3ca.
DR   InterPro; IPR0000008; C2.
DR   InterPro; IPR000403; PI3_PI4_kinase.
DR   InterPro; IPR002420; PI3K_C2_.
DR   InterPro; IPR003113; PI3K_p85B.
DR   InterPro; IPR000341; PI3K_ras_bind.
DR   InterPro; IPR001263; PI3Ka.
DR   Pfam; PF00454; PI3_PI4_kinase; 1.
DR   Pfam; PF00792; PI3K_C2; 1.
DR   Pfam; PF02192; PI3K_p85B; 1.
DR   Pfam; PF00794; PI3K_rbd; 1.
DR   Pfam; PF00613; PI3Ka; 1.
DR   SMART; SM00239; C2; 1.
DR   SMART; SM00142; PI3K_C2; 1.
DR   SMART; SM00143; PI3K_p85B; 1.
DR   SMART; SM00144; PI3K_rbd; 1.
DR   SMART; SM00145; PI3Ka; 1.
DR   SMART; SM00146; PI3Kc; 1.
DR   PROSITE; PS50004; C2_DOMAIN_2; FALSE_NEG.
DR   PROSITE; PS00915; PI3_4_KINASE_1; 1.
DR   PROSITE; PS00916; PI3_4_KINASE_2; 1.
DR   PROSITE; PS50290; PI3_4_KINASE_3; 1.
KW   Transferase; Kinase; Multigene family.
FT   DOMAIN      319    428     C2 DOMAIN.
FT   DOMAIN      797   1068     PI3K/PI4K.
SQ   SEQUENCE   1068 AA;  124453 MW;  67F54FCF8747FB1C CRC64;
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Query Match             25.1%;  Score 1450.5;  DB 1;  Length 1068;
Best Local Similarity   33.4%;  Pred. No. 1.5e-88;
Matches  381;  Conservative  204;  Mismatches  406;  Indels  149;  Gaps  39;

Qy   23  MKPRSTAASLSSMELIP----IEFVLPTSQRNTKTPETALLHVAGHGNVEQMKAQVWLRA   78
          |  ||| .|| |  ||      :.|| : ::|
Db    1  MPPRPSSGELWGIILMPPRILVECLLPNGMIVT-------LECLREATLVTIKHELFREA   53

Qy   79  LEISVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLDCLRYWKVLHRSPGQIHVV  138
          : ::.:   |   |        ::
Db   54  RKYPL------HQLLQDETSYIPVSVTQEAEREEFFDETRRLCLDRLFQPF-----LKVI  102

Qy  139  QRHAPSEETLAFQQLNALIGYDVTDVSNVHDDELEFTRRRLVTPRMAEVAGRD------  192
          :.  | .   |    | :|:| : ||     || |
Db  103  EPVGNREEKI-LNRBIGFVIGMPVCEFDMVKDPEVQDFRRNILNVCKEAVDLRDLNSPHS  161

Qy  193  PKLYAMHPWVTSKP-LPEYLLKKITNNCVFIVI------HRSTTSQTIKVSADDTPGTIL  245
          .:: : .|  . .| || |: |::||
Db  162  RAMVYYPENVESSPELPKHIYNKLDKGQIIVVIWVIVSPNNDKQKYTLKINHDCVPEQVI  221

Qy  246  QSFFTKVAKKKSLMDIPES---------QNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKN  299
          . .  |  | ||:|||      ||:.|| : |.:||| |  .: || .: .
Db  222  AEAIRK--KTRSMLLSSEQLKLCVLEYQGKYILKVCGCDEYFLEKYPLSQYKYIRSCIML  279

Qy  300  GEEIHIVLDTPPDALDEVRKEEWPLVDDCTGVTGYHEQLT----IHGKDHESVFTVSL  354
          |  :. :| .    | .        : |    :.|:  |       |    ::.|.:||
Db  280  GRMENLML------MAKESLYSQLPI-DSFTMPSYSRRISTATPYMNGB----TSTKSL  327

Qy  355  WDCDRKFRVK-------IRGIDIPVLPRTADLTVFVEANIQYGGQVLCQRRTSPKPF  404
          |  .| ::        | : :  ::      | | || .: | : |
Db  328  WVINSALRIKILCATYVNVNIRDID--------KIYVRTGIYHGGEPLCDNVNTQRVP  377

Qy  405  TEBVLWNVWLEFSIKIKDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYYV  464
          . . .||:|:::  || |||: |  ::|:   |  | .||.|           ::| .
Db  378  CSNPRWNEWINYDIYIPDLPRLARLCLSI-C----SVKGRKGA-------KEEHCPLAWG  425

Qy  465  NLLLIDHRFLLRHGEYVLHMWQLSGKGEDQGSFNADKLTSAINPDKENSMSISILLDNYC  524
          |: |.|  .|.. ||||||:|  .|:| |       ::|      ||: .    :  |
Db  426  NINLFDYTDTLVSGKMALNLWPVHGLED--LLNPIGVT-GSNPNKE-TPCLELEFDWFS  481

Qy  525  HPIALPKHRPTPDPEGDRV---------RAEMPNQLR---KQLEAIIATDPLN  565
          . : .     . . : .:          |    |::     |:|   .:||:|
Db  482  SVKFPDMSVIEEHANWSVSREAGFSYSHTGLSNRLARDNELRENDKEQLRALCTRDPLS  541

Qy  566  PLTABDKELLWHFRYESLKDPKAYPKLFSSVKWGQQEIVAKTYQLLAKREVWDQSALDVG  625
          . |  :|:.||.|| |  .  |  |:|: |||| .:|:| .:| :    ::. :
Db  542  EITEQEKDFLWSHRHYCVTIPEILPKLLLSVKWNSRDEVAQMYCL-----VKDWPPIKPE  596

Qy  626  LTMQLLDCNFSDENVRATAVQKLES-LEDDDVLHYLLQLVQAVKFEPYHDSALARFLLKR  684
          . :.|||||: | :||   ||: |: |.||: | |||:|||.||:|        | |||:
Db  597  QAMELLDCNYPDPMVRSFAVRCLEKYLTDDKLSQYLIQLVQVVKYEQVLDNLVRFLLKK  656

Qy  685  GLRNKRIGHPLFWFLRSEIAQSRHYQQRPAVILEAYLRGCGTAMLHDFTQQYQVIDMLQK  744
          .| |:|||||:||:|:.||  . :  | :|  ||:|   ||  ||:.  .:|  : |::
Db  657  ALTNQRIGHPFFWFILKSEM-HNKTVSQRFGLLLESYCRACGMYLKH-LNRQVBAMEKLIN  714

Qy  745  VTIDIKSLSAEKYDVSSQVISQLQKLENLQN---LNLPQSFRVPYDPGLKAGALVIEKC  801
          :| || .: |:   ..  |.:||:|:           :  |   |. .|:|| |:.:.
Db  715  LT-DI--LKQEKKDBTQKV--QMKFLVEQMRQPDFMDALQGFLSPLNPAHQLGNLRLEBC  769

Qy  802  KVMASKKKPLWLEPKCADPTALS------NETIGIIFKHGDDLRQDMLILQILRIMESIW  855
          :.::| :||||:      ::          | ||:||:|||||||||:.||::|||| ||
Db  770  RIMSSAKRPLWLNWE--NPDIMSELLFQNNE----IIFKNGDDLRQDMLTLQIIRIMENIW  824

Qy  856  ETESLDLCLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTGA--FKDEVLSHWLKE  913
          :.:.|||.:||||:| || :|:||:|:.:|||  | |  .  .     |:: :|.|||:
Db  825  QNQGLDLRMLPYGCLSIGDCVGLIEVVRNSHTIMQI-QCKGGLKGALQFNSHTIHQWLKD  883
```

```
KW   Transferase; Kinase; Multigene family.
FT   DOMAIN      800   1050       PI3K/PI4K.
SQ   SEQUENCE   1070 AA;  122607 MW;  4E8EB2333E96E4D5 CRC64;
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Query Match     Best Local Similarity   23.5%;   Score 1362;  DB 1;
                                         32.5%;   Pred. No. 1.2e-82;   Length 1070;
Matches  358;  Conservative  196;  Mismatches  397;  Indels  152;  Gaps  36;
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Qy    78  ALETSVSADFYHRLG------PDHFLLLYQKKGQWYEI--YDKYQVVQTLD-----CLR  123
Db    25  ASDGSISVDFLJPTGIYIQLEVPREATISYIKQMLWKQVHNYPMFNLLMDIDSYMFACVN   84

Qy   124  YWKVLHRSPGQ------IHVVQRHAPSEETLAFQRQLNALIGYDTDVSNVHD  170
Db    85  QTAVYELEDETRRLCDVRPFLPVLKLVTRSCDPAEKL--DSKIGVLIGKGLHEFDALKD  142

Qy   171  DEL-EFTR--RRLVTPRMAEVAGRDPKLYAMHPWVTSKPLPEY-----LLKKITNNCV  220
Db   143  PEVNEFRRKMRKFSEDKIQSLVG-----LSWIDWLKTYPPHEPSVLENLEDKLYGGKL  197

Qy   221  FIVIHRSTTSQ--TIKVSADDTPGTILQSFFTKMAKKKSLMDIPESQNERDFVLRVCGRD  278
Db   198  VVAVHFENSQDVFSFQVSPNLNPIKINE--LAIQKRLTIRGKEBEASPCDYLQVSGRV  254

Qy   279  EYLVGETPIKNFQWVRQCLKNGBEIHLVLDTPPDPALDEVRKEEWPlVDDCTGVTGYHEQ  338
Db   255  EYVFGDHPLIQFQYIRNCVMNRTLPHFIL-----------------VECCKIKMYEQ  295

Qy   339  --LTIHGKDHESVFTVSL-------------WDCDRKPR-VKIRGIDIPVLPRTADLTVF  382
Db   296  EMIAIEAAINRNSSLPLPLPPKKTRVISHVWGNNNPFQIVLVKG---NKLNTEETVKVH  352

Qy   383  VEANIQYGQQVLCQRRTSPK-PFTEEVLWNVWLEFSIKIDLPKGALLNLQIYCGKAPAL  441
Db   353  VRAGLFRGTELLCKTTVVSSEISGKNDHIWNEQLEFDINICDLPRMARLCFAVY-AVLDKV  411

Qy   442  SGKTSAEMPSP--ESKGKAQLLYY-----VNLLLIDHRFLLRHGEYVLHMWQLSGKGEDQ  494
Db   412  KTTKKSTKTINPSKYQTIRKAGKVHYPVAWVNTMVFDFKGQLRSGDVILHSW-------  462

Qy   495  GSFNADKL----------TSATNPDKENSMSISILL-DNYCHPIALP---------KHRPTPDP  538
Db   463  SSF-PDBLEEMLNPMGTVQTNYAENATALHIKPPENKKQPYYYPPFDKIIEKAABIASG  521

Qy   539  EGDRVRAEMPNQLRKQLBAIIATDPLNPLTAEDKELLMHFRYESLKD-PKAYPKLFSSVK  597
Db   522  DSANVSSRGGKKFLAVLKEILDRDPLSQLCENEMDLIWTLRQDCRENFPQSLPKLLLSIK  581

Qy   598  WGGQEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDVL  657
Db   582  WNKLEDVA--QLQALLQIWPK--LPPREALEILDFNYPDQYVREYAVGCLRQMSDEELS  636

Qy   658  HYLLQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVIL  717
Db   637  QYLLQLVQVLKYEPFLDCALSRFLLERALDNRRIGQFLFWHLRSEV-HTPAVSIQFGGVIL  695

Qy   718  EAYLRGCGTAMLHDFTQQVQVIDMLQKVT--IDIKSLSAEKYDVSSQVISQLKQK-----  770
Db   696  EAYCRG-SVGHMKVLSKQVEALNKLKTLNSLIKLNAMKLNRAKGKEAMHTCLKQSAYREA  754

Qy   771  LENLQNLNLPQSFRVPYDPGLKAGALVIEKCKVMASKKKKPLMLEFKCADPTALSNETIGI  830
Db   755  LSDLQS---------PLNPCVILSELYVEKCRYMDSRMKPLMLVY---SNRAFGEBDAVGV  802

Qy   831  IFKHGDDLRQDMLILQILRIMESIWETESLDLCLLPYGCISTGDKIGMEIVKDATTIAK  890
Db   803  IFKNGDLRQDMLTIQMLRLMDLIWKEAGLDLRMLPYGCLATGDRSGLIEVSTSETIAD  862

Qy   891  IQ--QSTVGNTGAFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRH  948
Db   863  IQLNSSNVAATAAFNKDALLNWLKEYNSGDD-LDRAIEEFTLSCAGYCVASYVLGIGDRH  921

Qy   949  NDNIMISETGNLFHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQK 1008
```

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Qy   914  KCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNLFHIDFGHILGNYK  973
Db   884  KNK-GEIYDAAIDLFTRSCAGYCVATFIGIGDRHNSNIMVKDDGQLFHIDFGHFLDHKK  942

Qy   974  SFLGINKERVPFVLTPDFLFVM--GTSGKKTSLHFQKFQDVVCVKAYLALRHTNLLIILF 1031
Db   943  KKFGYKRERVPFVLTQDFLIVISKGAQEVTKTREFERFQEMCVKAYLAIRQHANLFINLF 1002

Qy  1032  SMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGWTVQFNWFLHLV 1091
Db  1003  SMMLGSGMPELQSFDDIAYIRKTLALDKTEQEALEYFTKQMNDAHHGWTTKMDWIFHTI 1062
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RESULT 7

P11B_RAT

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ID   P11B_RAT     STANDARD;      PRT;   1070 AA.
AC   Q9ZL0;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit, beta
DE   isoform (EC 2.7.1.153) (PI3-kinase p110 subunit beta) (PtdIns-3-kinase
DE   p110) (PI3K) (PI3Kbeta).
GN   PIK3CB.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley;
RA   Mulder H., Stenson Holst L., Degerman E.;
RT   "Phosphatidylinositol-3 kinase and activation of phosphodiesterase 3B
RT   in adipocytes.";
RL   Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PHOSPHORYLATES PTDINS, PTDINS4P AND PTDINS(4,5)P2 WITH A
CC       PREFERENCE FOR PTDINS(4,5)P2 (BY SIMILARITY).
CC   -!- CATALYTIC ACTIVITY: ATP + 1-phosphatidyl-1D-myo-inositol 4,5-
CC       bisphosphate = ADP + 1-phosphatidyl-1D-myo-inositol 3,4,5-
CC       trisphosphate.
CC   -!- PATHWAY: SIGNALING PATHWAYS REGULATING CELL GROWTH.
CC   -!- SUBUNIT: HETERODIMER OF A P110 (CATALYTIC) AND A P85 (REGULATORY)
CC       SUBUNIT (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE PI3/PI4-KINASES FAMILY.
```

```
DR   EMBL; AJ012482; CAA10046.1; -.
DR   InterPro; IPR000403; PI3_PI4_kinase.
DR   InterPro; IPR002420; PI3K_C2.
DR   InterPro; IPR003113; PI3K_p85B.
DR   InterPro; IPR000341; PI3K_ras_bind.
DR   InterPro; IPR001263; PI3Ka.
DR   Pfam; PF00454; PI3_PI4_kinase; 1.
DR   Pfam; PF00792; PI3K_C2; 1.
DR   Pfam; PF02192; PI3K_p85B; 1.
DR   Pfam; PF00794; PI3K_rbd; 1.
DR   Pfam; PF00613; PI3Ka; 1.
DR   SMART; SM00142; PI3K_C2; 1.
DR   SMART; SM00143; PI3K_p85B; 1.
DR   SMART; SM00144; PI3K_rbd; 1.
DR   SMART; SM00145; PI3Ka; 1.
DR   SMART; SM00146; PI3Kc; 1.
DR   PROSITE; PS00915; PI3_4_KINASE_1; 1.
DR   PROSITE; PS00916; PI3_4_KINASE_2; 1.
DR   PROSITE; PS50290; PI3_4_KINASE_3; 1.
```

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Db    922  SDNIMVKKTGQLFHIDFGHIIGNFKSKFGIKRERVPFILYDFIHVIQQGKTGNTEKFGR  981
           :||||:. :||   ||||||||   ||  ||| ||  .|| |:||||:|.|.|  || :
Qy   1009  FQDVCVKAYIALRHHTNLLILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYF 1068
           :|||| : |:|| | |:|||:|  ||:|| |:| |:|||:||  ||.||||||::||:|
Db    982  FRQCCEDAYLILRRHGNLFITLFALMTAGLPELTSVKDIQYLKDSLALGKSEEEALKQF 1041

Qy   1069  LDQIEVCRDKGWTVQFNWFLHLV 1091
           ||:|| ||||||||||:|:|:||
Db   1042  KQKFDEALRESWTTKVNWMAHTV 1064


RESULT 8
P11B_HUMAN
ID   P11B_HUMAN     STANDARD;      PRT;   1070 AA.
AC   P42338;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit, beta
DE   isoform (EC 2.7.1.153) (PI3-kinase p110 subunit beta) (PtdIns-3-kinase
DE   p110) (PI3K) (PI3Kbeta).
GN   PIK3CB.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94067128; PubMed=8246984;
RA   Hu P., Mondino A., Skolnik E.Y., Schlessinger J.;
RT   "Cloning of a novel, ubiquitously expressed human
RT   phosphatidylinositol 3-kinase and identification of its binding site
RT   on p85.";
RL   Mol. Cell. Biol. 13:7677-7688(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Kossila M., Sinkovic M., Karkkainen P., Laukkanen P., Miettinen R.,
RA   Rissanen J., Kekalainen P., Kuusisto J., Yla-Herttuala S., Laakso M.;
RT   "Gene encoding the catalytic subunit p110beta of human
RT   phosphatidylinositol 3-kinase: cloning, genomic structure and
RT   screening for variants in patients with type 2 diabetes.";
RL   Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PHOSPHORYLATES PTDINS, PTDINS4P AND PTDINS(4,5)P2 WITH A
CC       PREFERENCE FOR PTDINS(4,5)P2.
CC   -!- CATALYTIC ACTIVITY: ATP + 1-phosphatidyl-1D-myo-inositol 4,5-
CC       bisphosphate = ADP + 1-phosphatidyl-1D-myo-inositol 3,4,5-
CC       trisphosphate.
CC   -!- PATHWAY: SIGNALING PATHWAYS REGULATING CELL GROWTH.
CC   -!- SUBUNIT: HETERODIMER OF A P110 (CATALYTIC) AND A P85 (REGULATORY)
CC       SUBUNIT.
CC   -!- TISSUE SPECIFICITY: Expressed ubiquitously.
CC   -!- SIMILARITY: BELONGS TO THE PI3/PI4-KINASES FAMILY.
```

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DR   EMBL; S67334; AAB29081.1; -.
DR   EMBL; AJ297549; CAC21449.1; -.
DR   EMBL; AJ297550; CAC21449.1; JOINED.
DR   EMBL; AJ297551; CAC21449.1; JOINED.
DR   EMBL; AJ297552; CAC21449.1; JOINED.
DR   EMBL; AJ297553; CAC21449.1; JOINED.
DR   EMBL; AJ297554; CAC21449.1; JOINED.
DR   EMBL; AJ297555; CAC21449.1; JOINED.
DR   EMBL; AJ297556; CAC21449.1; JOINED.
DR   EMBL; AJ297557; CAC21449.1; JOINED.
DR   EMBL; AJ297558; CAC21449.1; JOINED.
DR   EMBL; AJ297559; CAC21449.1; JOINED.
DR   EMBL; AJ297560; CAC21449.1; JOINED.
DR   PIR; A54600; A54600.
DR   Genew; HGNC:8976; PIK3CB.
DR   MIM; 602925; -.
DR   GO; GO:0004429; F:1-phosphatidylinositol 3-kinase; TAS.
DR   GO; GO:0000187; P:activation of MAPK; TAS.
DR   GO; GO:0006935; P:chemotaxis; TAS.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; TAS.
DR   GO; GO:0000074; P:regulation of cell cycle; TAS.
DR   InterPro; IPR000403; PI3_PI4_kinase.
DR   InterPro; IPR002420; PI3K_C2.
DR   InterPro; IPR003113; PI3K_p85B.
DR   InterPro; IPR000341; PI3K_ras_bind.
DR   InterPro; IPR001263; PI3Ka.
DR   Pfam; PF00454; PI3_PI4_kinase; 1.
DR   Pfam; PF00792; PI3K_C2; 1.
DR   Pfam; PF02192; PI3K_p85B; 1.
DR   Pfam; PF00794; PI3K_rbd; 1.
DR   Pfam; PF00613; PI3Ka; 1.
DR   SMART; SM00142; PI3K_C2; 1.
DR   SMART; SM00143; PI3K_p85B; 1.
DR   SMART; SM00144; PI3K_rbd; 1.
DR   SMART; SM00145; PI3Ka; 1.
DR   SMART; SM00146; PI3Kc; 1.
DR   PROSITE; PS00915; PI3_4_KINASE_1; 1.
DR   PROSITE; PS00916; PI3_4_KINASE_2; 1.
DR   PROSITE; PS50290; PI3_4_KINASE_3; 1.
KW   Transferase; Kinase; Multigene family.
FT   DOMAIN        800   1050       PI3K/PI4K.
SQ   SEQUENCE   1070 AA;  122762 MW;  81135FE93452C00E CRC64;


Query Match             23.4%;  Score 1354.5;  DB 1;  Length 1070;
Best Local Similarity   31.8%;  Pred. No. 3.8e-82;
Matches   361;  Conservative   202;  Mismatches   407;  Indels   165;  Gaps    37;

Qy     30  ASLSSMELIPIERVLPTSQRNTKTPETALLHVAGHGNVEQMKAQVWLRALETSVSADFYH   89
           :.::.:.|:|
Db     22  SQIASDGSIPVDFLLPTG------IYIQLEVPREATISYIKQMLWKQVHNYPM------   68

Qy     90  RLGPDHFLLLYQKKGQWYEIYDXYQVVQTLD------C----LRYWKVLHRS--PQGIH  136
           |:  |:.|  |  |:    :  ||    ||        |    |  |:|||:  ||:|
Db     69  ---FNLLMDIDSYMFACVNQTAVYELEDETRRLCDVRPFLPVLKLVTRSCDPGE--  120

Qy    137  VVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDEL-EFTR--RRLVTPRMAEVAGRD-  192
           :||  :::||:.:|  ||:.|  |:|  |  |::|:  |:    |::|    ||  :|
Db    121  ----------KLDSKIGVLIGKGLHFDSLKDPEVNEFRRKMRKFSEEKILSLVGLSW  168

Qy    193  -PKLYAMHPWVTSKPLPEYLLKKITNNCVFIVIHRSTTSQ--TIKVSADDTPGTILQSFF  249
           |:  |.|||:  |||:|:||:.||    .|.|  |::|:    |:||:||:||:|:|||:
Db    169  MDWLKQTYPPEHBPSIPENLEDKLYGGKLIVAVHFENCQDVFSFQVSPNMNPIKVNE---  225

Qy    250  TKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNGEBIHLVLDT  309
           |  |:.||    |  ::.  |||:.|||  ::|  ||:.|  |:|  |:||  :||:|:|
Db    226  LAIQKRLTIHGKEDEVSPYDYVLQVSGRVEYVYFGDHPLIQFQYIRNCVMNRALPHFIL--  283

Qy    310  PPDPALDEVRKEEWPLVDDCTGVTGYHEQ--LTIHGKDHESVFTVSL----------  354
           ||                      |  |     :..|  :      |
Db    284  ------------VECCKIKKMYEQEMIAEAAINRNSSNLPLPPKKTRIISHV  326

Qy    355  WDCDRKFR-VKIRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTSPK-PFTEBVLMNV  412
           |:  ::   |:|.|:
Db    327  WENNNPFQIVLVKG---NKLNTEETVKVHVRAGLFHGTELLCKTIVSSEVSGKNDHIWNE  383

Qy    413  WLPSIKIKDLPKGALLNLQIYCGKAPALSGKTSAEMPSP---ESKGKAQLLYY----VN  465
           | :|   |||  |  |:||:  |  .  |:  |:.   |      ::|  |  |
Db    384  PLEFDINICDLPRMARLCFAVY-AVLDKVKTKKSTKTINPSKYQTIRKAGKVHYPVAWVN  442

Qy    466  LLLIDHRPLLRHGEYVLHMWQLSGKGEDQGSFNADKL----TSATNPDXENSMSIS  517
           ||   :|        |      |
Db    443  TMVFDFKGQLRTGDIILHSW---------SSF-PDELEEMLNPMGIVQTNPYTENATALH  492

Qy    518  ILL-DNYCHPIALP------KHRPTPDPEGDRVRAEMPNQLRKQLEAIIATDPLNPLTA  569
```

```
Db  727 ARLRDCDLKSEEYRRISLLMEAYLRG-NEEHIKIITRQVDMVDELTRISTLVKGMPK---  782
Qy  758 DVSS----QVISQLKQKLENLQNLNLPQSFRVPYDPGLKAGALVIEBKCKVMASKKKPLWL  813
Db  783 DVATMKLRDELRSISHKMENMDS--------PLDPVYKLGEMIDKAIVLGSAKRPIML  833
Qy  814 EFKCADPTA-LSNETIGIIFKHGDLRQDMLIQILRIMESIWETESLDLCLLPYGCIST  872
Db  834 HWKNKNPKSDLHLPFCAMIFKNGDDLRQDMLVLQVLEVMDNIWKAANIDCCLNPYAVLPM  893

Qy  873 GDKIGMIEIVKDATTIAKIQQST-VGNTG--AFKDEVLSHWLKEKCPIBE---------  919
Db  894 GEMGIIEVVPNCKTIFBIQVGTGFMNTAVRSIDPSFMNKWIRKQCGIEDERKKSKKDST  953

Qy  920 --------------KFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNLFHID  964
Db  954 KNPIEKKIDNTQAMKKYFESVDRFLYSCVGYSVATYIMGIKDRHSDNLMLTEDGKYFHID 1013

Qy  965 FGHILGNYKSPLGINKERVPFVLTPDFLFVM--GTSGKKTSLHFQKFQDVCVKAYLALRH 1022
Db 1014 FGHILGHGKTKLGIQRDRQPFILTEHFMVIRSGKSVDGNSHELQKFKTLCVBAYEVMWN 1073

Qy 1023 HTNLLILFSMMLMTGMPQLTSKEDIEYIRDALTV-GKSEEDAKKYFLDQIEVCRDKGWT 1081
Db 1074 NRDLFVSLFTLMLGMELPLSTKADLDHLKKTLFCNGSSKEEARKFFAGIYEEAFNGSWS 1133

Qy 1082 VQFNWFLHJV 1091
Db 1134 TKTNWLFHAV 1143
```

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RESULT 15
PK3B_HUMAN
ID   PK3B_HUMAN    STANDARD;    PRT;    1634 AA.
AC   O00750; O95666;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Phosphatidylinositol-4-phosphate 3-kinase C2 domain-containing beta
DE   polypeptide (EC 2.7.1.154) (Phosphoinositide 3-Kinase-C2-beta)
DE   (Pdins-3-kinase C2 beta) (PI3K-C2beta) (C2-PI3K).
GN   PI3C2B.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC   TISSUE=Breast;
RX   MEDLINE=97289668; PubMed=9144573;
RA   Brown R.A., Ho L.K.F., Weber-Hall S.J., Shipley J.M., Fry M.J.;
RT   "Identification and cDNA cloning of a novel mammalian C2 domain-
RT   containing phosphoinositide 3-kinase, HsC2-PI3K.";
RL   Biochem. Biophys. Res. Commun. 233:537-544(1997).
RN   [2]
RP   SEQUENCE OF 26-1634 FROM N.A., AND CHARACTERIZATION.
RC   TISSUE=Monocytes;
RX   MEDLINE=99047700; PubMed=9830063;
RA   Arcaro A., Volinia S., Zvelebil M.J., Stein R., Watton S.J.,
RA   Layton M.J., Gout I., Ahmadi K., Downward J., Waterfield M.D.;
RT   "Human phosphoinositide 3-kinase C2beta, the role of calcium and the
RT   C2 domain in enzyme activity.";
RL   J. Biol. Chem. 273:33082-33090(1998).
CC   -!- FUNCTION: PHOSPHORYLATES PTDINS AND PTDINS4P WITH A PREFERENCE FOR
CC       PTDINS. DOES NOT PHOSPHORYLATE PTDINS(4,5)P2.
CC   -!- CATALYTIC ACTIVITY: ATP + 1-phosphatidyl-1D-myo-inositol 4-
CC       phosphate = ADP + 1-phosphatidyl-1D-myo-inositol 3,4-bisphosphate.
CC   -!- SUBCELLULAR LOCATION: FOUND MOSTLY IN THE MICROSOME, BUT ALSO IN
CC       THE PLASMA MEMBRANE AND CYTOSOL.
CC   -!- TISSUE SPECIFICITY: WIDELY EXPRESSED, BUT LEVELS ARE HIGHEST IN
CC       THYMUS AND PLACENTA AND LOWEST IN PERIPHERAL BLOOD, SKELETAL
CC       MUSCLE AND KIDNEY.
CC   -!- SIMILARITY: BELONGS TO THE PI3/PI4-KINASES FAMILY.
```

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DR   Pfam; PF00792; PI3K_C2; 1.
DR   Pfam; PF02192; PI3K_p85B; 1.
DR   Pfam; PF00794; PI3K_rbd; 1.
DR   Pfam; PF00613; PI3Ka; 1.
DR   SMART; SM00239; C2; 1.
DR   SMART; SM00142; PI3K_C2; 1.
DR   SMART; SM00143; PI3K_p85B; 1.
DR   SMART; SM00144; PI3K_rbd; 1.
DR   SMART; SM00145; PI3Ka; 1.
DR   SMART; SM00146; PI3Kc; 1.
DR   PROSITE; PS00915; PI3_4_KINASE_1; 1.
DR   PROSITE; PS00916; PI3_4_KINASE_2; 1.
DR   PROSITE; PS50290; PI3_4_KINASE_3; 1.
KW   Transferase; Kinase.
FT   DOMAIN      851   1127    PI3K/PI4K.
FT   VARIANT     826    826    S -> N (IN AGE1 (MG109)).
FT   CONFLICT   1010   1010    F -> V (IN REF. 1).
SQ   SEQUENCE   1146 AA;  132961 MW;  0D3628419407253A CRC64;

Query Match            18.0%;  Score 1041;  DB 1;  Length 1146;
Best Local Similarity  27.3%;  Pred. No. 3.1e-61;
Matches  314;  Conservative  227;  Mismatches  399;  Indels  210;  Gaps  44;

Qy   78 ALETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLDCLRYWKVLHRSPGQIHV  137
Db   68 SLEIKLS-DFKGHQL----FELIAPMKWGTYSVKPQDYVFRQLNNFGEISVIFNDDQPLSK  122

Qy  138 VQRHAPSEETLAFQ------------RQLNALIGYDVTDVSNVHDDEL-EF-------TRR  178
Db  123 LELHGTFPMLFLYQPDGINRDKELMSDISHCLGYSLDKLEESLDEELRQFRASLWARTKK  182

Qy  179 RLVT------------------PRMAEVAGRDPKLYAMHPWVTSKPLPEYLLKKI  215
Db  183 TCLTRGLEGTSHYAFPEEQYLCVGESCPKDLESKVKAAKLSYQMFWRKRK------AEI  235

Qy  216 TNNCVFIVIHRSTTSQTIKVSADDTPGTILQSFFTKMAKKKSLMDIPESQNERD--FVLR  273
Db  236 NGVC------EKMMKIQIEFNPNETPKSLLHTFLYEMRK----LDVYDTDDPADBGWFLQ  285

Qy  274 VCGRDEYLVG-ETPIKNFQWVRQCLKN----GEBIH--LVLD--TPPDPALDE--VRKE  321
Db  286 LAGRTTFVTNPDVKLTSYDGVRSELESYRCGPGVFVRRQSLVLKDYCRPKPLYEPHYVRAH  345

Qy  322 EWPLVDDCTGVTGYHEQLTIHGKDHESVFT----------VSLWDCDRKFRVK---IRGI  368
Db  346 ERKLALDVLGVS--IDSTPKQSKNSDMVMTDFRPTASLKQVSLWDLDANLMIRPVNISGF  403

Qy  369 DIPVLPRTADLTVFVEANIQYGQQVLCQRRTSPKPFTEBVLMNVWL-EFSIKIKDLPKGA  427
Db  404 DFPA--DVDMYVRIEFSVVYGTLTLASKSTT-KVNAQFAKWNKEMYTFDLYMKDMPFSA  459

Qy  428 LLNLQIYCGAPALSGKTSAEMPSPESKGKAQLLYVNLLLIDHRFLLRHGEVYLHWWQL  487
Db  460 VLSIRVLYGK--------VKLKSEFE----VGWVNMSLTDWRDELRQGQFLFHLW--  503

Qy  488 SGKGEDQGSFNADKLTSATNPDKEN------SMSISILLDNYCHPIALP---------KH  532
Db  504 --------APEPTANRSRIGENGARIGTNAAVTIEISSYGGRVRMPSQGQYTYLVKH  552

Qy  533 R----PTPDFEGDRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKE---LLWHFRYESLKD  585
Db  553 RSTWTFTLNIMGDDYESCIRDPGYKKLQMLVKKHSGIVLEEDEQRHVWMWR-RYIQKOE  611

Qy  586 PKAYPKLFS-SVKWGQQEIVAKTYQLLAKREVWDQSALDVGLIMQLLDCNFSDENVRAIA  644
Db  612 PDLLIVLSELAFVWDRENFSELYVMLEK--WKPPSVAAALT--LLGKRCTDRVIRKFA  666

Qy  645 VQKLBSLEDDDVLH-YLLQLVQAVKFEPYHDSALARFLLKRGLENKRIGHFLFWFLRSEI  703
Db  667 VEKLNEQLSPVTFHLFILFLPLIQALKYEPRAQSEVGMLLTRALCDYRIGHRLFWLLRAEI  726

Qy  704 AQSR-------HYQQRFAVILEAYLRGCGTAMLHDFTQQYQVIDMLQKVTIDIKSLSABKY  757
```

```
CC   -!- SIMILARITY: Contains 1 C2 domain.
CC   -!- SIMILARITY: Contains 1 phox homology (PX) domain.
CC   -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-26 IS THE INITIATOR.
CC
```

```
DR   EMBL; Y11112; CAA72168.1; -.
DR   EMBL; Y13892; CAA74194.1; -.
DR   PIR; JC5500; JC5500.
DR   HSSP; P21707; 1RSY.
DR   Genew; HGNC:8972; PIK3C2B.
DR   MIM; 602838; -.
DR   GO; GO:0005792; C:microsome; NAS.
DR   GO; GO:0005886; C:plasma membrane; NAS.
DR   GO; GO:0016305; F:phosphatidylinositol 3-kinase, class II act. . .; NAS.
DR   InterPro; IPR000008; C2.
DR   InterPro; IPR000403; PI3_PI4_kinase.
DR   InterPro; IPR002420; PI3K_C2.
DR   InterPro; IPR000341; PI3K_ras_bind.
DR   InterPro; IPR001263; PI3Ka.
DR   InterPro; IPR001683; PX.
DR   Pfam; PF00168; C2; 1.
DR   Pfam; PF00454; PI3_PI4_kinase; 1.
DR   Pfam; PF00792; PI3K_C2; 1.
DR   Pfam; PF00794; PI3K_rbd; 1.
DR   Pfam; PF00613; PI3Ka; 1.
DR   Pfam; PF00787; PX; 1.
DR   SMART; SM00239; C2; 1.
DR   SMART; SM00142; PI3K_C2; 1.
DR   SMART; SM00144; PI3K_rbd; 1.
DR   SMART; SM00145; PI3Ka; 1.
DR   SMART; SM00146; PI3Kc; 1.
DR   SMART; SM00312; PX; 1.
DR   PROSITE; PS00499; C2_DOMAIN_1; FALSE_NEG.
DR   PROSITE; PS50004; C2_DOMAIN_2; 1.
DR   PROSITE; PS00915; PI3_4_KINASE_1; 1.
DR   PROSITE; PS00916; PI3_4_KINASE_2; 1.
DR   PROSITE; PS50290; PI3_4_KINASE_3; 1.
DR   PROSITE; PS50195; PX; 1.
KW   Transferase; Kinase; Multigene family.
FT   DOMAIN     1365   1481    PX.
FT   DOMAIN      156    162    PRO-RICH.
FT   DOMAIN      169    174    PRO-RICH.
FT   DOMAIN     1079   1343    PI3K/PI4K.
FT   DOMAIN     1517   1608    C2 DOMAIN.
FT   CONFLICT     63     63    P -> S (IN REF. 2).
FT   CONFLICT     75     75    R -> W (IN REF. 2).
FT   CONFLICT     99     99    Q -> L (IN REF. 2).
FT   CONFLICT    246    246    V -> A (IN REF. 2).
FT   CONFLICT    278    278    K -> S (IN REF. 2).
FT   CONFLICT    567    567    P -> B (IN REF. 2).
FT   CONFLICT    664    665    DM -> EL (IN REF. 2).
SQ   SEQUENCE   1634 AA;  184856 MW;  COB5DF63C668B824 CRC64;
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Query Match             17.6%;  Score 1021;  DB 1;  Length 1634;
Best Local Similarity   28.0%;  Pred. No. 1.2e-59;
Matches   304;  Conservative 178;  Mismatches 391;  Indels 212;  Gaps  29;
```

```
Qy  159  GYDVTDVSNVHDDELEFTRRRLVTPRMAEVAGRDPKLYAM--HPWVTSKPLPBYLLKKIT  216
              |:::|:|||||      |::||  |   ..|...:|:|| ::||
Db  322  GHELFEVSEERDBEVAAFCHMLDILR----SGSDIQDYPFLTGYWSAVTPSPEHLGDEV-  376

Qy  217  NNCVFIVIHRSTTSQTIKVSADDTPGTILQSFFTKMAKKKSLMDIPESQNERDFVLRVCG  276
         |  ::        |        ::|:|.:.:| : |  |||||| :|
Db  377  NLKVTVLCDRLQEALTFTCNCSSTVDLLI--YQTLCYTHDDLRNV----DVGDFVLKPCG  430

Qy  277  RDEYLVGETPIKNFQWVRQCLK----------------------------------  298
```

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Db   431  LEEFLQNKHALGSHEYIQYCRKFDIDIRLQLMEQKVVRSDLARTVNDDQSPSTLNYLVHL  490
              :||:|.      ..:::.|
Qy   299  --------NGEEIHLVLDT---------------------------------------  309
Db   491  QERPVKQTISRQALSLLFDTYHNEVDAFLLADGDFPLKADRVVQSVKAICNALAAVETPE  550
Qy   310  ----------PP----DPALDEVRKEEWPLV------------------------DDCT  330
Db   551  ITSALNQLPPCPSRMQPKIQKDPSVLAVRENREKVVEALTAAILDLVELYCNTFNADFQT  610
Qy   331  GVTGYHEQLTIHGKDH--ESVFTVSLWDCDRKFRVKIRGIDIPVLPRTADLTVFVEANI  387
Db   611  AVPGSRKHDLVQBACHFARSLAFTV--YATHR--------IPIIWATSYEDFYLSCSL  658
Qy   388  QYGGQVLC-----QRRTSPKPFTEEVLMNVWLEFSIKIKDLPKGALLNLQIYC--GKAPA  440
Db   659  SHGGKDMCSFPLQTRRAHFSKYLFHLIVNDQQICFPVQVNRLPRETLLCATLYALPIPPPG  718
Qy   441  LSGKTSAEMPSPESKGKAQLLYVNLLLIDHRFLLRHGEYVLHMWQLSGKGEDQGSFNAD  500
Db   719  SSSEANKQRRVPEALG-------WVTTPLFNFRQVLTCGRKLLGLWPATQE-------NPS  765
Qy   501  KLTSATNPDKENSMSISILLDNVCHPIALPKHRPTPDPEGDRVR----AEMPNQLRKQL  555
Db   766  ARWSAPNFHQPDSVILQIDFPTSAFDIKF------TSPPGDKFSPRIEFGSLREEDQRKL  819
Qy   556  EAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQQEIVAKTYQLLAKRE  615
Db   820  KDIMQKESLYWLTDADKKRLWEKRYYCHSEVSSLPLVLASAPSWEWACLPDIYVLLKQ--  877
Qy   616  VW---DQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDVLHYLLQLVQAVKFEP  671
Db   878  -WTHMNHQDALG------ILHATFPDQEVRRMAVQWIGSLSDAELLDYIPQLVQALKYEC  930
Qy   672  YHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRPAVILEAYLRGCGTAMLHD  731
Db   931  YLDSPLVRFPLLKRAVSDLRVTHYFFWLLKDGLKDSQ-FSIRYQYLLAALLCCGKGLREE  989
Qy   732  FTQQVQVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENL-QNLNLPQSFRVPVYDPG  790
Db   990  FNRQCWLVNALAKLAQQVR----EAAPSARQGI--LRTGLBEEVKQFFALNGSCRLPLSPS  1043
Qy   791  LKAGALVIEBKCKVMASKKKPLWILEFKCADPTALSNETIGIIFKHGDDLRQDMLILQILRI  850
Db   1044 LLVKGIVPRDCSYFNSNAVPLKLLSFQNVDPL--GENIRVIFKCGDDLRQDMLTLQMIRI  1100
Qy   851  MESIWETESLDLCLLPYGCISTGDKIGMEIVKDATTIAKIQQSTVGNTGAFKDEVLSHW  910
Db   1101 MSKIWVQEGLDMRMVIFRCFSTGRGRGNVEMIPNAETLRKIQVEH-GVTGSFKDRPLADW  1159
Qy   911  LKEKCPIEBKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNLFHIDFGHILG  970
Db   1160 LQKNPGEDEYEKAVENFIYSCAGCCVATYVLGICDRHNDNIMLKTTGHMFHIDFGRFIG  1219
Qy   971  NYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCKAYLALRHTNLLIIL  1030
Db   1220 HAQMFGNIKEDRAPFVFTSDMAVVI-NGGDKPSPSSRFHDFVDLCCQAYNLIRKHTHLFLNL  1278
Qy   1031 FSMMLMTGMPQLTSKEDIBYIRDALTVGKSEEDAKKYFLDQIEVCRDKGWTVQPNWFLHL  1090
Db   1279 LGLMLSCGIPELSDLEDLKYVYDALRPQDTEANATTYFTRLIESSLGSVAT-KLNFFIHN  1337
Qy   1091 VLGIK  1095
Db   1338 LAQMK  1342
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OM protein - protein search, using sw model

                  Copyright   GenCore version 5.1.6
                        (c) 1993 - 2004 Compugen Ltd.

Run on: February 14, 2004, 17:24:00 ; Search time 77 seconds
                                       (without alignments)
                                       2271.645 Million cell updates/sec

Title: US-09-974-573-1
Perfect score: 5790
Sequence: 1 MELENYEQPVVLREDNRRRR.........QFNWFLHLVLGIKQGEKHSA 1102

Scoring table: BLOSUM62
              Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database : A_Geneseq_19Jun03:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                                SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5726	98.9	1102	19	AAW23948	Porcine phosphoino
2	5726	98.9	1102	20	AAW90083	Porcine G-protein
3	5726	98.9	1101	20	AAY76802	Pig p120 regulator
4	5523.5	95.4	1101	21	AAW90089	Human G-protein re
5	5523.5	95.4	1101	21	AAY76803	Human p110gamma is
6	5500.5	95.0	1101	19	AAU09689	Human p110gamma is
7	5500.5	95.0	1101	19	AAW23947	Human phosphoinosi
8	5222	90.2	1050	17	AAW11577	Human phosphatidyl
9	5093.5	88.0	1049	17	AAW11576	Human phosphatidyl
10	1467.5	25.3	1068	15	AAR46294	PtdIns 3-kinase 11
11	1465.5	25.3	1068	14	AAR43341	p110. Homo sapien
12	1460.5	25.2	1068	14	AAR43342	Human p110. Homo
13	1460.5	25.2	1068	23	AAU09687	Human p110alpha is
14	1354.5	23.4	1070	21	AAB11124	Human PI3 kinase p
15	1354.5	23.4	1070	23	ABP65170	Hypoxia-regulated
16	1354.5	23.3	1070	23	AAU09688	Human p110beta iso
17	1351.5	23.3	1044	19	AAW58570	Human phosphatidyl
18	1351.5	23.3	1044	20	AAW97390	p110-delta amino a
19	1351.5	23.3	1044	21	AAY50179	Human PI 3-kinase-
20	1349.5	23.3	1044	19	AAW46625	Mammalian novel cl
21	1349.5	23.3	1044	21	AAY88372	Phosphatidyl inosi
22	1349.5	23.3	1044	23	AAU09685	Human p110delta is
23	1283	22.2	1088	22	ABB60424	Drosophila melanog
24	1076.5	18.6	1726	21	AAW38756	Phosphatidyl inosi
25	1074	18.5	1686	19	AAW70991	Human class II PI3
26	1074	18.5	1686	24	ABJ19811	Androgen-independe
27	1034	17.9	1146	19	AAW47544	Caenorhabditis ele
28	1034	17.9	1157	21	AAB06072	Caenorhabditis ele
29	873.5	15.1	1876	22	ABB61970	Drosophila melanog
30	873.5	15.1	1876	18	ABB66876	Phosphatidyl inosi
31	866.5	15.0	1876	22	AAW38757	Novel human protei
32	856.5	14.8	1445	23	ABB97312	Novel human diagno
33	856.5	14.8	1450	22	ABG04173	Novel human diagno
34	856.5	14.8	1450	22	ABG07330	Human protein sequ
35	855	14.8	1462	22	AAM25582	Human PI3-kinase h
36	855	14.8	1475	22	ABB11449	Novel human diagno
37	767.5	13.3	311	22	ABG09801	Human polypeptide
38	709.5	12.3	887	22	AAM39431	Human polypeptide
39	709.5	12.3	901	22	AAM41217	Human NOVX polypep
40	705.5	12.2	887	24	ABU54626	Human NOVX polypep
41	705.5	12.2	913	24	ABU54625	Maize phosphatidy
42	690.5	11.9	803	20	AAW97880	Drosophila melanog
43	645	11.1	1157	22	ABB61471	Human NOVX polypep
44	550.5	9.5	818	24	ABU54627	Novel human diagno
45	478.5	8.3	1146	22	ABG14251	Novel human diagno

                                ALIGNMENTS

RESULT 1
AAW23948
ID   AAW23948 standard; Protein; 1102 AA.
XX
AC   AAW23948;
XX
DT   17-AUG-1998 (first entry)
XX
DE   Porcine phosphoinositide 3OH-kinase p120 subunit.
XX
DB
XX
KW   G-beta-gamma regulated phosphatidylinositol-3' kinase; pig;
KW   phosphoinositide 3OH-kinase; PI3K; signal transduction;
KW   phosphatidylinositol (3,4,5)-triphosphate; G-protein; receptor;
KW   transgenic animal; knockout animal; inflammation; arthritis;
KW   septic shock; adult respiratory distress syndrome; pneumonia;
KW   asthma; allergy; reperfusion injury; atherosclerosis; cancer;
KW   Alzheimer's disease; cancer; antisense; ribozyme; diagnosis;
KW   therapy; drug screening.
XX
OS   Sus scrofa.
XX
FH   Key   Location/Qualifiers
FT   Cleavage-site   40..41
FT   /note= "cryptic thrombin cleavage site"
FT   Domain   310..315
FT   /note= "WW domain, may be involved in interaction
FT   with p101 subunit"
FT   Domain   173..302
FT   /note= "weak pleckstrin homology domain, may be
FT   involved in membrane binding and/or
FT   G-beta.gamma subunit interaction of the
FT   p101/120 complex"

```
Qy  301  EEIHLVLDTPPPALDEVRKEEWPLVDDCTGVTGYHEQLTHGKDHESVFTVSLWDCDRK  360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301  EEIHLVLDTPPPALDEVRKEEWPLVDDCTGVTGYHEQLTHGKDHESVFTVSLWDCDRK  360

Qy  361  FRVKIRGIDIPVLPRTADLTVFVEANIQYGGQVLCQRRTSPKFTEVLWNVWLEFSIKI  420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361  FRVKIRGIDIPVLPRTADLTVFVEANIQYGGQVLCQRRTSPKFTEVLWNVWLEFSIKI  420

Qy  421  KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYYVNLLIDHRFLLRHGEY  480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421  KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYYVNLLIDHRFLLRHGEY  480

Qy  481  VLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKRPTDPPEG  540
              |||||||||||||||||||||||||   |||||  ||||||||||||||||| ||||  
Db  481  VLHMWQLSGKGEDQGSFNADKLTSGTNPDKEDSMSISILLDNYCHPIALPKHRPTDPEG  540

Qy  541  DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQ  600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541  DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQ  600

Qy  601  QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL  660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601  QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL  660

Qy  661  LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLPWFLRSEIAQSRHYQQRFAVILEAY  720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661  LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLPWFLRSEIAQSRHYQQRFAVILEAY  720

Qy  721  LRGCGTAMLHDFTQQVVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLP  780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721  LRGCGTAMLHDFTQQVVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLP  780

Qy  781  QSFRVPVDPGLKAGALVIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ  840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781  QSFRVPVDPGLKAGALVIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ  840

Qy  841  DMLILQIIRIMESIWETESLDICLLPYGCISTGDKIGMEIVKDATTIAKIQQSTVGNTG  900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841  DMLILQIIRIMESIWETESLDICLLPYGCISTGDKIGMEIVKDATTIAKIQQSTVGNTG  900

Qy  901  AFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL  960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901  AFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL  960

Qy  961  FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLAL 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961  FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLAL 1020

Qy 1021  RHHTNLLILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEBDAKKYFLDQIEVCRDKGW 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021  RHHTNLLILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEBDAKKYFLDQIEVCRDKGW 1080

Qy 1081  TVQFNWFLHLVLGIKQGEKHSA 1102
              |||||||||||||||||||| |
Db 1081  TVQFNWFLHLVLGIKQGEKHPA 1102
```

RESULT 2
AAW90083

```
XX
PN  WO9749818-A2.
XX
PD  31-DEC-1997.
XX
PF  26-JUN-1997; 97WO-US11219.
XX
PR  27-JUN-1996; 96US-0672211.
XX
PA  (ONYX-) ONYX PHARM.
XX
PI  Braselmann S, Hawkins PT, Stephens L;
XX
DR  WPI; 1998-077181/07.
DR  N-PSDB; AAV04634.
XX
PT  DNA encoding G-beta-gamma regulated phosphatidyl-inositol-3' kinase,
    p101 and p120 subunits - useful for diagnosis, drug screening,
    clinical trial monitoring and treatment of inflammatory disorders
XX
PS  Claim 54; Fig 4; 151pp; English.
XX
CC  This is the deduced amino acid sequence of the p120 catalytic
CC  subunit of pig G-protein regulated phosphatidylinositol-3' kinase
CC  (PI3K), a heterodimeric enzyme which produces the intracellular
CC  messenger phosphatidylinositol (3,4,5)-triphosphate in response to
CC  activation of trimeric G protein-linked receptors. This novel
CC  protein, which also contains a regulatory subunit, p101 (see
CC  AAW23946), is found in cells of haematopoietic origin and is involved
CC  in immune system responses which cause inflammation. p101 cDNA (see
CC  AAV04634) was obtained from a neutrophil cDNA library. The invention
CC  encompasses pig and human p101 and p120 nucleotides (see AAV04633-34),
CC  host cell expression systems, p101 and p120 proteins (see AAW23946-49),
CC  fusion proteins, polypeptides and peptides, antibodies to these
CC  proteins, and transgenic and knockout animals. Compounds which are
CC  useful for treating inflammatory response disorders can be
CC  identified by screening assays using a G protein activated PI3K, or
CC  a cultured host cell that expresses the p101 gene. Antagonists of
CC  G protein stimulated PI3K (acting through the p101 subunit,
CC  especially by disrupting the interaction between the p101 and p120
CC  subunits) can be used to treat arthritis, septic shock, adult
CC  respiratory distress syndrome (ARDS), pneumonia, asthma, allergies,
CC  reperfusion injury, atherosclerosis, cancer and Alzheimer's disease.
CC  The nucleic acids and their products can also be used for diagnosis,
CC  drug screening and clinical trial monitoring of inflammatory
CC  diseases.
XX
SQ  Sequence  1102 AA;

Query Match             98.9%;  Score 5726;  DB 19;  Length 1102;
Best Local Similarity   98.9%;  Pred. No. 0;
Matches  1090;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy   1  MELENYEQPVLREDNRRRRMKPRSTAASLSSMELIPIEFVLPTSQRNTKTPETALLH   60
             ||||||||||||||||| |||||||||||||||||||||||| ||||||||||||||
Db   1  MELENYEQPVLREDNRRRRRRMKPRSTAASLSSMELIPIEFVLATSQRNTKTPETALLH  60

Qy  61  VAGHGNVEQMKQAQYWLRALETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLD 120
             ||||||||:|||:||||||||||:   ::|  ||||||||::||||:|||||||||||||||
Db  61  VAGHGNVEKKKAQVLLRALETSVWDFYIRFGPDHFLLVFQKKGEWYEIYDKYQVVQTLD 120

Qy 121  CLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRL 180
             |||:|:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121  CLRWEVLHRSPGQIHVVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRL 180

Qy 181  VTPRMAEVAGRDPKLYAMHPWVTSKPLPEYLLKKITNNCVFIVHRSTTSQTIKVSADDT 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181  VTPRMAEVAGRDPKLYAMHPWVTSKPLPEYLLKKITNNCVFIVHRSTTSQTIKVSADDT 240

Qy 241  PGTILQSFFTKMAKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241  PGTILQSFFTKMAKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG 300

RESULT 2
AAW90083
ID  AAW90083 standard; Protein; 1102 AA.
XX
AC  AAW90083;
XX
DT  09-MAR-1999  (first entry)
XX
DE  Porcine G-protein regulated PI3K p120 adapter subunit protein.
XX
KW  Phosphoinositide 3-hydroxykinase; PI3K; trimeric G protein; porcine;
KW  adapter subunit; regulatory subunit; p101; p120; catalytic subunit;
KW  detection; diagnosis; activation disorder; haematopoietic system;
KW  treatment; immune disorder; inflammation; arthritis; septic shock;
KW  adult respiratory distress syndrome; pneumonia; asthma; allergy;
KW  reperfusion injury; atherosclerosis; Alzheimer's disease; cancer.
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Qy  421  KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYYVNLLLIDHRFLLRHGEY  480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421  KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYYVNLLLIDHRFLLRHGEY  480

Qy  481  VLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKHRPTPDPEG  540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481  VLHMWQLSGKGEDQGSFNADKLTSGTNPDKEDSMSISILLDNYCHPIALPKHRPTPDPEG  540

Qy  541  DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQ  600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541  DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQ  600

Qy  601  QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDVLHYL  660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601  QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDVLHYL  660

Qy  661  LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY  720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661  LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY  720

Qy  721  LRGCGTAMLHDFTQQVVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLP  780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721  LRGCGTAMLHDFTQQVVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLP  780

Qy  781  QSFRVPYDPGLKAGALVIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ  840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781  QSFRVPYDPGLKAGALVIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ  840

Qy  841  DMLILQLIRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG  900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841  DMLILQLIRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG  900

Qy  901  AFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL  960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901  AFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL  960

Qy  961  FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLAL  1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961  FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLAL  1020

Qy 1021  RHHTNLLILLFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW  1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021  RHHTNLLILLFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW  1080

Qy 1081  TVQFNWFLHLVLGIKQGEKHSA  1102
         ||||||||||||||||||||||
Db 1081  TVQFNWFLHLVLGIKQGEKHPA  1102
```

RESULT 3
AAY76802
ID   AAY76802 standard; Protein; 1102 AA.
XX
AC   AAY76802;
XX
DT   20-APR-2000 (first entry)
XX
DE   Pig p120 regulatory subunit proteinsequence.
XX
KW   p101 protein; p120 protein; regulatory subunit; immune system disorder;
KW   trimeric G-protein regulated PI3K; phosphoinositide 3OH-kinase; asthma;
KW   inflammatory response disorder; arthritis; septic shock; allergy;
KW   adult respiratory distress; cancer; reperfusion injury; atherosclerosis;
KW   Alzheimer's disease; haematopoietic lineage cell activation disorder;
KW   therapy; pig.
XX
OS   Sus sp.
XX
PN   US6017763-A.
XX
PD   25-JAN-2000.
XX
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XX
OS   Sus scrofa.
XX
PN   US5856132-A.
XX
PD   05-JAN-1999.
XX
PF   15-AUG-1997;    97US-0916917.
XX
PR   15-AUG-1997;    97US-0916917.
PR   27-JUN-1996;    96US-0672211.
XX
PA   (ONYX-) ONYX PHARM.
XX
PI   Braselmann S, Hawkins PT, Stephens L;
XX
DR   WPI; 1999-105107/09.
DR   N-PSDB; AAV74100.
XX
PT   Nucleic acid encoding regulatory (p101) and catalytic (p120)
PT   subunits of a heterodimeric phosphatidylinositol-3' kinase - useful
PT   in treatment and diagnosis of immune system disorders, e.g.
PT   arthritis, cancer and Alzheimer's disease
XX
PS   Example IX; Fig 4; 75pp; English.
XX
CC   This sequence represents a novel catalytic subunit, p120, from porcine
CC   phosphoinositide 3-hydroxykinase (PI3K) which is regulated by beta-gamma
CC   subunits of trimeric G-protein. Nucleic acid coding for p101 or p120, or
CC   their fragments, are used as probes and primers for identifying p101 or
CC   p120 gene mutations, allelic variations or regulatory defects,
CC   particularly for the diagnosis of activation disorders (or
CC   susceptibility) in cells of the haematopoietic system. The related
CC   proteins, antibodies, agonists and antagonists can be used similarly. The
CC   p101 and p120 proteins, peptides or fusion proteins are used to treat or
CC   screen for potential agents for treating immune disorders, particularly
CC   inflammation, e.g. arthritis, septic shock, adult respiratory distress
CC   syndrome, pneumonia, asthma, allergies, reperfusion injury,
CC   atherosclerosis, Alzheimer's disease and cancer.
XX
SQ   Sequence 1102 AA;

Query Match         98.9%;    Score 5726;    DB 20;    Length 1102;
Best Local Similarity   98.9%;    Pred. No. 0;
Matches 1090;    Conservative   6;    Mismatches    6;    Indels    0;    Gaps    0;
```

```
Qy    1  MELENYEQPVLREDNRRRRMKPRSTAASLSMELIPIEFVLPTSQRNTKTPETALLH  60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  MELENYEQPVLREDNRRRRMKPRSTAASLSMELIPIEFVLATSQRNTKTPETALLH  60

Qy   61  VAGHGNVEQMKAQVWLRALETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLD  120
         ||||||||| |||||||||||||||||||||||||||||:|:||||||||||||||||||
Db   61  VAGHGNVERMKAQVLLRALETSVSWDPYHRFGPDHFLLVFQKKGEWYEIYDKYQVVQTLD  120

Qy  121  CLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRL  180
         |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  CLRYWEVLHRSPGQIHVVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRL  180

Qy  181  VTPRMAEVAGRDPKLYAMIPWVTSKPLPEYLLKKITNNCVFIVIHRSTTSQTIKVSADDT  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  VTPRMAEVAGRDPKLYAMIPWVTSKPLPEYLLKKITNNCVFIVIHRSTTSQTIKVSADDT  240

Qy  241  PGTILQSFFTKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  PGTILQSFFTKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG  300

Qy  301  EEIHLVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK  360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301  EEIHLVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK  360

Qy  361  FRVKIRGIDIPVLPRTADJLTVFVEANIQYGQQVLCQRRTSPKPFTEEVLMNVWLEFSIKI  420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361  FRVKIRGIDIPVLPRTADJLTVFVEANIQYGQQVLCQRRTSPKPFTEEVLMNVWLEFSIKI  420
```

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PF         04-JAN-1999; 99US-0225170.
XX
PR         15-AUG-1997; 97US-0916917.
PR         27-JUN-1996; 96US-0672211.
XX
PA    (ONYX-) ONYX PHARM INC.
PA    (BABR-) BABRAHAM INST.
XX
PI    Braselmann S, Stephens L, Hawkins PT;
XX
DR    WPI; 2000-136682/12.
DR    N-PSDB; AAZ86813.
XX
PT    Isolated p101 regulatory polypeptide, a subunit of the trimeric
PT    G-protein regulated PI3K, is useful for screening compounds which can
PT    be used to treat inflammatory response disorders -
XX
PS    Example; Fig 4; 75pp; English.
XX
CC    This sequence represents the pig p120 regulatory protein.
CC    The invention relates to the human p101 regulatory protein,
CC    which is a subunit of the trimeric G-protein regulated phosphoinositide
CC    3OH-kinase (PI3K). The p101 regulatory protein can be used in screening
CC    assays to detect compounds which can be used to treat inflammatory
CC    response disorders. The compounds identified may be antagonists or
CC    agonists of G protein-regulated PI3K gene expression and/or p101 or p120
CC    gene product activity. These compounds may then be used to control immune
CC    system disorders, in particular arthritis, septic shock, adult
CC    respiratory distress, asthma, allergies, repefusion injury,
CC    atherosclerosis, Alzheimer's disease and cancer. p101 proteins and
CC    peptides can be used in the detection of mutant or inappropriately
CC    expressed p101 regulatory subunits for the diagnosis of immune disorders
CC    and haematopoietic lineage cell activation disorders which will also
CC    assist in devising a proper treatment or therapeutic regime. Using
CC    genetically engineered host cells to screen for compounds also allows
CC    compounds which affect the signal transduced by the activated p101
CC    regulatory subunit to be identified.
XX
SQ    Sequence 1102 AA;

Query Match             98.9%;  Score 5726;  DB 21;  Length 1102;
Best Local Similarity   98.9%;  Pred. No. 0;
Matches 1090; Conservative    6; Mismatches    6; Indels    0;  Gaps    0;

Qy         1 MELENYEQPVLREDNRRRRRMKPRSTAASLSMELIPIEFVLPTSQRNTKTPETALLH 60
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 MELENYEQPVLREDNRRRRRMKPRSTAASLSMELIPIEFVLATSQRNTKTPETALLH 60

Qy        61 VAGHGNVEQMKAQVWLRALETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLD 120
             |||||||||||||||||||||||||||||||||||||:|||||||||||||||||||||
Db        61 VAGHGNVEKMKAQVLLRALETSVSWDFYHRFGPDHFLLVFQKKGEWYEIYDKYQVVQTLD 120

Qy       121 CLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRL 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 CLRYWEVLRRSPGQIHVVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRL 180

Qy       181 VTPRMAEVAGRDPKLYAMHPWVTSKPLPEYLLKKITNNCVFIVIHRSTTSQTIKVSADDT 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 VTPRMAEVAGRDPKLYAMIPWVTSKPLPEYLLKKITNNCVFIVIHRSTTSQTIKVSADDT 240

Qy       241 PGTILQSFFTKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 PGTILQSFFTKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG 300

Qy       301 EEIHLVLDTPPDPALDEVRKEEWPIVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 EEIHLVLDTPPDPALDEVRKEEWPIVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK 360

Qy       361 FRVKIRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTSPKPTEEVLWNVWLEFSIKI 420
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 FRVKIRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTSPKPFTEEVLMNVWLEFSIKI 420

Qy       421 KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYVNLLIDHRFLLRHGEY 480
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Db       421 KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYVNLLIDHRFLLRHGEY 480
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy       481 VLHMWQLSGKGBEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKHRPTPDPEG 540
             |||||||||||||||||||||||||||||| ::||||||||||||||||||| |||||||
Db       481 VLHMWQLSGKGBEDQGSFNADKLTSGTNPDKEDSMSISILLDNYCHPIALPKGRPTPDPEG 540

Qy       541 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQ 600
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQ 600

Qy       601 QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 660

Qy       661 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY 720
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY 720

Qy       721 LRGCGTAMLHDFTQQVVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQRLENLQNLNLP 780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721 LRGCGTAMLHDFTQQVVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQRLENLQNLNLP 780

Qy       781 QSFRVPYDPGLKAGALVIEKCKVMASKKKPIWLEFKCADPTALSNETIGIIFKHGDDLRQ 840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781 QSFRVPYDPGLKAGALVIEKCKVMASKKKPIWLEFKCADPTALSNETIGIIFKHGDDLRQ 840

Qy       841 DMLILQLRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 DMLILQLRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG 900

Qy       901 AFKDEVLSHWLKEKCPIEEKFQAAVERFVVSCAGYCVATFVLGIGDRHNDNIMISETGNL 960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       901 AFKDEVLSHWLKEKCPIEEKFQAAVERFVVSCAGYCVATFVLGIGDRHNDNIMISETGNL 960

Qy       961 FHIDFGHILGNYKSFLGINKRVPFVLTPDFLFVMGTSGKKTSLHFQDCVKAYLAL 1020
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       961 FHIDFGHILGNYKSFLGINKRVPFVLTPDFLFVMGTSGKKTSLHFQKFQDCVCKAYLAL 1020

Qy      1021 RHHTNLLIILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 RHHTNLLIILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSSEDAKKYFLDQIEVCRDKGW 1080

Qy      1081 TVQFNWFLHLVLGIKQGEKHSA 1102
             ||||||||||||||||||||||
Db      1081 TVQFNWFLHLVLGIKQGEKHPA 1102
```

```
RESULT 4
AAW90089
ID   AAW90089 standard; Protein; 1101 AA.
XX
AC   AAW90089;
XX
DT   09-MAR-1999   (first entry)
XX
DE   Human G-protein regulated PI3K p120 adapter subunit protein.
XX
KW   Phosphoinositide 3-hydroxykinase; PI3K; trimeric G protein; human;
KW   adapter subunit; regulatory subunit; p101; p120; catalytic subunit;
KW   detection; diagnosis; activation disorder; haematopoietic system;
KW   treatment; immune disorder; inflammation; arthritis; septic shock;
KW   adult respiratory distress syndrome; pneumonia; asthma; allergy;
KW   reperfusion injury; atherosclerosis; Alzheimer's disease; cancer.
XX
OS   Homo sapiens.
XX
PN   US5856132-A.
XX
PD   05-JAN-1999.
XX
PF   15-AUG-1997; 97US-0916917.
XX
```

```
Qy  541 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYSLKDPKAYPKLFSSVKWGQ 600
            |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db  540 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYSLKHPKAYPKLFSSVKWGQ 599

Qy  601 QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 660
            |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db  600 QEIVAKTYQLLARREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 659

Qy  661 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  660 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY 719

Qy  721 LRGCGTAMLHDFTQQVQVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLP 780
            ||||||||||||||||||| |||||| ||||||||||||||||||||||||||||||   ||
Db  720 LRGCGTAMLHDFTQQVQVIEMLQKVTLDIKSLSAEKYDVSSQVISQLKQKLENLQNSQLP 779

Qy  781 QSFRVPYDPGLKAGALVIEKCKVMASKKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ 840
            :||||||||||||||| |||||||||||| ||||||||||||||||||||||||||||||||
Db  780 ESFRVPYDPGLKAGALAIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ 839

Qy  841 DMLILQIRIMESIWETESLDLCLLPYGCISTGDKIGMEIVKDATTIAKIQQSTVGNTG 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  840 DMLILQIRIMESIWETESLDLCLLPYGCISTGDKIGMEIVKDATTIAKIQQSTVGNTG 899

Qy  901 AFKDEVLSHWLKEKCPIEKFQAAVERPVYSCAGYCVATFVLGIGDRHNDNIMISETGNL 960
            |||||| ||||||| | ||||||||||| ||||||||||||||||||||||||| |||||
Db  900 AFKDEVLNHWLKEKSPTEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMITETGNL 959

Qy  961 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLAL 1020
            ||||||||||||||||||||||||||||||||||||||||||||| ||||||| |||||||
Db  960 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSPHFQKFQDICVKAYLAL 1019

Qy 1021 RHHTNLILILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSBEDAKKYFLDQIEVCRDKGW 1080
            |||||||||||||||||||||||||||||||||||||||::|||||||||||||||||||
Db 1020 RHHTNLILILFSMMLMTGMPQLTSKEDIEYIRDALTVGKNEEDAKKYFLDQIEVCRDKGW 1079

Qy 1081 TVQFNWFLHLVLGIKQGEKHSA 1102
            |||||||||||||||||||||||
Db 1080 TVQFNWFLHLVLGIKQGEKHSA 1101
```

PT   Nucleic acid encoding regulatory (p101) and catalytic (p120)
PT   subunits of a heterodimeric phosphatidylinositol-3' kinase - useful
PT   in treatment and diagnosis of immune system disorders, e.g.
PT   arthritis, cancer and Alzheimer's disease
XX
PS   Claim 15; Fig 13; 75pp; English.
XX
CC   This sequence represents a novel catalytic subunit, p120, from human
CC   phosphoinositide 3-hydroxykinase (PI3K) which is regulated by beta-gamma
CC   subunits of trimeric G-protein. Nucleic acid coding for p101 or p120, or
CC   their fragments, are used as probes and primers for identifying p101 or
CC   p120 gene mutations, allelic variations or regulatory defects,
CC   particularly for the diagnosis of activation disorders (or
CC   susceptibility) in cells of the haematopoietic system. The related
CC   proteins, antibodies, agonists and antagonists can be used similarly. The
CC   p101 and p120 proteins, peptides or fusion proteins are used to treat or
CC   screen for potential agents for treating immune disorders, particularly
CC   inflammation, e.g. arthritis, septic shock, adult respiratory distress
CC   syndrome, pneumonia, asthma, allergies, reperfusion injury,
CC   atherosclerosis, Alzheimer's disease and cancer.
XX
SQ   Sequence 1101 AA;

```
Query Match             95.4%;  Score 5523.5;  DB 20;  Length 1101;
Best Local Similarity   95.2%;  Pred. No. 0;
Matches  1049;  Conservative   21;  Mismatches   31;  Indels    1;  Gaps    1;

Qy    1 MELENYEQPVLREDNRRRRRRMKPRSTAASLSSMELIPIEBFVLPTSQRNTKTPETALLH 60
            ||||| |||||||||| ||||||||:  |||||||||||||||:|||||||| ::|||||||
Db    1 MELENYKQPVLREDNCRRRRRMKPRS-AASLSSMELIPIEFVLPTSQRKCKSPETALLH 59

Qy   61 VAGHGNVEQMKAQVWLRALETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLD 120
            ||||||||||||||||||||||||:|||||||||:||||||||||:|||||||||||||||
Db   60 VAGHGNVEQMKAQVWLRALETSVAADFYHRLGPHHFLLLYQKKGQWYEIYDKYQVVQTLD 119

Qy  121 CLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRL 180
            ||||| |||||||||| ||||||:|| :|||||:| |||||||:||||||||||||||:||
Db  120 CLRYWKATHRSPGQIHLVQRHPPSEESQFQRQLTALIGYDVTVSNVHDDELEFTRRGL 179

Qy  181 VTPRMAEVAGRDPKLYAMHPWVTSKPLPEYLLKKITNNCVFIVIHRSTTSQIKVSADDT 240
            |||||||||:||||||||||||||||||||| |||| ||| |||||||||||||||:|||
Db  180 VTPRMAEVASRDPKLYAMHPWVTSKPLPEYLWKKIANNCIFIVIHRSTTSQIKVSPDDT 239

Qy  241 PGTILQSFFTKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG 300
            ||:||||||||||||||||||||||: |:||||||||||||||||||||||||||:||||||
Db  240 PGAILQSFFTKMAKKKSLMDIPESQSEQDFVLRVCGRDEYLVGETPIKNFQWVRHCLKNG 299

Qy  301 EEIHVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK 360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  300 EEIHVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK 359

Qy  361 FRVKIRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTSPKPFTEEVLWNVWLEFSIKI 420
            ||||||||||||||| :|||||||||||:||||||||||||||||||||||||||||||||
Db  360 FRVKIRGIDIPVLPRNTDLTVFVEANIQHGQQVLCQRRTSPKPFTEEVLWNVWLEFSIKI 419

Qy  421 KDLPKGALNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYYVNLLLIDHRFLLRHGEY 480
            |||||||||||||||||||||:| :|| || ::|:||:|| |:|||||||||||||||:|||
Db  420 KDLPKGALNLQIYCGKAPALSSKASAESPSSESKGKVRLLYYVNLLLIDHRFLLRRGEY 479

Qy  481 VLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKHRPTPDPEG 540
            |||||||:||||||||||||||||||||||||||||||||||||||||||||:|| |||||
Db  480 VLHMWQISGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKHQPTPDPEG 539
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Db  540 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKHPKAYPKLFSSVKWGQ 599

Qy  601 QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 660
        |||||||||||||||:|||||||||||||||||||||||||||||||||||||||||||
Db  600 QEIVAKTYQLLARREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 659

Qy  661 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY 720
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  660 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY 719

Qy  721 LRCGGTAMLHDFTQQVVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLP 780
        |||||||||||||||:|||||||:|||||||||||||||||||||||||||||||||:|
Db  720 LRGGGTAMLHDFTQQVVEMLQKVTLDIKSLSAEKYDVSSQVISQLKQKLENLQNSQLP 779

Qy  781 QSFRVPYDPGLKAGALVIEKCKVMASKKKPLMLEFKCADPTALSNETIGIIFKHGGDLRQ 840
        ::|||||||||||||||:||||||||||||||||||||||||||||||||||||||||:
Db  780 ESFRVPYDPGLKAGALAIEKCKVMASKKKPLMLEFKCADPTALSNETIGIIFKHGGDLRQ 839

Qy  841 DMLILQILRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG 900
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  840 DMLILQILRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG 899

Qy  901 AFKDEVLSHWLKEKCPIEBKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL 960
        |||||||||||||:|||||||||||||||||||||||||||||||||||||||:||||
Db  900 AFKDEVLNHWLKEKSPTEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMITETGNL 959

Qy  961 FHIDFGHIIGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLAL 1020
        ||||||||||||||||||||||||||||||||||||||||||||:||:||||||||||
Db  960 FHIDFGHIIGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSPHFQKFQDICVKAYLAL 1019

Qy  1021 RHHTNLLILLFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW 1080
         |||||||||||||||||||||||||||||||||||||||:||||||||||||||||||
Db  1020 RHHTNLLILLFSMMLMTGMPQLTSKEDIEYIRDALTVGKNEEDAKKYFLDQIEVCRDKGW 1079

Qy  1081 TVQFNWFLHLVLGIKQGEKHSA 1102
         ||||||||||||||||||||||
Db  1080 TVQFNWFLHLVLGIKQGEKHSA 1101
```

RESULT 6
AAU09689
ID   AAU09689   standard; Protein; 1101 AA.
XX
AC   AAU09689;
XX
DT   12-MAR-2002 (first entry)
XX
DE   Human p110gamma isoform of PI3-kinase.
XX
KW   Human; phosphatidylinositol 3-kinase; PI3K; p110gamma isoform;
KW   LASP-1; cancer; inflammatory disease; ophthalmic disorder; SH3 domain;
KW   autoimmune disease; inflammatory bowel disease; bacterial pneumonia;
KW   Type I diabetes mellitus; cytostatic; immunosuppressive.
XX
OS   Homo sapiens.
XX
PN   WO200185986-A2.
XX
PD   15-NOV-2001.
XX
PF   10-MAY-2001; 2001WO-US15065.
XX
PR   10-MAY-2000; 2000US-203346P.
XX
PA   (ICOS-) ICOS CORP.
XX
PI   Sadhu C;
XX
DR   WPI; 2002-075252/10.
DR   N-PSDB; AAS14367.
XX
PT   Identifying a modulator of p110delta polypeptide binding to SH3
PT   domain-containing polypeptides e.g. LASP-1, comprising allowing the

---

XX
DR   WPI; 2000-136682/12.
DR   N-PSDB; AAZ86814.
XX
PT   Isolated p101 regulatory polypeptide, a subunit of the trimeric
PT   G-protein regulated PI3K, is useful for screening compounds which can
PT   be used to treat inflammatory response disorders -
XX
PS   Disclosure; Fig 13; 75pp; English.
XX
CC   This sequence represents the human p120 regulatory protein.
CC   The invention relates to the human p101 regulatory protein,
CC   which is a subunit of the trimeric G-protein regulated phosphoinositide
CC   3OH-kinase (PI3K). The p101 regulatory protein can be used in screening
CC   assays to detect compounds which can be used to treat inflammatory
CC   response disorders. The compounds identified may be antagonists or
CC   agonists of G protein-regulated PI3K gene expression and/or p101 or p120
CC   gene product activity. These compounds may then be used to control immune
CC   system disorders, in particular arthritis, septic shock, adult
CC   respiratory distress, asthma, allergies, reperfusion injury,
CC   atherosclerosis, Alzheimer's disease and cancer. p101 proteins and
CC   peptides can be used in the detection of mutant or inappropriately
CC   expressed p101 regulatory subunits for the diagnosis of immune disorders
CC   and haematopoietic lineage cell activation disorders which will also
CC   assist in devising a proper treatment or therapeutic regime. Using
CC   genetically engineered host cells to screen for compounds also allows
CC   compounds which affect the signal transduced by the activated p101
CC   regulatory subunit to be identified.
XX
SQ   Sequence 1101 AA;

Query Match   95.4%;   Score 5523.5;   DB 21;   Length 1101;
Best Local Similarity 95.2%;   Pred. No. 0;
Matches 1049;   Conservative 21;   Mismatches 31;   Indels 1;   Gaps 1;

```
Qy    1 MELENYEQPVLREDNRRRRRRMKPRSTAASLSSMELIPIEFVLPTSQRNTKTPETALLH 60
        ||||||:|||||||||:|||||||||:|||||||||||||||||||||||:|||||||||
Db    1 MELENYKQPVLREDNCRRRRRMKPRS-AASLSSMELIPIEFVLPTSQRKCKSPETALLH 59

Qy   61 VAGHGNVEQMKAQVWLRALETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLD 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   60 VAGHGNVEQMKAQVWLRALETSVAADFYHRLGPHHFLLLYQKKGQWYEIYDKYQVVQTLD 119

Qy  121 CLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRQLNALIGYDVTVSNVHDDELEFTRRRL 180
        |||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||
Db  120 CLRYWKATHRSPGGQIHLVQRHPPSSESQAFQRQLTALIGYDVTVSNVHDDELEFTRRGL 179

Qy  181 VTPRMAEVAGRDPKLYAMHPWVTSKPLPEYLLKKITNNCVFIVIHRSTTSQTIKVSADDT 240
        ||||||||:||||||||||||||||||||||||||:|||||||||||||||||||||:||
Db  180 VTPRMAEVASRDPKLYAMHPWVTSKPLPEYLWKKIANNCIFIVIHRSTTSQTIKVSPDDT 239

Qy  241 PGTILQSFFTKMAKKKSLMDIPESQNBRDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG 300
        ||:|||||||||||||||||||||||:|||||||||||||||||||||||||||:|||||
Db  240 PGAILQSFFTKMAKKKSLMDIPESQSEQDFVLRVCGRDEYLVGETPIKNFQWVRHCLKNG 299

Qy  301 EEIHLVLDTPPDPALDEVRKSEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK 360
        ||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  300 EEIHVVLDTPPDPALDEVRKSEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK 359

Qy  361 FRVKIRGIDIPVLPRTADLTVFVEANIQYGGQVLCQRRTSPKPFTEEVLWNVWLEFSIKI 420
        ||||||||||||||||:|||||||||||||||||||||||||||||||||:|||||||||
Db  360 FRVKIRGIDIPVLPRNTDLTVFVEANIQHGGQVLCQRRTSPKPFTEEVLWNVWLEFSIKI 419

Qy  421 KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYYVNLLLIDHRFLLRHGEY 480
        ||||||||||||||||||||||||||||||:|||||:||||||||||||||||||||||:
Db  420 KDLPKGALLNLQIYCGKAPALSSKASAAESPSSESKGKVRLLYYVNLLLIDHRFLLRRGEY 479

Qy  481 VLHMWQLSGKGEDQQSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKHRPTPDPEG 540
        ||||||:|||||||||||||||||||||||||||||:||||||||||||||||||||||||
Db  480 VLHMWQISGKGEDQQSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKHQPTPDPEG 539

Qy  541 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQ 600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

PT   binding partners to interact in the presence and absence of a test
PT   compound -
XX
PS   Example 1; Page 77-80; 85pp; English.
XX
CC   The present invention relates to identifying a modulator of the
CC   phosphatidylinositol 3-kinase (PI3K; p110delta) enzyme that binds to
CC   the catalytic subunit via a SH3 domain-containing polypeptide such as
CC   LASP-1. Also described are methods of assaying the specific binding
CC   affinity of the PI-kinase binding partner. Such modulators are useful
CC   for the treatment of diseases characterised by the undesirable or
CC   excessive activity of PI3kdelta. For example the modulators can be used
CC   for inhibiting the growth or proliferation of cancer cells
CC   (e.g. malignant neoplasms of lymphoid and reticuloendothelial tissues,
CC   Hodgkin's lymphoma, leukaemias), inflammatory diseases (e.g. rheumatoid
CC   arthritis), ophthalmic disorders (e.g. allergic conjunctivitis)
CC   autoimmune diseases (e.g. systematic lupus erythematosus), inflammatory
CC   bowel diseases (e.g. chronic inflammatory bowel disease), inflammatory
CC   dermatoses (e.g. contact dermatitis; central or peripheral nervous
CC   system inflammatory disorders (e.g. meningitis), bacterial pneumonia,
CC   and Type I diabetes mellitus. The present sequence represents human
CC   pl1ogamma isoform of PI3k.
XX
SQ   Sequence 1101 AA;

```
Query Match             95.4%;  Score 5523.5;  DB 23;  Length 1101;
Best Local Similarity   95.2%;  Pred. No. 0;
Matches 1049;  Conservative   21;  Mismatches   31;  Indels   1;  Gaps   1;

Qy      1 MELENYEQPVLREDNRRRRMKPRSTAASLSMELIPIEFVLPTSQRNTKPETALLH 60
          ||||||||||||||||||||||||| ||||||||||||||||| :|||||||||||
Db      1 MELENYKQPVLREDNCRRRRRMKPRS-AASLSSMELIPIEFVLPTSQRKCKSPETALLH 59

Qy     61 VAGHGNVEQMKAQVWLRALETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLD 120
          |||||||||||||||||||||||||||||||| :||||||||||||||||||||||||||
Db     60 VAGHGNVEOMKAQVWLRALETSVAADFYHRLGPHHFLLLYQKKGQWYEIYDKYQVVQTLD 119

Qy    121 CLRYWKVLHRSPGCQIHVVQRHAPEEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRL 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    120 CLRYWKATHRSPGCQIHLVQRHPPSEESQAFQRQLTALIGYDVTDVSNVHDDELEFTRRGL 179

Qy    181 VTPRMAEVAGRDPKLYAMHPWVTSKPLPBYLKKITNNCVFIVIHRSTTSQTIKVSADDT 240
          |||||||||||||||||||||||||||||||||:||||||||||||||||||||:|||||
Db    180 VTPRMAEVASRDPKLYAMHPWVTSKPLPBYLKKIANNCIFIVIHRSTTSQTIKVSPDDT 239

Qy    241 PGTILQSFFTKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG 300
          ||||||||||||||||||||||||||||||||:|||||||||||||||||||||:|||||
Db    240 PGAILQSFFTKMAKKKSLMDIPESQSEQFVLRVCGRDYLVGETPIKNFQWVRHCLKNG 299

Qy    301 EEIHLVLDTPDDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    300 EEIHVVLDTPDDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK 359

Qy    361 FRVKIRGIDIPVLPRTADLITVFVEANIQYGGQVLCQRRTSPKFPTEEVLMNVWLEFSIKI 420
          |||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||
Db    360 FRVKIRGIDIPVLPRNTDLTVFVEANICHGGQQVLCQRRTSPKFFTEEVLMNVWLEFSIKI 419

Qy    421 KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYYVNLLLIDHRFLLRHGEY 480
          |||||||||||||||||||||||| || ||||||| |||||||||||||||||||||||
Db    420 KDLPKGALLNLQIYCGKAPALSSKASAAESPSSESKGKVRLLYYVNLLLIDHRFLLRRGEY 479

Qy    481 VLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKRPTDPDPEG 540
          |||||:||||||||||||||||||||||||||||||||||||||||||:||||||||||||
Db    480 VLHMWQISGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKHQPTPDPEG 539

Qy    541 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQ 600
          |||||||||||||||||||||||||||||||||||||:||||||||:|||||||||||||
Db    540 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKHPKAYPKLFSSVKWGQ 599

Qy    601 QEIVAKTYQLLAKREVWDQSALDVGLIMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 660
          ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db    600 QEIVAKTYQLLARREVWDQSALDVGLIMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 659
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Qy    661 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    660 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY 719

Qy    721 LRGGCGTAMLHDFTQQVQVIDMLQKVTIDIKSLSAEKYDVSSQVISQKQKLENLQNLP 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||:|||||
Db    720 LRGCGTAMLHDFTQQVQVIEMLQKVTLDIKSLSAEKYDVSSQVISQKQKLENLQNSQLP 779

Qy    781 QSFRVPYDPGLKAGALVIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    780 BSFRVPYDPGLKAGALAIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ 839

Qy    841 DMLILQILRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG 900
          |||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||||
Db    840 DMLILQILRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG 899

Qy    901 AFKDEVLSHWLKEKCPIEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL 960
          |||||||| :|| :||||||||||| |||||||||||||||||||||||||:|| :|||||
Db    900 AFKDEVLNHWLKEKSPTEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMITETGNL 959

Qy    961 FHIDFGHILGNYKSFLGINKERVPFVLTPDELFVMGTSGKKTSLHFQKFQDVCVKAYLAL 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    960 FHIDFGHILGNYKSFLGINKERVPFVLTPDELFVMGTSGKKTSPHFQKFQDICVKAYLAL 1019

Qy   1021 RHHTNLLIILFSMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1020 RHHTNLLIILFSMLMTGMPQLTSKEDIEYIRDALTVGKNEEDAKKYFLDQIEVCRDKGW 1079

Qy   1081 TVQFNWFLHLVLGIKQGEKHSA 1102
          |||||||||||||||||||||||
Db   1080 TVQFNWFLHLVLGIKQGEKHSA 1101
```

```
RESULT 7
AAW23947
ID   AAW23947 standard; Protein; 1101 AA.
XX
AC   AAW23947;
XX
DT   17-AUG-1998  (first entry)
XX
DE   Human phosphoinositide 3OH-kinase p120 subunit.
XX
KW   G-beta-gamma regulated phosphatidylinositol-3' kinase; pig;
KW   phosphoinositide 3OH-kinase; PI3K; signal transduction;
KW   phosphatidylinositol (3,4,5)-triphosphate; G-protein; receptor;
KW   transgenic animal; knockout animal; inflammation; arthritis;
KW   septic shock; adult respiratory distress syndrome; pneumonia;
KW   asthma; allergy; reperfusion injury; atherosclerosis; cancer;
KW   Alzheimer's disease; cancer; antisense; ribozyme; diagnosis;
KW   therapy; drug screening.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Cleavage-site   40..41
FT                   /note= "cryptic thrombin cleavage site"
FT   Domain          310..315
FT                   /note= "WW domain, may be involved in interaction
FT                   with p101 subunit"
FT   Domain          173..302
FT                   /note= "weak pleckstrin homology domain, may be
FT                   involved in membrane binding and/or
FT                   G-beta,gamma subunit interaction of the
FT                   p101/120 complex"
XX
PN   WO9749818-A2.
XX
PD   31-DEC-1997.
XX
PF   26-JUN-1997;  97WO-US11219.
XX
PR   27-JUN-1996;  96US-0672211.
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XX
PA   (ONYX-) ONYX PHARM.
XX
PI   Braselmann S, Hawkins PT, Stephens L;
XX
DR   WPI; 1998-077181/07.
XX
PT   DNA encoding G-beta-gamma regulated phosphatidyl-inositol-3' kinase,
PT   p101 and p120 subunits - useful for diagnosis, drug screening,
PT   clinical trial monitoring and treatment of inflammatory disorders
XX
PS   Claim 55; Fig 11; 151pp; English.
XX
CC   This is the deduced amino acid sequence of the p120 catalytic
CC   subunit of human G-protein regulated phosphatidylinositol-3' kinase
CC   (PI3K), a heterodimeric enzyme which produces the intracellular
CC   messenger phosphatidylinositol (3,4,5)-triphosphate in response to
CC   activation of trimeric G protein-linked receptors.  This novel
CC   protein, which also contains a regulatory subunit, p101 (see
CC   AAW23949), is found in cells of haematopoietic origin and is involved
CC   in immune system responses which cause inflammation.  Human p120
CC   cDNA was obtained from a leukocyte cDNA library.  The invention
CC   encompasses pig and human p101 and p120 nucleotides (see AAV04633-34),
CC   host cell expression systems, p101 and p120 proteins (see AAW23946-49),
CC   fusion proteins, polypeptides and peptides, antibodies to these
CC   proteins, and transgenic and knockout animals.  Compounds which are
CC   useful for treating inflammatory response disorders can be
CC   identified by screening assays using a G protein activated PI3K, or
CC   a cultured host cell that expresses the p101 gene.  Antagonists of
CC   G protein stimulated PI3K (acting through the p101 subunit,
CC   especially by disrupting the interaction between the p101 and p120
CC   subunits) can be used to treat arthritis, septic shock, adult
CC   respiratory distress syndrome (ARDS), pneumonia, asthma, allergies,
CC   reperfusion injury, atherosclerosis, cancer and Alzheimer's disease.
CC   The nucleic acids and their products can also be used for diagnosis,
CC   drug screening and clinical trial monitoring of inflammatory
CC   diseases.
XX
SQ   Sequence   1101 AA;

Query Match      95.0%;  Score 5500.5;  DB 19;  Length 1101;
Best Local Similarity  94.7%;  Pred. No. 0;
Matches 1044;  Conservative  23;  Mismatches  34;  Indels  1;  Gaps  1;

Qy    1 MELENYEQPVVLREDNRRRRRMKPRSTRAASLSSMELIPIEFVLPTSQRNTKIPETALLH 60
Db    1 MELENYKQPVVLREDNCRRRRRMKPRS-AASLSSMELIPIEFVLPTSQRKCKSPETALLH 59

Qy   61 VAGHGNVEQMKAQVWLRALETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLD 120
Db   60 VAGHGNVEQMKAQVWLRALETSVAADFYHRLGPHHFLLLYQKKGQWYEIYDKYQVVQTLD 119

Qy  121 CLRYWKVLHRSPGQIHVVQRHAPSEBTLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRL 180
Db  120 CLRYWKATHRSPGQIHLVQRHPPSEESQAFQRQLTALIGYDVTDVSNVHDDELEFTRRGL 179

Qy  181 VTPRMAEVAGRDPKLYAMHPWVTSKPLPEYLLKKITNNCVFIVIHRSTTSQTIKVSADDT 240
Db  180 VTPRMAEVASRDPKLYAMHPWVTSKPLPEYIWKKIANNCIFIVIHRSTTSQTIKVSPDDT 239

Qy  241 PGTILQSFFTKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG 300
Db  240 PGAIIQSFFTKMAKKKSLMDIPESQSEQDFVLRVCGRDEYLVGETPIKNFQWVRHCLKNG 299

Qy  301 EEIHLVLDTPPDPALDEVRKEEWPLVDDCTGVTGVHEQLTIHGKDHESVFTVSLWDCDRK 360
Db  300 EEIHVVLDTPPDPALDEVRKEEWPLVDDCTGVTGVHEQLTIHGKDHESVFTVSLWDCDRK 359

Qy  361 FRVKIRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTSPKPFTEEVLMNVWLEFSIKI 420
Db  360 FRVKIRGIDIPVLPRNTDLTVFVEANIQHGQQVLCQRRTSPKPFTBEVLMNVWLEFSIKI 419

Qy  421 KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYVNLLIDHRFLRHGEY 480
Db  420 KDLPKGALLNLQIYCGKAPALSSKASAEBPSSESKGKVRLLYVNLLIDHRFLLRRGEY 479

Qy  481 VLHMWQLSGKGEDQGSFNADKLITSATNPDKENSMSISILLDNYCHPIALPKJRPTPDPEG 540
Db  480 VLHMWQISGKGEDQGSFNADKLITSATNPDKENSMSISILLDNYCHPIALPKHQPTPDPEG 539

Qy  541 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQ 600
Db  540 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKHPKAYPKLFSSVKWGQ 599

Qy  601 QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 660
Db  600 QEIVAKTYQLLARREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 659

Qy  661 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY 720
Db  660 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY 719

Qy  721 LRGCGTAMLHDFTQQVQVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLP 780
Db  720 LRGCGTAMLHDFTQQVQVIEMLQKVTLDIKSLSAEKYDVSSQVISQLKQKLENLQNSQLP 779

Qy  781 QSFVPYDPGLKAGALVIEKCKVMASKKPLWLEFPKCADPTALSNETIGIIFKHGDDLRQ 840
Db  780 ESFVPYDPGLKAGALAIEKCKVMASKKKPLWLEFPKCADPTALSNETIGIIFKHGDDLRQ 839

Qy  841 DMLLQLRIMBSIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG 900
Db  840 DMLLQLRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG 899

Qy  901 AFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL 960
Db  900 AFKDEVLNHWLKEKSPTEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMITETGNL 959

Qy  961 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYIAL 1020
Db  960 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSPHFQKFQDICVKAYIAL 1019

Qy 1021 RHHTNLLILLFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW 1080
Db 1020 RHHTNLLLIFSMMILMTGMPQLTSKEDIEYIRDALTVGKNEEDAKKYFLDQIEVCRDKGW 1079

Qy 1081 TVQFNWFLHLVLGIKQGEKHSA 1102
Db 1080 TVQFNWFLHLVLGIKQGEKHSA 1101
```

RESULT 8
AAW11577

```
ID   AAW11577 standard; Protein; 1050 AA.
XX
AC   AAW11577;
XX
DT   25-MAR-1997  (first entry)
XX
DE   Human phosphatidylinositol 3-kinase PI3K-gamma.
XX
KW   Phosphatidylinositol 3-kinase; gamma; PI3K; immunogen; immunoassay;
KW   cell proliferation; receptor-mediated signal transmission;
KW   histamine secretion; nerve cell differentiation; glucose transport;
KW   modulation; regulation; Alzheimer's disease; lipolysis.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         742..756
FT                   /label= immunogen
FT                   /note= "antibodies are pref. raised against this
FT                   peptide; location given as 742-746 in the
FT                   claims"
XX
PN   DE4445562-C1.
```

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XX
PD   04-APR-1996.
XX
PF   20-DEC-1994;  94DE-4445562.
XX
PR   13-OCT-1994;  94DE-4436696.
XX
PA   (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI   Hanck T, Stoyanov B, Wetzker R;
XX
DR   WPI; 1996-172545/18.
DR   N-PSDB; AAT58546.
XX
PT   New phosphatidyl:inositol 3-kinase protein - useful as immunogen and
PT   for determ. of kinase activity
XX
PS   Claim 1; Page -; 10pp; German.
XX
CC   A 402 bp cDNA fragment was amplified from a human bone marrow
CC   library using PCR primers corresponding to amino acid sequences
CC   KNGDDIR and HIDPG. The amplified fragment was used to probe a human
CC   U937 cell cDNA library and several overlapping clones were isolated.
CC   The largest clone coded for a protein of 1049 residues. The protein
CC   is a novel phosphatidylinositol 3-kinase (PI3K) that differs in its
CC   regulatory mechanism from the known PI3k-alpha and -beta enzymes.
CC   The new enzyme has been designated PI3k-gamma. Another clone, coding
CC   for a PI3k-gamma having the present sequence of 1050 residues, was
CC   then isolated. The enzyme can be used as an immunogen. The enzyme,
CC   antibodies against it or nucleic acid encoding it can be
CC   used for modulating cell proliferation, receptor-mediated signal
CC   transmission, histamine secretion, nerve cell differentiation,
CC   glucose transport and anti-lipolytic activity or for treating
CC   Alzheimer's disease.
CC   N.B. Although the claimed sequences are referred to by SEQ.ID.
CC   Numbers, a sequence listing did not appear in the original printed
CC   patent application.
XX
SQ   Sequence  1050 AA;
```

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Query Match        90.2%;  Score 5222;  DB 17;  Length 1050;
Best Local Similarity  95.2%;  Pred. No. 0;
Matches  990;  Conservative  20;  Mismatches  30;  Indels  0;  Gaps  0;
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Qy    35  MELIPIEFVLPTSQRNTKTPETALLHVAGHGNVEQMKAQVWLRALETSVSADFYHRLGPD   94
          ||||||||||||||||:  :|||||||||||||||||||||||||||||:||||||
Db     1  MELIPIEFVLPTSQRKCKSPETALLHVAGHGNVEQMKAQVWLRALETSVAADFYHRLGPH   60

Qy    95  HFLLLYQKKGQWYEIYDKYQVVQTLDCLRYWKVLHRSPGQIHVVQRHAPSEETLAFORQL  154
          |||||||||||||||||||||||||||||||:||||||:||:|||||||||||||||
Db    61  HFLLLYQKKGQWYEIYDKYQVVQTLDCLRYWKATHRSPGQIHLVQRHPPSBESQAFQRQL  120

Qy   155  NALIGYDVTDSVNVHDDELEFTRRRLVTPRMAEVAGRDPKLYAMGHPWVTISKPLPEYLLKK  214
          ||||||||||||||||||:|||||:|||||||||:||||||||||||:|||||||
Db   121  TALIGYDVTDSVNVHDDELEFTRRGLVTPRMAEVASRDPKLYAMGHPWVTSKPLPEYLWKK  180

Qy   215  ITNNCVFIVIHRSTTSQTIKVSADDTPGTILQSFFTKMAKKKSLMDIPESQNERDFVLRV  274
          |:||  ||||||||||||||:||||:|||||||||||||||||:||||||||:|:||||
Db   181  IANNCIFIVIHRSTTSQTIKVSPDDTPGAILQSFFTKMAKKKSLMDIPESQSEQDFVLRV  240

Qy   275  CGRDEYLVGETPIKNFQWVRQCLKNGEEIHLVLDTPPDPALDEVRKEEWPLVDDCTGVTG  334
          ||||||||||||||||||||| |||||||:|||||||||||||||||||||||||||||
Db   241  CGRDEYLVGETPIKNFQWVRHCLKNGEEIHVVLDTPPDPALDEVRKEEWPLVDDCTGVTG  300

Qy   335  YHEQLTIHGKDHESVFTVSLWDCDRKFRVKIRGIDIPVLPRTADLTVFVEANIQYGQQVL  394
          ||||||||||||||||||||||||||||||||||||||:  ||||||||:|||||
Db   301  YHEQLTIHGKDHESVFTVSLWDCDRKFRVKIRGIDIPVLPRNTDLTVFVEANIQHGQQVL  360

Qy   395  CQRRTSPKPFTEEVLWNVWLEFSIKIKDLPKGALLNLQIYCGKAPALSGKTSAEMPSPES  454
          |||||||||||||| ||||||||||||||||||||||||||||||  || ||:
Db   361  CQRRTSPKPFTEEVLWNVWLEFSIKIKDLPKGALLNLQIYCGKAPALSSKASASPSSES  420

Qy   455  KGKAQLLYYVNLLLIDHRFLLRHGEYVLHMWQLSGKGEDQGSFNADKLTSATNPDKENSM  514
          ||| :||||||||||||||| :||||||:|||:||||||||||||||||||||||||||
Db   421  KGKVRLLYYVNLLLIDHRFLLRRGEYVLHWWQISGKGEDQGSFNADKLTSATNPDKENSM  480

Qy   515  SISILLDNYCHPIALPKHRPTPDPEGDRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKEL  574
          |||||||||||||||||:|||||||||||||||||||||||||||||||||||||||||
Db   481  SISILLDNYCHPIALPKHQPTPDPEGDRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKEL  540

Qy   575  LWHFRYESLKDPKAYPKLFSSVKNGQQEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCN  634
          ||||||||||:||||||||||||||||||||||||||:|||||||||||||||||||||
Db   541  LWHFRYESLKHPKAYPKLFSSVKNGQQEIVAKTYQLLARREVWDQSALDVGLTMQLLDCN  600

Qy   635  FSDENVRAIAVQKLESLEDDDVLHYLLQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHF  694
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  FSDENVRAIAVQKLESLEDDDVLHYLLQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHF  660

Qy   695  LFWFLRSETAQSRHYQQRFAVILEAYLRGCGTAMLHDFTQQVVQIDMLQKVTIDIKSLSA  754
          ||||||||:||||||||||||||||||||||||||||||||||||:|||||||:||||||
Db   661  LFWFLRSEIAQSRHYQQRFAVILEAYLRGCGTAMLHDFTQQVVQIEMLQKVTLDIKSLSA  720

Qy   755  EKYDVSSQVISQLKQKLENLQNLNLPQSFRVPYDPGLKAGALVIEKCKVMASKKKPLWLE  814
          |||||||||||||||||||||||: :||:||||||||||||||:|||||||||||||||||
Db   721  EKYDVSSQVISQLKQKLENLQNSQLPESFRVPYDPGLKAGALAIEKCKVMASKKKPLWLE  780

Qy   815  FKCADPTALSNETIGIIFKHGDDLRQDMLILQIIRIMESIWETESLDLCLLPYGCISTGD  874
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781  FKCADPTALSNETIGIIFKHGDDLRQDMLILQIIRIMESIWETESLDLCLLPYGCISTGD  840

Qy   875  KIGMIEIVKDATTIAKIQQSTVGNTGAFKDEVLSHWLKEKCPIEEKFQAAVERPVYSCAG  934
          ||||||||||||||||||||||||||||||||||:||||||:|||||||||||||||||||
Db   841  KIGMIEIVKDATTIAKIQQSTVGNTGAFKDEVLNHWLKEKSPTEEKFQAAVERPVYSCAG  900

Qy   935  YCVATFVLGIGDRHNDNIMISETGNLFHIDFGHILGNYKSFLGINKERVPFVLTPDFLFV  994
          ||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||
Db   901  YCVATFVLGIGDRHNDNIMITETGNLFHIDFGHILGNYKSFLGINKERVPFVLTPDFLFV  960

Qy   995  MGTSGKKTSLHFQKFQDVCVKAYLALRHHTNLLLILFSMMLMTGMPQLTSKEDIEYIRDA 1054
          |||||||||:|||||||:|||||||||||||||||||||||||||||||||||||||||
Db   961  MGTSGKKTSPHFQKFQDICVKAYLALRHHTNLLLILFSMMLMTGMPQLTSKEDIEYIRDA 1020

Qy  1055  LTVGKSEEDAKKYFLDQIEV 1074
          |||||:: |||||||||||
Db  1021  LTVGKNEBDAKKYFLDQIEV 1040
```

```
RESULT 9
AAW11576
ID   AAW11576 standard; Protein; 1049 AA.
XX
AC   AAW11576;
XX
DT   25-MAR-1997  (first entry)
XX
DE   Human phosphatidylinositol 3-kinase PI3K-gamma.
XX
KW   Phosphatidylinositol 3-kinase; gamma; PI3K; immunogen; immunoassay;
KW   cell proliferation; receptor-mediated signal transmission;
KW   histamine secretion; nerve cell differentiation; glucose transport;
KW   modulation; regulation; Alzheimer's disease; lipolysis.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         741..755
FT                   /label= immunogen
FT                   /note= "antibodies are pref. raised against this
FT                   peptide; location given as 741-745 in the
FT                   claims"
XX
PN   DE4445562-C1.
XX
PD   04-APR-1996.
XX
PF   20-DEC-1994;  94DE-4445562.
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Qy  355 WDCDRKFRVK--------IRGIDIPVLPRTADLTVFVEANIQYGQVLCQRRTSPKPF 404
                      :||:  :|   |:
Db  328 WVINSALRIKILCATYVNVIRDID---------KIYVRTGIYHGGEPLCDNVNTQRVP 377

Qy  405 TEEVLWNVWLEFSIKIKDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYYV 464
                      : ||: :|   |:                     :
Db  378 CSNPRWNEWLNYDIYIPDLPRAARLCLSI-C----SVKGRKGA--------KEEHCPLAWG 425

Qy  465 NLLLIDHRPLLRHGEYVLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYC 524
        |  ||: | |:|    |:
Db  426 NINLFDYTDTLVSGKMAINLWPVPHGLED--LLNPIGVT-GSNPNKE-TPCLELEPDWFS 481

Qy  525 HPIALPKIRPTPDPEGDRV------RAEMPNQLR---KQLEAIIATDPLN 565
                                    ||::  |   | ::||
Db  482 SVVKFPDMSVIEBHANWSVSREAGFSYSHAGLSNRLARDNELRENDKEQLRAICTRDPLS 541

Qy  566 PLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQQEIVAKTYQLLAKREVWDQSALDVG 625
          |: ||: |||: |: | :|||  || : |||:  |  || |||  |
Db  542 EITEQEKDFLWSHRHYCVTIPEILPKLLLSVKWNSRDEVAQNYCL----VKDWPIKPE 596

Qy  626 LTMQLLDCNFSDENVRAIAVQKLES-LEDDDVLHYLLQLVQAVKFEPYHDSALARFLLKR 684
          |:|||||| | ||||::| ||::|   | :|::|||:||:|:||  | :| ||||||
Db  597 QAMELLDCNYPDPMVRGFAVRCLEKYLTDDKLSQYILQVQVLKYEQYLDNLLVRFLLKK 656

Qy  685 GLRNKRIGHFLFWFLRSEIAQSRHYQQRPAVILEAYLRGCGTAMLHDFTQQVQVIDMLQK 744
         | ::|||||  ||:|:| : | :|: ||  ||| ||| || : ||  |::|:| : |:
Db  657 ALTNQRIGHFFFWHLKSEM-HNKTVSQRFGLLLESYCRACGMYLKH-LNRQVEAMBKLIN 714

Qy  745 VTIDIKSLSAEKYDVSSQVISOLQKQKLENLQN--LNLPQSFRVPVYDPGLKAGALVIEKC 801
          | ||  :  ||    |::   |:|:||  : ||:  |: ||  || |: :: |||:  ||
Db  715 LT-DI--LKQEKKDETQKV--QMKFLVEQMRRPDFMDALQGFLSPLNPAHQLGNLRLLBEC 769

Qy  802 KVMASKKKPLWLEFKCADPTALS------NEFIGIIFKHGDDLRQDMLILQILRIMESIW 855
         ::  ||:||||  |   |:::      || |||:|| :|||||||| ||| || :||:||
Db  770 RIMSSAKRPLWLNWE--NPDIMSELLFQNNE---IIFKNGDDLRQDMLTLQIIRIMENIW 824

Qy  856 ETESLDLCLLPYGCISTGDKIGMEIVKDATTIAKIQQSTVGNTGA--FKDEVLSHWLKE 913
          : ||||: |||||:| ||::|:|| |: | | :| | |:  :  | || |  | :||
Db  825 QNQGLDLRMLPYGCLSIGDCVGLIEVVRNSHTIMQI-QCKGGLKGALQFNSHTLHQWLKD 883

Qy  914 KCPIEEKFQAAVERFVVSCAGYCVATFVLGIGDRHNDNIMISETGNLFHIDFGHILGNYK 973
           | :|:| ||:  |::|||||||||||:||||||| |||:  :| |:|||||||:| :|
Db  884 KNK-GEIYDAAIDLFTRSCAGYCVATFIIGIGDRHNSNIMVKDDGQLPHIDFGHFLDHKK 942

Qy  974 SFLGINKSRVPFVLTPDFLFVMGTSGKK--TSLHFQKFQDVCVKAYLALRHHTNLLILLF 1031
            :|: | |||||| |||:|: : |:   || || : | :| ||||:|: ||| :| ||
Db  943 KKFGYKBRVPFVLTQDFLIVISKGAQBCTKTREFERFQEMCYKAYLAIRQHANLFINLF 1002

Qy 1032 SMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGWTVQFNWFLHLV 1091
        ||| :|||| |:| :| :|||  | ||| |: ||:|| | | | | ||| :  ||: | :
Db 1003 SMMLGSGMPELQSFDDIAYIRKTLALDKTEQEALEYMKQMNDAHHGGWTTKMDWIFHTI 1062
```

RESULT 12
AAR43342

```
ID   AAR43342 standard; Protein; 1068 AA.
XX
AC   AAR43342;
XX
DT   25-MAR-2003 (updated)
DT   12-APR-1994 (first entry)
XX
DE   Human p110.
XX
KW   Phosphoinositide kinase; PI; p85 subunit; screening; agonist;
KW   antagonist; cell proliferation; inhibition; prophylaxis; therapy;
KW   platelets; neutrophil activity; 3-phosphorylated phosphoinositides.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          19..100
```

```
PT   Recombinant polypeptide(s) - with phosphoinositide-3 kinase
PT   activity, useful for controlling cell proliferation
XX
PS   Claim 4; Fig 9; 146pp; English.
XX
CC   Southern blot analysis was performed using a bovine cDNA probe contg.
CC   a fragment of a PI3-kinase-encoding sequence and human cDNA isolated
CC   from a cDNA library constructed from mRNA isolated from the human
CC   cell line KG1a. Positive clones were sequenced to give a human
CC   PI3 kinase p110 sequence. This sequence has 95 percent
CC   homology with the bovine sequence. The domain encoding residues 19-
CC   100 of human p110 is sufficient to encode the kinase which will
CC   associate with the p85 kinase subunit. The gene may be used to
CC   provide a protein with PI3 kinase activity, and is useful for
CC   screening for (ant)agonists of PI3 kinase activity which could be
CC   useful for stimulation or inhibition of cell proliferation and hence
CC   prophylaxis or therapy. Platelet or neutrophil activity or blood
CC   glucose levels can be controlled using the kinase.
CC   See also AAR43342 and AAR46552-3.
CC   (Updated on 09-JAN-2003 to add missing OS field.)
CC   (Updated on 25-MAR-2003 to correct PN field.)
CC   (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ   Sequence  1068 AA;

Query Match   25.3%;  Score 1465.5;  DB 14;  Length 1068;
Best Local Similarity  33.5%;  Pred. No. 1.3e-113;
Matches  382;  Conservative 204;  Mismatches 405;  Indels 149;  Gaps 39;

Qy   23 MKPRSTAASLSSMELIP----IEFVLPTSQRNTKTPETALLHVAGHGNVEQMKAQVWLRA 78
         | |  :   :|:|:|   :|: |         |:   : :
Db    1 MPPRPSSGELWGIHIMPPRILVECLLPNGMIVT------LECLREATLITIKHELFKEA 53

Qy   79 LETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLDCLRYWKVLHRSPGQIHVV 138
          :    ||    :   ::|::                                  LKVI
Db   54 RKYPL-----HQLLQDESSYIFVSVTQEAEREEFPDETRRLCDLRLFQPF------LKVI 102

Qy  139 QRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRLVTPRMAEVAGRD------ 192
          : |  :    : | || :| |::          :  | :
Db  103 EPVGNREEKI-LNREIGFAICMPVCEPDMVKDPEVQDPFRRNILNVCKEAVDLRDLNSPHS 161

Qy  193 PKLYAMHPWTSKP-LPEYLLKITNNCVFIVI-----HRSTTSQTIKVSADDTPGTIL 245
            :      ::| ||: ::| |:  : ||       :   |
Db  162 RAMYVYPPNVESSPELPKHIYNKLDKGQIIVVIWIVSPNNDKQKYTLKINHDCVPEQVI 221

Qy  246 QSFFTKMAKKKSLMDIPES------QNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKN 299
           : : :  :  :|:    :|||  :| | |:|:|| | ||: |
Db  222 AEAIRK--KTRSMLLSSEQLKLCVLEYQGKYILKVCGCDEYFLEKYPLSQYKYIRSCIML 279

Qy  300 GEEIHLVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLT-----IHGKDHESVFTVSL 354
         | |  ||      |:           |  |     :     :     |  :    :  ||
Db  280 GRMPNLML------MAKELSYSQLPM--DCFTMPSYSRRISTATPYMNGE----TSTKSL 327
```

```
FT              /note= "binds with p85 subunit"
XX
PN   WO9321328-A1.
PD   28-OCT-1993.
XX
PF   13-APR-1993; 93WO-GB00761.
XX
PR   13-APR-1992; 92GB-0008135.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Hiles ID, Fry MJ, Dhand R, Waterfield MD, Parker PJ, Otsu M;
PI   Panayotou G, Volinia S, Gout I;
XX
DR   WPI; 1993-351738/44.
DR   N-PSDB; AAQS1156.
XX
PT   Recombinant polypeptide(s) - with phosphoinositide-3 kinase
PT   activity, useful for controlling cell proliferation
XX
PS   Claim 24; Fig 16; 146pp; English.
XX
CC   Southern blot analysis was performed using a bovine cDNA probe contg.
CC   a fragment of a PI3-kinase-encoding sequence and human cDNA isolated
CC   from a cDNA library constructed from mRNA isolated from the human
CC   cell line KG1a. Positive clones were sequenced to give the human
CC   PI3 kinase pi10 sequence. This sequence has 95 percent homology
CC   with the bovine sequence. The domain contg. residues 19-100 of human
CC   pi10 is sufficient to associate with the p85 kinase subunit. The
CC   protein with PI3 kinase activity is useful for screening for
CC   (ant)agonists of PI3 kinase activity which could be useful for
CC   stimulation or inhibition of cell proliferation and hence
CC   prophylaxis or therapy. Platelet or neutrophil activity or blood
CC   glucose levels can be controlled using the kinase.
CC   See also AAR43341 and AAR46552-3.
CC   (Updated on 25-MAR-2003 to correct PN field.)
CC   (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ   Sequence  1068 AA;

Query Match        25.2%;
Best Local Similarity   33.3%;
Matches  381;  Conservative 206;  Mismatches 400;  Indels 157;  Gaps 40;
Score 1460.5;  DB 14;  Length 1068;  Pred. No. 3.3e-113;
```

```
Qy   23 MKPRSTAALSLSSMELIP----IEFVLPTSQRNTKTPETALLHVAGHGNVEQMKAQWVLRA 78
Db    1 MPPRPSSGELWGIHLMPPRIIVEC-LPNGMIVT------LECLREATLVTIKHELFKEA 53

Qy   79 LETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLDCLRYWKVLHRSPGQIHVV 138
Db   54 RKYPL-----HQLLQDBSSYIFVSVTQEAEREEFFDETRRLCDLRLFQPF------LKVI 102

Qy  139 QRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRLVTPRMAEVAGRD------ 192
Db  103 EPVGNVREEKI-LNREIGFAIGMPVCEFDMVKDPEVQDFRRNILNVCKEAVDLRDLNSPHS 161

Qy  193 PKLYAVHPWVTSKP-LPEYLLKKITNNCVFIVI------HRSTTSQTIKVSADDTPGTIL 245
Db  162 RAMYIVYPPHVESSPELPKHIYNKLDRGQIIVIWVIVSPNNDKQKYTLKINHDCVPBQVI 221

Qy  246 QSFFTKMAKKKSLMDIPES-------QNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKN 299
Db  222 AEAIRK--KTRSMLLSSEQLKLJCVLEYQGKYILKVCGCDEYFLEKYPLSQYKYIRSCIML 279

Qy  300 GEEIHLVLDTPPDPALDEVRKE----EWPLVDDCTGVTGYHEQLT----IHGKDHESVF 350
Db  280 GRM-------PNLKMMAKESLYSQLPM-DCFTMPSYSRRISTATPYMNGE----TS 323

Qy  351 TVSLWDCDRKFRVK--------IRGIDIPVLPRTADLITVFVEANIQYGQQVLCQRRTS 400
Db  324 TKSLWVINRALRIKILCATYVNLNIRDID---------KIYVRTGIYHGGEPLCDNVNT 373
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Qy  401 PKFPTEEVLMNVWLEFSIKIKIDLPKGALLNLNQIYCGKAPALSGKTSAEMPSPESKGKAQL 460
Db  374 QRVPCSNPRWNEWLNYDIYIPDLPRAARLCLSI-C------SVKGRKGA------KEEHCP 421

Qy  461 LYYVNLLLIDHRFLLRHGEYVLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILL 520
Db  422 LAWGNINLFDYTDTLVSGKMALNLWPVHGLED--LLNPIGVT-GSNPNKE-TPCLELEF 477

Qy  521 DNYCHPIALPKGHRPTPDPEGDRV-------------RAEMPNQLR----KQLEAIIAT 561
Db  478 DWFSSVVKFPDMSVIEBHANWSVSREAGFSYSHAGLSNRLARDNELRENDKEQLKAISTR 537

Qy  562 DPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQQEIVAKTYQLLAKREWVDQSA 621
Db  538 DPLSEITEQEKDFIWSRHYCVTIPEILPKLLLSVKWNSRDEVAQMYCL------VKDWPP 592

Qy  622 LDVGLTMQLLDCNFSDENVRAIAVQKLES-LEDDDVLHYLLQLVQAVKFEPYHDSALARF 680
Db  593 IKPEQAMELLDCNYPDMVRGFAVRCLEKYLTDDKLSQYLIQLVQVLKYEQYLDNLLVRF 652

Qy  681 LLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAYLRGCGTAMLHDFTQQVQVID 740
Db  653 LKKALTNQRIGHFFFWHLKSEM-HNKTVSQRFGLLLESYCRACGMYLKH-LNRQVEAME 710

Qy  741 MLQKVTIDKSLSAEKYDVSSQVISQLKQKLENLQN---LNLPQSFRVPYDPGLKAGALV 797
Db  711 KLINLT-DI--LKQERKDETQKV--QMKFLVEQMRRPDFMDALQGLLSPLNPAHQLGNLR 765

Qy  798 IECKVMASKKKPLWLEFKCADPTALS-----NETIGIIFKHGDDLRQDMLILQILRIM 851
Db  766 LKECRIMSSAKRPIWLAWB--NPDIMSELLFQNNE---IIFKNGDDLRQDMLTLQIIRIM 820

Qy  852 ESIWETESLDLCLLPYGCISTGDKIGMEIVKDATTIAKIQQSTVGNTGA--FKDEVLSH 909
Db  821 ENTWQNQGLDRMLPYGCLSIGDCVGLIEVRNSHTIMQI-QCKGGLKGALQFNSHTLHQ 879

Qy  910 WLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNLFHIDFGHIL 969
Db  880 WLKDKNK-GEIYDAAIDLFTRSCAGYCVATFIGIGDRHNSNIMVKDDGQLFHIDFGHFL 938

Qy  970 GNYKSFLGINKERVPFVLTPDFLFVMGTSGKK--TSLHFQKFQDVCVKAYLALRHHTNLL 1027
Db  939 DHKKKKFGVKRERVFVLTQDFLIVISKGAQECTKTREFERFQEMCYKAYLAIRQHANLF 998

Qy 1028 IILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGWTVQFNWF 1087
Db  999 INLFSMMLGSSGMPELQSFDDIAYIRKTLALDKTEQEALEYFMKQMNDAHHGGWTTKMDWI 1058

Qy 1088 LHLV 1091
Db 1059 FHTI 1062
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```
RESULT 13
AAU09687
ID   AAU09687 standard; Protein; 1068 AA.
XX
AC   AAU09687;
XX
DT   12-MAR-2002 (first entry)
XX
DE   Human pi10alpha isoform of PI3-kinase.
XX
KW   Human; phosphatidylinositol 3-kinase; PI3K; pi10alpha isoform;
KW   LASP-1; cancer; inflammatory disease; ophthalmic disorder; SH3 domain;
KW   autoimmune disease; inflammatory bowel disease; bacterial pneumonia;
KW   Type I diabetes mellitus; cytostatic; immunosuppressive.
XX
CS   Homo sapiens.
XX
PN   WO200185986-A2.
XX
PD   15-NOV-2001.
```

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XX
PF    10-MAY-2001; 2001WO-US15065.
XX
PR    10-MAY-2000; 2000US-203346P.
XX
PA    (ICOS-) ICOS CORP.
XX
PI    Sadhu C;
XX
DR    WPI; 2002-075252/10.
DR    N-PSDB; AAS14365.
XX
PT    Identifying a modulator of p110delta polypeptide binding to SH3
PT    domain-containing polypeptides e.g. LASP-1, comprising allowing the
PT    binding partners to interact in the presence and absence of a test
PT    compound -
XX
PS    Example 1; Page 60-63; 85pp; English.
XX
CC    The present invention relates to identifying a modulator of the
CC    phosphatidylinositol 3-kinase (PI3K; p110delta) enzyme that binds to
CC    the catalytic subunit via a SH3 domain-containing polypeptide such as
CC    LASP-1. Also described are methods of assaying the specific binding
CC    affinity of the PI3-kinase binding partner. Such modulators are useful
CC    for the treatment of diseases characterised by the undesirable or
CC    excessive activity of PI3kdelta. For example the modulators can be used
CC    for inhibiting the growth or proliferation of cancer cells
CC    (e.g. malignant neoplasms of lymphoid and reticuloendothelial tissues,
CC    Hodgkin's lymphoma, leukaemias), inflammatory diseases (e.g. rheumatoid
CC    arthritis), ophthalmic disorders (e.g. allergic conjunctivitis),
CC    autoimmune diseases (e.g. systematic lupus erythematosus), inflammatory
CC    bowel diseases (e.g. chronic inflammatory bowel disease), inflammatory
CC    dermatoses (e.g. contact dermatitis; central or peripheral nervous
CC    system inflammatory disorders (e.g. meningitis), bacterial pneumonia,
CC    and Type I diabetes mellitus. The present sequence represents human
CC    p110alpha isoform of PI3K.
XX
SQ    Sequence 1068 AA;

Query Match     25.2%;    Score 1460.5;   DB 23;   Length 1068;
Best Local Similarity    33.3%;    Pred. No. 3.3e-113;
Matches 381;  Conservative 206;  Mismatches 400;  Indels 157;  Gaps  40;

Qy    23  MKPRSTAASLSSMELIP----IEPVLPTSQRNTKTPETALLHVAGHGNVEQMKAQVWLRA  78
Db     1  MPPRPSSGEIWGIHLMPPRILVECLLPNGMIVT------LECLREATLVTIKHELFKEA  53

Qy    79  LETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLDCLRYWKVLHRSPGQIHVV 138
Db    54  RKYPL-----HQLLQDESSYIFVSVTQEAREREFFDETRRLCDLRLFQPF------LKVI 102

Qy   139  QRHAPSEETLAFQPQLNALIGYDVTDVSNVHDDELEFTRRRLVTPRMAEVAGRD------ 192
Db   103  EPVGNREEKI-LNREIGPAIGMPVCEFDMVKDPEVQDFRRNILNVCKEAVDLRDLNSPHS 161

Qy   193  PKLYAMHPWVTSKP-LPEYLLKKITNNCVFIVI------HRSTSQTIKVSADDTPGTIL 245
Db   162  RAMVYYPPHVESSPELPKHIYNKLDRGQIIVWIWIVSPNNDKQKYTLKINHDCVPEQVI 221

Qy   246  QSFFTKMAKKKSLMDIPES-------QNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKN 299
Db   222  AEAIRK--KTRSMLLSSEQLKLCVLEYQGKYILKVCGCDEYFLEKYPLSQYKYIRSCIML 279

Qy   300  GEEIHLVLDTPPDPALDEVRKE------EWPLVDDCTGVTGYHEQLT-----IHGKDHESVF 350
Db   280  GRM------PNLKMMAKESLYSQLPM--DCFTMPSYSRRISTATPYMNGE----TS 323

Qy   351  TVSLWDCDRKFRVK------------IRGIDIPVLPRTADLTVFVEANIQYGGQVLCQRRTS 400
Db   324  TKSLWVINRALRIKLCATYVNLNIRDID------KIYVRTGIYHGGEPLCDNVNT 373

Qy   401  PKPFTEEVLMNVWLEFSIKIKDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQL 460
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Db   374  QRVPCSNPRWNEWLNVDIYIPDLPRAARLCLSI-C----SVKGRKGA------KEEHCP 421
Qy   461  LYYVNLLLIDHRFLLRHGEYVLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILL 520

Db   422  LAWGNINLFDYTDTLVSGKMALNLWPVPHGLED--LLNPIGVT-GSNPNKE-TPCLELEF 477
Qy   521  DNYCHPIALPKHRPTPDPEGDRV---------------RAEMPNQLR--KQLEAIIAT 561

Db   478  DWFSSVVKFPDMSVIEEHANWSVSREAGFSYSHAGLSNRLARDNELRENDKEQLKAISTR 537
Qy   562  DPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQQEIVAKTYQLLAKREVWDQSA 621

Db   538  DPLSEITEQEKDFLWSRHYCVTIPELLPKLLLSVKWNSRDEVAQMYCL----VKDWPP 592
Qy   622  LDVGLTMQLLDCNFSDENVRAIAVQKLES-LEDDDVLHYLLQLVQAVKPEYHDSALARF 680

Db   593  IKPEQAMELLDCNYPDPMVRGFAVRCLEKYLTDDKLSQYILIQLVQVLKYEQYLDNLLVRF 652
Qy   681  LLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAYLRGCGTAMLHDFTQQVQVID 740

Db   653  LLKKALTNQRIGHFFWFHLKSEM-HNKTVSQRFGLLLESYCRACGMYLKH-LNRQVEAME 710
Qy   741  MIQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQN---LNLPQSPRVPYDPGLKAGALV 797

Db   711  KLINLI-DI--LKQERKDETQKV--QMKFLVEQMRRPDFMDALQGLLSPLNPAHQLGNLR 765
Qy   798  IEKCKVMASKKKPLWLEFKCADPTALS------NETIGIIFKHGDLRQDMLILQILRIM 851

Db   766  LKECRIMSSAKRPLWLNWE--NPDIMSELLFQNNE--IIFKNGDLDRQDMLTLQIIRIM 820
Qy   852  ESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTGA--FKDEVLSH 909

Db   821  ENIWQNQGLDLRMLPYGCLSIGDCVGLIEVVRNSHTIMQI-QCKGGLKGALQFNSHTLHQ 879
Qy   910  WLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNLFHIDFGHIL 969

Db   880  WLKDKNK-GEIYDAAIDLFTRSCAGYCVATFILGIGDRHRSNIMVXDDGQLFHIDFGHFL 938
Qy   970  GNVKSFLGINKERVPFVLTPDFLFVMGTSGKK--TSLHFQKFQDVCVKAYLALRHHTNLL 1027

Db   939  DHKKKKFGYKKERVPFVLTQDFLIVISKGAQECTKREFERFQEMCYKAYLAIRQHANLF 998
Qy  1028  IILFSMMLTMGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGWTVQFNWF 1087

Db   999  INLFSMMLGSGWPELQSFDDIIAYIRKTLALDKTEQEALEYFMKQMNDAHHGGWTTKMDWI 1058
Qy  1088  LHLV 1091

Db  1059  FHTI 1062
```

```
RESULT 14
AAB11124
ID   AAB11124 standard; Protein; 1070 AA.
XX
AC   AAB11124;
XX
DT   16-FEB-2001 (first entry)
XX
DE   Human PI3 kinase p110beta protein.
XX
KW   Human; pI3 kinase P110 beta; antisense inhibition; primer; cytostatic;
KW   antiinflammatory; antiinfective.
XX
OS   Homo sapiens.
XX
PN   US6133032-A.
XX
PD   17-OCT-2000.
XX
PF   09-SEP-1999;  99US-0392350.
XX
PR   09-SEP-1999;  99US-0392350.
```

```
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Monia BP, Cowsert LM;
XX
DR   WPI; 2000-686014/67.
DR   N-PSDB; AAC65590.
XX
PT   Antisense compound 8-30 nucleobases in length targeted to a start codon
PT   of the coding region of human P13 kinase p110beta, useful for
PT   inhibiting the expression of the human polynucleotide -
XX
PS   Example 1; Column 43-50; 34pp; English.
XX
CC   This invention describes a novel antisense compound (I) 8-30 nucleobases
CC   in length targeted to a start codon or nucleobases 4-3174 of the coding
CC   region of human P13 kinase p110beta (II), in which (I) specifically
CC   hybridizes with and inhibits the expression of (II). The products of the
CC   invention have cytostatic, antiinflammatory and antiinfective activity.
CC   (I) is useful for inhibiting the expression of (II) in human cells or
CC   tissues. The antisense compound can be utilized for diagnostics,
CC   therapeutics, prophylaxis and as research reagents and kits. The
CC   antisense compounds may also be useful prophylactically, e.g. to prevent
CC   or delay infection, inflammation or tumor formation. The antisense
CC   compounds are useful for research and diagnostics, because these
CC   compounds hybridize to nucleic acids encoding (II).
XX
SQ   Sequence 1070 AA;

Query Match            23.4%;  Score 1354.5;  DB 21;  Length 1070;
Best Local Similarity  31.8%;  Pred. No. 2.7e-104;
Matches  361;  Conservative 202;  Mismatches 407;  Indels 165;  Gaps 37;

Qy   30  ASLSSMELIPIEFVLPTSQRNTKTPETALLHVAGHGNVEQMKAQVWLRALETSVSADFYH  89
             :::|:|::|||||             :|: :: |:|:     :||:
Db   22  SQIASDGSIPVDFLLPTG------IYIQLEVPREATISYIKQMLWKQVHNYPM-------  68

Qy   90  RLGPDHFLLIYQKKGGQWYEIYDKYQVVQTLD-----C-----LRYWKVLHRS--PGQIH 136
             ||||
Db   69  ------FNLLMDIDSYMFACVNQTAVYEELEDETRRLCDVRPFLPVLKLVTRSCDPGE-- 120

Qy  137  VVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDEL-EFTR--RRLVTPRMAEVAGRD- 192
             |||   :  : ||||
Db  121  -------KLDSKIGVLIGKGLHEFDSLKDPEVNEFRRKMRKFSBEKILSLVGLSW      168

Qy  193  -PKLYAMHPWVTSKPLPEYLLKKITNNCVFIVIHRSTTSQ--TIKVSADDTPGTILQSFF 249
             :::|: |:  ||||
Db  169  MDWLKQTYPEHEPSIPENLEDKLYGGKLIVAVHFENCQDVFSFQVSPNMNPIKVNE---- 225

Qy  250  TKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNGEEIHLVLDT 309
             :::|:| ||:  ||:
Db  226  LAIQKRLTIHGKSDEVSPYDYVLQVSGRVEYVFGDHPLIQFQYIRNCVWNRALPHFIL-- 283

Qy  310  PPDPALDEVRKEEWPLVDDCTGVTGYHEQ--LTIHGKDHRESVFTVSL------------ 354
             :::  |:|||
Db  284  --VECCKIKKMYEQEMIAIEAAINRNSSNLPLPLPPKKTRIISHV                326

Qy  355  WDCDRKFR-VKIRGIDIPVLPRTADLTVFVEANIQYGGQVLCQRRTSPK-PFTEEVLMNV 412
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Db  327  WENNNPFQIVLVKG--NKLNTEETVKVHVRAGLFHGTELLCKTIVSSEVSGKNDHIWNE  383

Qy  413  WLEPSIKIKDLPKGALLNLQIYCGKAPALSGKTSAEMPSP---ESKGKAQLLYY----VN 465
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Db  384  PLEFDINICDLPRMARLCFAVY-AVLDKVKTKKSTKTINPSKYQTIRRAGKVHYPVAWVN 442

Qy  466  LLLIDHRFLLRHGEYVLHMWQLSGKGEDQGSFNADKL--------TSATNPDKENSMSIS 517
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Db  443  TMVFDFKGQLRTGDIILHSW--------SSF-PDELEMLNPMGTVQTNPYTENATALH   492

Qy  518  ILL-DNYCHPIALP------KHRPTDPPEGDRVRAEMPNQLRKQLEAIIATDPLNPLTA  569
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Db  493  VKFPENKKQPYYYPPFDKIIEXAAEIASSDSANVSSRGGKKFLPVLKEILDRDPLSQLCE 552

Qy  570  EDKELLWHFRYESLK-DPKAYPLFSSVKWGQQEIVAKTYQLLAKREVWDQSALDVGLTM  628
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Db  553  NEMDLIWTLRQDCREIFPQSLPKLLLSIKWNKLEDVA--QLQALLQIWPK--LPPREAL  607

Qy  629  QLIDCNFSDENVRAIAVQKLBSLEDDDVLHYLLQLVQAVKFEPYHDSALARFLLKRGLRN 688
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Db  608  ELLDFNYPDQYVREYAVGCLRQMSDEELSQVILQLVQVLKYEPFLDCALSRFLLERALGN 667

Qy  689  KRIGHFLFWFLRSEIAQSRH--YQQRFAVILEAYLRGCGTAMLHDFTQQYVIDMLQKV   745
             :|||:|||||:|||        |   ::|||||:|  |||
Db  668  RRIGQFLFWHLRSEV----HIPAVSVQFGVILEAYCRG-SVGHMKVLSKQVEALNKLKTL 722

Qy  746  T--IDIKSLSAEKYDVSSQVISQLKQK----LENLQNLNLPQSFRVPYDPGLKAGALVI  798
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Db  723  NSLIKLNAVKLNRAKGKEAMHTCLKQSAYREALSDLQS------PLNPCVILSELYV    773

Qy  799  EKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDLRQDMLIIQILRIMESIWETE  858
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Db  774  EKCKYMDSKMKPLWLVI---NNKVFGEDSVGVIFKNGDDLRQDMLTLQMLRIMDLLWKEA 830

Qy  859  SLDICLLPYGCISTGDKIGMEIVKDATTIAKIQ--QSTVGNTGAFKDEVLSHWLKEKCP  916
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Db  831  GLDLRMLPYGCLATGDRSGLIEVSTSETIADIQLNSSNVAAAAFNKDALLNWLKEYNS   890

Qy  917  IEBKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISBTGNLFHIDFGHILGNYKSFL 976
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Db  891  GDD-LDRAIEEFTLSCAGYCVASYVLGIGDRHSDNIMVKKTGQLFHIDFGHILGNFKSKF 949

Qy  977  GINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLALRHHTNLLIILFSMMLM 1036
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Db  950  GIKRERVPFILTYDFIHVIQQGKTGNTEKFGGRFRQCCEDAYLILRRHGNLFTTLFALMLT 1009

Qy 1037  TGMPQLTSKEDIEYIRDALTVGKSEBDAKKYFLDQIEVCRDKGWTVQFNWFLHLV     1091
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Db 1010  AGLPELTSVKDIQYLKDSLALGKSEEEALKQFKQKFDEALRESWTTKVNWMAHTV     1064

RESULT 15
ABP65170
ID   ABP65170 standard; Protein; 1070 AA.
XX
AC   ABP65170;
XX
DT   12-NOV-2002 (first entry)
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DE   Hypoxia-regulated protein #44.
XX
KW   Cytostatic; vasotropic; tranquiliser; antiinflammatory; antiatherosclerotic; gene therapy;
KW   antiinflammatory; vulnerary; gynecological; ophthalmological; vaccine;
KW   hypoxia; tumourigenesis; angiogenesis; apoptosis; cancer;
KW   ischaemic condition; reperfusion injury; retinopathy; neonatal stress;
KW   preeclapmsia; atherosclerosis; inflammatory condition; wound healing;
KW   inflammation; erythropoiesis; hair loss; human.
XX
OS   Homo sapiens.
XX
PN   WO20024645-A2.
XX
PD   13-JUN-2002.
XX
PF   10-DEC-2001; 2001WO-GB05458.
XX
PR   08-DEC-2000; 2000GB-0030076.
PR   08-FEB-2001; 2001GB-0003156.
PR   25-OCT-2001; 2001GB-0025666.
XX
PA   (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI   White J, Mundy CR, Ward NR, Krige D, Kingsman SM, Harris RA;
PI   Rayner WN;
XX
DR   WPI; 2002-627238/67.
XX
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PT   Identifying a gene involved in disease for treating hypoxia-regulated
PT   conditions, comprises comparing the transcriptome/proteome of two cell
PT   types under different conditions and identifying a differentially
PT   regulated gene -
XX
PS   Claim 35; Page 363; 533pp; English.
XX
CC   The present invention relates to methods for identifying genes and
CC   proteins that are implicated in a specific disease or physiological
CC   condition. The method comprises comparing the transcriptome/proteome of a
CC   specialised cell type implicated in a disease or condition with that of a
CC   second specialised cell type, under two experimental conditions, and
CC   identifying a gene that is differentially regulated in the two
CC   specialised cell types under experimental conditions. ABV77873-ABV78116
CC   and ABP65061-ABP65257 were identified using the methods of the invention.
CC   The coding sequences and proteins are useful for treating a disease in a
CC   patient, for manufacture of a medicament for treating hypoxia-regulated
CC   conditions, and for regulating tumourigenesis, angiogenesis, apoptosis,
CC   biological response to hypoxia conditions, or hypoxi-associated
CC   pathology in a patient. The coding sequences and proteins are also useful
CC   for monitoring the therapeutic treatment of a disease or physiological
CC   condition, such as cancer, ischaemic conditions, reperfusion injury,
CC   retinopathy, neonatal stress, preeclapmsia, atherosclerosis, inflammatory
CC   conditions, wound healing, inflammation, erythropoiesis or hair loss.
XX
SQ   Sequence 1070 AA;

Query Match   23.4%; Score 1354.5; DB 23; Length 1070;
Best Local Similarity   31.8%; Pred. No. 2.7e-104;
Matches 361; Conservative 202; Mismatches 407; Indels 165; Gaps 37;

Qy   30 ASLSSMELIPIEFVLPTSQRNTKTPETALLHVAGHGNVEQMKAQVWLRALETSVSADFYH   89
Db   22 SQIASDGSIPVDFLLPTG------IYIQLEVPREATISYIKQMLWKQVHNYPM------   68

Qy   90 RLGPDHPLLLYQKGQWYEIYDKYQVVQTLD------C-----LRYWKVLHRS--PGQIH 136
Db   69 -----FNLLMDIDSYMFACVNQTAVYEELEDETRRLCDVRPFLPVLKJVTRSCDPGE-- 120

Qy 137 VVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDEL-EFTR--RRLVTPRMAEVAGRD- 192
Db 121 --------------KLDSKIGVLIGKGLHEFDSLKDPEVNEFRRKMRKFSEEKILSLVGLSW 168

Qy 193 -PKLYAMHPWTSKPLPEYLLKKITNNCVFIVIHRSTTSQ--TIKVSADDTPGTILQSFF 249
Db 169 MDWLKQTYPPEHEPSIPENLEDKLYGGKLIVAVHFENCQDVFSFQVSPNMNPIKVNE-- 225

Qy 250 TKMAKKKSLMDIPESQNERDPVLRVCGRDEYLVGETPIKNFQWVRQCLKNGEEIHLVLDT 309
Db 226 LAIQKRLTIHGKEDEVSPYDYVLQVSGRVEYVFGDHPLIQFQYIRNCVMNRALPHFIL-- 283

Qy 310 PPDPALDEVRKEEWPLVDDCTGVTGYHEQ--LTIHGKDHESVFTVSL------------- 354
Db 284 ------------VECCKIKKMYEQEMIAIEAAINRNSSNLPLPLPPKKTRIISHV 326

Qy 355 WDCDRKFPR-VKIRGIDIPVLPRTADLTVFVBEANIQYGQQVLCQRRTSPX-PFTEEVLMNV 412
Db 327 WENNNPFQIVLVKG---NKLNTEETVKVHVRAGLPHGTELLCKTIVSSEVSGKNDHIKWNE 383

Qy 413 WLEFSIKIKDLPKGALLNLQIYCGKAPALSGKTSAEMPSP--ESKGKAQLLYY----VN 465
Db 384 PLEFDINICDLPRMARLCFAVY-AVLDKVKTKKSTKTINPSKYQTIRKAGKVHYPVAWVN 442

Qy 466 LLLIDHRPLLRHGEVVLHMWQLSGKGSEDQGSFNADKL--------TSATNPDKENSMSIS 517
Db 443 TMVFDFKGQLRTGDIILHSW--------SSF-PDELEEMLNPMGTVQTNPYTENATALH 492

Qy 518 ILL-DNYCHPIALP-------KHRPTPDPEGDRVRAEMPNQLRKQLEAIIATDPLNPLTA 569
Db 493 VKFPENKKQPYYYPPFDKIIEKAAEIASSDSANVSSRGGKKFLPVLKEILDRDPLSQLCE 552

Qy 570 EDKELLWHFRYESLK-DPKAYPKLFSSVKWGQQEIVAKTYQLLAKREVWDQSALDVGLTM 628
Db 553 NEMDLIWTLRQDCREIFPQSLPKLLLSIKWNKLEDVA---QLQALLQIWPK--LPPREAL 607

Qy 629 QLLDCNFSDENVRAIAVQKLESLEDDVLHYLLQLVQAVKFEPYHDSALARFLLKRGLRN 688
Db 608 ELLDFNYPDQYVREYAVGCLRQMSDEELSQYILQLVQVLKYEPFLDCALSRFLLERALGN 667

Qy 689 KRIGHFLFWFLRSEIAQSRH---YQQRFAVILEAYLRGCGTAMLHDFTQQYQVIDMLQKV 745
Db 668 RRIGQFLFWHLRSEV---HIPAVSVQFGVILEAYCRG-SVGHMKVLSKQVEALNKLKTL 722

Qy 746 T--IDIKSLSAEKYDVSSQVISQLKQK------LENLQNLNLPQSFRVPYDPGLKAGALVI 798
Db 723 NSLIKLNAVKLNRAKGKEAMHTCLKQSAYREALSDLQS------PLNPCVILSELYV 773

Qy 799 EKCKVMASKKKPLMLEFKCADPTALSNETIGIIFKHGDDLRQDMLIIQILRIMESIWETE 858
Db 774 EKCKYMDSKMKPLWLVY---NNKVFGEDSVGVIFKNGDDLRQDMLTLQMLRLMDLLWKEA 830

Qy 859 SLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQ--QSTVGNTGAFKDEVLSHWLKEKCP 916
Db 831 GLDLRMLPYGCLATGDRSGLIEVVSTSETIADIQLNSSNVAAAAAFNKDALLNWLKEYNS 890

Qy 917 IEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNLFHIDFGHILGNYKSFL 976
Db 891 GDD-LDRAIEEFTLSCAGYCVASYVLGIGDRHSDNIMVKKTGQLFHIDFGHILGNFKSKF 949

Qy 977 GINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLALRHHTNLLILLFSMMLM 1036
Db 950 GIKRERVPFILYDFIHVIQQGKTGNTEKFGRFRQCCEDAYLILRHHGNLFTTLFALMLT 1009

Qy 1037 TGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGWTVQPNWFLHLV 1091
Db 1010 AGLPELTSVKDIQYLKDSLALGKSEEEALKQFKQXFDEALRSWTTKVNWMAHTV 1064

Search completed: February 15, 2004, 02:02:56
Job time : 86 secs

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            Copyright  GenCore version 5.1.6
                       Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:     February 15, 2004, 02:03:09 ; Search time 28 Seconds
                                          (without alignments)
                                      1665.234 Million cell updates/sec

Title:      US-09-974-573-1
Perfect score: 5790
Sequence:   1 MELENYEQPVVLREDNRRRR.........QFNWFLHLVLGIKQGEKHSA 1102

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:   328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters:      328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  Issued Patents AA:*
            1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
            2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
            3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
            4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
            5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
            6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	5726	98.9	1102	2	US-08-916-917-4	Sequence 4, Appli
2	5726	98.9	1102	2	US-08-972-631-4	Sequence 4, Appli
3	5726	98.9	1102	2	US-08-972-629-4	Sequence 4, Appli
4	5726	98.9	1102	2	US-08-972-630-4	Sequence 4, Appli
5	5726	98.9	1102	2	US-08-672-211-4	Sequence 4, Appli
6	5726	98.9	1102	3	US-09-225-170-4	Sequence 4, Appli
7	5523.5	95.4	1101	2	US-08-916-917-14	Sequence 14, Appl
8	5523.5	95.4	1101	3	US-09-225-170-14	Sequence 14, Appl
9	5222	90.2	1050	2	US-08-817-090B-4	Sequence 4, Appli
10	5093.5	88.0	1049	2	US-08-817-090B-37	Sequence 2, Appli
11	1465.5	25.3	1069	2	US-08-162-081B-37	Sequence 37, Appl
12	1465.5	25.3	1069	2	US-08-780-872-37	Sequence 37, Appl
13	1465.5	25.3	1069	3	US-09-085-957-37	Sequence 37, Appl
14	1463.5	25.3	1080	2	US-08-162-081B-36	Sequence 36, Appl
15	1463.5	25.3	1080	2	US-08-780-872-36	Sequence 36, Appl
16	1463.5	25.3	1080	3	US-09-085-957-36	Sequence 36, Appl
17	1450.5	25.1	1068	3	US-08-390-874C-11	Sequence 11, Appl
18	1450.5	25.1	1068	4	US-09-265-772-11	Sequence 11, Appl
19	1351.5	23.3	1044	2	US-08-777-405A-2	Sequence 2, Appli
20	1351.5	23.3	1044	2	US-08-977-871A-2	Sequence 2, Appli
21	1351.5	23.3	1044	4	US-09-225-951-2	Sequence 2, Appli
22	1351.5	23.3	1044	4	US-09-841-341-2	Sequence 2, Appli
23	1349.5	23.3	1044	4	US-09-194-640A-1	Sequence 1, Appli
24	1076.5	18.6	1726	4	US-08-609-049A-30	Sequence 30, Appl
25	1076.5	18.6	1726	3	US-09-170-996-30	Sequence 30, Appl
26	1075.5	18.6	1658	2	US-08-609-049A-13	Sequence 13, Appl
27	1075.5	18.6	1658	3	US-09-170-996-13	Sequence 13, Appl
28	1074	18.5	1686	4	US-09-355-160D-2	Sequence 2, Appli
29	1034	17.9	1167	3	US-08-857-076-48	Sequence 48, Appl
30	874	15.1	1876	2	US-08-609-049A-28	Sequence 28, Appl
31	874	15.1	1876	2	US-09-170-996-28	Sequence 28, Appl
32	873.5	15.1	1876	2	US-08-609-049A-12	Sequence 12, Appl
33	873.5	15.1	1876	3	US-09-170-996-12	Sequence 12, Appl
34	851.5	14.7	171	3	US-08-609-049A-23	Sequence 23, Appl
35	851.5	14.7	171	3	US-09-170-996-23	Sequence 23, Appl
36	690.5	11.9	803	3	US-09-118-442-2	Sequence 2, Appli
37	690.5	11.9	803	3	US-09-677-064-2	Sequence 2, Appli
38	649.5	11.2	868	2	US-08-162-081B-33	Sequence 33, Appl
39	649.5	11.2	868	3	US-08-780-872-33	Sequence 33, Appl
40	649.5	11.2	868	2	US-09-085-957-33	Sequence 33, Appl
41	499.5	8.6	171	2	US-08-609-049A-22	Sequence 22, Appl
42	499.5	8.6	171	3	US-09-170-996-22	Sequence 22, Appl
43	486.5	8.4	171	2	US-08-609-049A-21	Sequence 21, Appl
44	486.5	8.4	171	3	US-09-170-996-21	Sequence 21, Appl
45	464	8.0	171	2	US-08-609-049A-20	Sequence 20, Appl

ALIGNMENTS

```
RESULT 1
US-08-916-917-4
; Sequence 4, Application US/08916917
; Patent No. 5855132
; GENERAL INFORMATION:
;   APPLICANT: Stephens, Len
;   APPLICANT: Hawkins, Phillip Thomas
;   APPLICANT: Braselmann, Sylvia
;   TITLE OF INVENTION: G-BETA-GAMMA REGULATED
;   TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
;   NUMBER OF SEQUENCES: 14
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Pennie & Edmonds, LLP
;   STREET: 1155 Avenue of the Americas
;   CITY: New York
;   STATE: NY
;   COUNTRY: USA
;   ZIP: 10036-2811
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: Windows
;   SOFTWARE: FastSEQ for Windows Version 2.0b
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/916,917
;   FILING DATE: 15-AUG-1997
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/672,211
;   FILING DATE: 27-JUN-1996
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Abrams, Samuel B
;   REGISTRATION NUMBER: 30,605
;   REFERENCE/DOCKET NUMBER: 8549-0006-999
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 650-493-4935
;   TELEFAX: 650-493-5556
;   TELEX: 66141 PENNIE
;   INFORMATION FOR SEQ ID NO: 4:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1102 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: No. 5856132e
US-08-916-917-4

Query Match      98.9%;  Score 5726;  DB 2;  Length 1102;
Best Local Similarity  98.9%;  Pred. No. 0;
Matches 1090;  Conservative 6;  Mismatches 6;  Indels 0;  Gaps 0;
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Qy  1081 TVQFNWFLHLVLGIKQGEKHSA 1102
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Db  1081 TVQFNWFLHLVLGIKQGEKHPA 1102
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RESULT 2
US-08-972-631-4
; Sequence 4, Application US/08972631
; Patent No. 5856133
; GENERAL INFORMATION:
   APPLICANT: Stephens, Len
   APPLICANT: Hawkins, Phillip T.
   TITLE OF INVENTION: G-BETA-GAMMA REGULATED
   TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
   NUMBER OF SEQUENCES: 10
   CORRESPONDENCE ADDRESS:
      ADDRESSEE: Pennie & Edmonds
      STREET: 2730 Sand Hill Road
      CITY: Menlo Park
      STATE: California
      COUNTRY: USA
      ZIP: 94025
   COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: PatentIn Release #1.0, Version #1.30
   CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/08/972,631
      FILING DATE:
      CLASSIFICATION:
   PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 08/672,211
      FILING DATE: 27-JUN-1996
   ATTORNEY/AGENT INFORMATION:
      NAME: Halluin, Albert P.
      REGISTRATION NUMBER: 25,277
      REFERENCE/DOCKET NUMBER: 8549-0005-999
   TELECOMMUNICATION INFORMATION:
      TELEPHONE: (415)854-3660
      TELEFAX: (415)854-3694
   INFORMATION FOR SEQ ID NO: 4:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 1102 amino acids
      TYPE: amino acid
      STRANDEDNESS:
      TOPOLOGY: unknown
      MOLECULE TYPE: peptide
US-08-972-631-4

  Query Match   98.9%; Score 5726; DB 2; Length 1102;
  Best Local Similarity 98.9%; Pred. No. 0;
  Matches 1090; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
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Qy    1 MELENYEQPVVLREDNRRRRRMKPRSTAASLSSMELIPIEFVLPTSQRNTKTPETALLH 60
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Qy  121 CLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRL 180
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Qy  181 VTPRMAEVAGRDPKLYAMHPWTSKPLPEYLLKKITNNCVFIVIHRSTTSQTIKVSADDT 240
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Db  181 VTPRMAEVAGRDPKLYAMHPWTSKPLPEYLLKKITNNCVFIVIHRSTTSQTIKVSADDT 240

Qy  241 PGTILQSFFTKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG 300
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Db  241 PGTILQSFFTKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG 300

Qy  301 EEIHLVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK 360
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Db  301 EEIHLVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK 360

Qy  361 FRVKIRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTSPKFPTEEVLMNVWLEFSIKI 420
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Db  361 FRVKIRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTSPKFPTEEVLMNVWLEFSIKI 420

Qy  421 KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYVNLLLIDHRFLLRHGEY 480
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Qy  481 VLHWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKHRPTPDPEG 540
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Db  481 VLHWQLSGKGEDQGSFNADKLTSGTNPDKEDSMSISILLDNYCHPIALPKIRPTPDPEG 540

Qy  541 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQ 600
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Db  541 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQ 600

Qy  601 QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 660
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Db  601 QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 660

Qy  661 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLWFWFLRSEIAQSRHYQQRPAVILEAY 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLWFWFLRSEIAQSRHYQQRPAVILEAY 720

Qy  721 LRGGCGTAMLHDFTQQVQVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLP 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721 LRGGCGTAMLHDFTQQVQVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLP 780

Qy  781 QSFRVPYDPGLKAGALVIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ 840
          |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781 QSFRVPYDPGLKAGALVIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ 840

Qy  841 DMLIQILRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841 DMLIQILRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG 900

Qy  901 AFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL 960
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Db  901 AFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL 960

Qy  961 FHIDFPGHILGNYKSPLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLAL 1020
          |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961 FHIDFPGHILGNYKSPLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLAL 1020

Qy 1021 RHHTNLLILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW 1080
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Db 1021 RHHTNLLILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW 1080
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;  COUNTRY: USA
;  ZIP: 94025
;  COMPUTER READABLE FORM:
;    MEDIUM TYPE: Floppy disk
;    COMPUTER: IBM PC compatible
;    OPERATING SYSTEM: PC-DOS/MS-DOS
;    SOFTWARE: PatentIn Release #1.0, Version #1.30
;  CURRENT APPLICATION DATA:
;    APPLICATION NUMBER: US/08/972,629
;    FILING DATE:
;    CLASSIFICATION:
;  PRIOR APPLICATION DATA:
;    APPLICATION NUMBER: US 08/672,211
;    FILING DATE: 27-JUN-1996
;  ATTORNEY/AGENT INFORMATION:
;    NAME: Halluin, Albert P.
;    REGISTRATION NUMBER: 25,277
;    REFERENCE/DOCKET NUMBER: 8549-0005-999
;  TELECOMMUNICATION INFORMATION:
;    TELEPHONE: (415)854-3660
;    TELEFAX: (415)854-3694
;  INFORMATION FOR SEQ ID NO: 4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH: 1102 amino acids
;      TYPE: amino acid
;      STRANDEDNESS:
;      TOPOLOGY: unknown
;    MOLECULE TYPE: peptide
US-08-972-629-4

Query Match             98.9%;  Score 5726;  DB 2;  Length 1102;
Best Local Similarity   98.9%;  Pred. No. 0;
Matches 1090;  Conservative 6;  Mismatches 6;  Indels 0;  Gaps 0;

Qy      1  MELENYEQPVVLREDNRRRRRRMKPRSTAASLSSMELIPIEFVLPTSQRNTKTPETALLH 60
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Db      1  MELENYEQPVVLREDNRRRRRRMKPRSTAASLSSMELIPIEFVLATSQRNTKTPETALLH 60

Qy     61  VAGHGNVEQMKAQVWLRALETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVCTLD 120
           |||||||| ||||| |||||||||| ||||| |||||| ||||| ||||||||||||:||
Db     61  VAGHGNVEKMKAQVLLRALETSVSWDFYHRFGPDHFLLVFQKKGEWYEIYDKYQVVQTLD 120

Qy    121  CLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRLNALIGYDVTDVSNVHDDELEFTRRRL 180
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Db    121  CLRYWEVLHRSPGQIHVVQRHAPSEETLAFQCQLNALIGYDVTDVSNVHDDELEFTRRRL 180

Qy    181  VTPRMAEVAGRDPKLYAMHPWTSKPLPEYLLKKITNNCVFIVIHRSTTSQTIKVSADDT 240
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Db    181  VIPRMAEVAGRDPKLYAMHPWTSKPLPEYLLKKITNNCVFIVIHRSTTSQTIKVSADDT 240

Qy    241  PGTILQSFFTKMAKKKSLMDIPESQNRDFVLRVCGRDEYLVGETFIKNFQWVRQCLKNG 300
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Db    241  PGTILQSFFTKMAKKKSLMDIPESQNRDFVLRVCGRDEYLVGETFIKNFQWVRQCLKNG 300

Qy    301  EEIHLVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK 360
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Db    301  EEIHLVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK 360

Qy    361  FRVKIRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTSPKPFTEEVLMNVWLEFSIKI 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  FRVKIRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTSPKPFTEEVLMNVWLEFSIKI 420

Qy    421  KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYVNLLLIDHRFLLRHGEY 480
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Db    421  KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYVNLLLIDHRFLLRHGEY 480

Qy    481  VLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKGHRPTPDPEG 540
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Db    481  VLHMWQLSGKGEDQGSFNADKLTSGTNPDKEDSMSISILLDNYCHPIALPKGHRPTPDPEG 540

Qy    541  DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQ 600
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Db    541  DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQ 600
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Qy    301  EEIHLVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK 360
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Db    301  EEIHLVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK 360

Qy    361  FRVKIRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTSPKPFTEEVLMNVWLEFSIKI 420
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Db    361  FRVKIRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTSPKPFTEEVLMNVWLEFSIKI 420

Qy    421  KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYVNLLLIDHRFLLRHGEY 480
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Db    421  KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYVNLLLIDHRFLLRHGEY 480

Qy    481  VLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKGHRPTPDPEG 540
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Db    541  DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQ 600

Qy    601  QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 660
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Db    601  QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 660

Qy    661  LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY 720
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Db    661  LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY 720

Qy    721  LRGGCGTAMLHDFTQQVQVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLP 780
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Db    721  LRGGCGTAMLHDFTQQVQVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLP 780

Qy    781  QSFRVPYDPGLKAGALVIEKCKVNASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ 840
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Db    781  QSFRVPYDPGLKAGALVIEKCKVNASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ 840

Qy    841  DMLIQILRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG 900
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Db    841  DMLIQILRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG 900

Qy    901  AFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL 960
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Db    901  AFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL 960

Qy    961  FHIDFGHILGNYKSPLGINKERVPPVLTPDFLFVMGTSGKKTSLHFQKFQDVCKAYLAL 1020
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Db    961  FHIDFGHILGNYKSPLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLAL 1020

Qy   1021  RHHTNLLILFSMVMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW 1080
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Db   1021  RHHTNLLILFSMVMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW 1080

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Qy   601  QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL  660
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Db   601  QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL  660

Qy   661  LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY  720
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Db   661  LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY  720

Qy   721  LRGCGTAMLHDFTQQVQVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLP  780
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Db   721  LRGCGTAMLHDFTQQVQVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLP  780

Qy   781  QSFRVPYDPGLKAGALVIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ  840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781  QSFRVPYDPGLKAGALVIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ  840

Qy   841  DMLILQILRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG  900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841  DMLILQILRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG  900

Qy   901  AFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL  960
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Db   901  AFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL  960

Qy   961  FHIDFPGHILGNYKSFPIGINKERVPFVLTPDFLFVMGTSGKKTSLHFQDVCVKAYLAL  1020
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Db   961  FHIDFPGHILGNYKSFPIGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLAL  1020

Qy  1021  RHHTNLLIILFSMMLMTGNMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW  1080
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Db  1021  RHHTNLLIILFSMMLMTGNMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW  1080

Qy  1081  TVQFNWFLHLVLGIKQGEKHSA  1102
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RESULT 4
US-08-972-630-4
; Sequence 4, Application US/08972630
; Patent No. 5869271
; GENERAL INFORMATION:
;   APPLICANT: Stephens, Len
;   APPLICANT: Hawkins, Phillip T.
;   TITLE OF INVENTION: G-BETA-GAMMA REGULATED
;   TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
;   NUMBER OF SEQUENCES: 10
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Pennie & Edmonds
;   STREET: 2730 Sand Hill Road
;   CITY: Menlo Park
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94025
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/972,630
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/672,211
;   FILING DATE: 27-JUN-1996
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Halluin, Albert P.
;   REGISTRATION NUMBER: 25,277
;   REFERENCE/DOCKET NUMBER: 8549-0005-999
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415)854-3660

;   TELEFAX: (415) 854-3694
; INFORMATION FOR SEQ ID NO: 4:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1102 amino acids
;   TYPE: amino acid
;   STRANDEDNESS:
;   TOPOLOGY: unknown
;   MOLECULE TYPE: peptide
US-08-972-630-4

Query Match   98.9%; Score 5726; DB 2; Length 1102;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 1090; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

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Qy     1  MELENYEQPVVLREDNRRRRRMKPRSTAASLSSMELIPIEFVLPTSQRNTKTPETALLH   60
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Qy   121  CLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRL  180
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Db   121  CLRYWEVLHRSPGQIHVVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRL  180

Qy   181  VTPRMAEVAGRDPKLYAMHPWVTSKPLPEYLLKKITNCVFIVIHRSTTSQTIKVSADDT  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  VTPRMAEVAGRDPKLYAMHPWVTSKPLPEYLLKKITNCVFIVIHRSTTSQTIKVSADDT  240

Qy   241  PGTILQSFFTKMAKKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  PGTILQSFFTKMAKKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG  300

Qy   301  EEIHLVLDTPPPDALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK  360
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Db   301  EEIHLVLDTPPPDALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK  360

Qy   361  FRVKIRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTSPKPFTEVLMNVWLEFSIKI  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  FRVKIRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTSPKPFTEVLMNVWLEFSIKI  420

Qy   421  KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYYVNLLLIDHRFLLRHGEY  480
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Db   421  KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYYVNLLLIDHRFLLRHGEY  480

Qy   481  VLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKGHRPTPDPEG  540
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Qy   661  LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY  720
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Db   661  LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY  720

Qy   721  LRGCGTAMLHDFTQQVQVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLP  780
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Db   781  QSFRVPYDPGLKAGALVIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ  840

Qy   841  DMLILQILRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG  900
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Db   841  DMLILQILRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG  900
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Qy 181 VTPRMAEVAGRDPKLYAMHPWVTSKPLPEYLLKKITNNCVFIVIHRSTTSQTIKVSADDT 240
Db 181 VTPRMAEVAGRDPKLYAMHPWVTSKPLPEYLLKKITNNCVFIVIHRSTTSQTIKVSADDT 240
Qy 241 PGTILQSFFTKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG 300
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Qy 301 EEIHLVLDTPPDALDEVRKEBWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK 360
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Qy 361 FRVKIRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRTSPKPFTEEVLWNVWLEFSIKI 420
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Qy 421 KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYVNLLLIDHRFLLRHGEY 480
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Qy 601 QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 660
Db 601 QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 660
Qy 661 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHPLFWFLRSEIAQSRHYQQRFAVILEAY 720
Db 661 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHPLFWFLRSEIAQSRHYQQRFAVILEAY 720
Qy 721 LRGCGTAMLHDFTQQVQVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLP 780
Db 721 LRGCGTAMLHDFTQQVQVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLP 780
Qy 781 QSFRVPYDPGLKAGALVIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ 840
Db 781 QSFRVPYDPGLKAGALVIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ 840
Qy 841 DMLILQILRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG 900
Db 841 DMLILQILRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG 900
Qy 901 AFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL 960
Db 901 AFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL 960
Qy 961 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCKAYLAL 1020
Db 961 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCKAYLAL 1020
Qy 1021 RHHTNLLIILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW 1080
Db 1021 RHHTNLLIILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW 1080
Qy 1081 TVQFNWFLHLVLGIKQGEKHSA 1102
Db 1081 TVQFNWFLHLVLGIKQGEKHPA 1102

RESULT 6
US-09-225-170-4
; Sequence 4, Application US/09225170
; Patent No. 6017763
; GENERAL INFORMATION:

Qy 901 AFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL 960
Db 901 AFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL 960
Qy 961 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLAL 1020
Db 961 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLAL 1020
Qy 1021 RHHTNLLIILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW 1080
Db 1021 RHHTNLLIILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW 1080
Qy 1081 TVQFNWFLHLVLGIKQGEKHSA 1102
Db 1081 TVQFNWFLHLVLGIKQGEKHPA 1102

RESULT 5
US-08-672-211-4
; Sequence 4, Application US/08672211
; Patent No. 5874273
; GENERAL INFORMATION:
;   APPLICANT: Stephens, Len
;   APPLICANT: Hawkins, Phillip T.
;   TITLE OF INVENTION: G-BETA-GAMMA REGULATED
;   TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
;   NUMBER OF SEQUENCES: 10
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Pennie & Edmonds
;   STREET: 2730 Sand Hill Road
;   CITY: Menlo Park
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94025
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/672,211
;   FILING DATE: 27-JUN-1996
;   CLASSIFICATION: 514
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Halluin, Albert P.
;   REGISTRATION NUMBER: 25,277
;   REFERENCE/DOCKET NUMBER: 8549-0005-999
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415)854-3660
;   TELEFAX: (415)854-3694
; INFORMATION FOR SEQ ID NO: 4:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1102 amino acids
;   TYPE: amino acid
;   STRANDEDNESS:
;   TOPOLOGY: unknown
;   MOLECULE TYPE: peptide
US-08-672-211-4

Query Match   98.9%; Score 5726; DB 2; Length 1102;
Best Local Similarity   98.9%; Pred. No. 0;
Matches 1090; Conservative   6; Mismatches   6; Indels   0; Gaps   0;

Qy   1 MELENYEQPVLREDNRRRRRMKPRSTAASLSSMELIPIEFVLFTSQRNTKTPETALLH 60
Db   1 MELENYEQPVLREDNRRRRRMKPRSTAASLSSMELIPIEFVLATSQRNTKTPETALLH 60
Qy   61 VAGHGNVEQMKAQVWLRALETSVSADFYHRLGPDHFILLYQKKGQWYEIYDKYQVVQTLD 120
Db   61 VAGHGNVEKMKAQVLLRALETSVSWDFYHRFGPDHFLLVFQKKGEWYEIYDKYQVVQTLD 120
Qy 121 CLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRL 180

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;  APPLICANT:  Stephens, Len
;  APPLICANT:  Hawkins, Phillip Thomas
;  APPLICANT:  Braselmann, Sylvia
;  TITLE OF INVENTION:  G-BETA-GAMMA REGULATED
;  TITLE OF INVENTION:  PHOSPHATIDYLINOSITOL-3' KINASE
;  NUMBER OF SEQUENCES:  14
;  CORRESPONDENCE ADDRESS:
;  ADDRESSEE:  Pennie & Edmonds, LLP
;  STREET:  1155 Avenue of the Americas
;  CITY:  New York
;  STATE:  NY
;  COUNTRY:  USA
;  ZIP:  10036-2811
;  COMPUTER READABLE FORM:
;  MEDIUM TYPE:  Diskette
;  COMPUTER:  IBM Compatible
;  OPERATING SYSTEM:  Windows
;  SOFTWARE:  FastSEQ for Windows Version 2.0b
;  CURRENT APPLICATION DATA:
;  APPLICATION NUMBER:  US/09/225,170
;  FILING DATE:
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER:  08/916,917
;  FILING DATE:  15-AUG-1997
;  ATTORNEY/AGENT INFORMATION:
;  NAME:  Abrams, Samuel B
;  REGISTRATION NUMBER:  30,605
;  REFERENCE/DOCKET NUMBER:  8549-0006-999
;  TELECOMMUNICATION INFORMATION:
;  TELEPHONE:  650-493-4935
;  TELEFAX:  650-493-5556
;  TELEX:  66141 PENNIE
US-09-225-170-4

INFORMATION FOR SEQ ID NO:  4:
;  SEQUENCE CHARACTERISTICS:
;  LENGTH:  1102 amino acids
;  TYPE:  amino acid
;  STRANDEDNESS:  single
;  TOPOLOGY:  linear
;  MOLECULE TYPE:  No. 6017763e
US-09-225-170-4

Query Match             98.9%;  Score 5726;  DB 3;  Length 1102;
Best Local Similarity   98.9%;  Pred. No. 0;
Matches  1090;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;
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Qy     1  MELENYEQPVVLREDNRRRRMKPRSTAASLSSMELIPIEFVLPTSQRNTKTPETALLH   60
          |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db     1  MELENYEQPVVLREDNRRRRMKPRSTAASLSSMELIPIEFVLATSQRNTKTPETALLH   60

Qy    61  VAGHGNVEQMKAQVWLRALETSVSADFYHRLGPDHFLLLYQKKGGWYEIYDKYQVVQTLD  120
          |||||||| |||||| ||||||||| |||||| |||||| |||||||||||||||||||
Db    61  VAGHGNVEKMKAQVLLRALETSVSVSWDFYHRFGPDHFLLVFQKKGEWYEIYDKYQVVQTLD  120

Qy   121  CLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRL  180
          ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  CLRYWEVLHRSPGQIHVVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRL  180

Qy   181  VTPRMAEVAGRDPKLYAMHPWTSKPLPEYLLKKITNNCVFIVIHRSTTSQTIKVSADDT  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  VTPRMAEVAGRDPKLYAMHPWTSKPLPEYLLKKITNNCVFIVIHRSTTSQTIKVSADDT  240

Qy   241  PGTILQSFFTKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  PGTILQSFFTKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG  300

Qy   301  EEIHLVLDTPPDPALDEVRKEEWPLVDDCTGVTGVHEQLTIHGKDHESVFTVSLWDCDRK  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  EEIHLVLDTPPDPALDEVRKEEWPLVDDCTGVTGVHEQLTIHGKDHESVFTVSLWDCDRK  360

Qy   361  FRVKIRGIDIPVLPRTADLITVFVEANIQYGGQVLCQRRTSPKPFTEEVLMNVWLEFSIKI  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  FRVKIRGIDIPVLPRTADLITVFVEANIQYGGQVLCQRRTSPKPFTEEVLMNVWLEFSIKI  420

Qy   421  KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYYVNLLLIDHRFLLRHGEY  480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYYVNLLLIDHRFLLRHGEY  480

Qy   481  VLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKHRPTPDPEG  540
          ||||||||||||||||||||||||| |||||| |||||||||||||||||||||||||
Db   481  VLHMWQLSGKGEDQGSFNADKLTSGTNPDKEDSMSISILLDNYCHPIALPKHRPTPDPEG  540

Qy   541  DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQ  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541  DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQ  600

Qy   601  QEIVAKTYQLLAKREVNDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL  660
          |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db   601  QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL  660

Qy   661  LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY  720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661  LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY  720

Qy   721  LRGCGTAMLHDFTQQVQVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLP  780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721  LRGCGTAMLHDFTQQVQVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLP  780

Qy   781  QSFRVPYDPGLKAGALVIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ  840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781  QSFRVPYDPGLKAGALVIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ  840

Qy   841  DMLILQILRIMESTWETESLDLCLLPYGCISTGDKIGMIEIVDATTIAKIQQSTVGNTG  900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841  DMLILQILRIMESTWETESLDLCLLPYGCISTGDKIGMIEIVDATTIAKIQQSTVGNTG  900

Qy   901  AFKDEVLSHWLKEKCPIEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL  960
          ||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db   901  AFKDEVLSHWLKEKCPIEKFQAAVERVYSCAGYCVATFVLGIGDRHNDNIMISETGNL  960

Qy   961  FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLAL 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961  FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLAL 1020

Qy  1021  RHHTNLLIILFSMWLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021  RHHTNLLIILFSMWLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW 1080

Qy  1081  TVQFNWFLHLVLGIKQGEKHSA 1102
          |||||||||||||||||||| |
Db  1081  TVQFNWFLHLVLGIKQGEKHPA 1102
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RESULT 7
US-08-916-917-14
;  Sequence 14, Application US/08916917
;  Patent No. 5856132
;  GENERAL INFORMATION:
;  APPLICANT:  Stephens, Len
;  APPLICANT:  Hawkins, Phillip Thomas
;  APPLICANT:  Braselmann, Sylvia
;  TITLE OF INVENTION:  G-BETA-GAMMA REGULATED
;  TITLE OF INVENTION:  PHOSPHATIDYLINOSITOL-3' KINASE
;  NUMBER OF SEQUENCES:  14
;  CORRESPONDENCE ADDRESS:
;  ADDRESSEE:  Pennie & Edmonds, LLP
;  STREET:  1155 Avenue of the Americas
;  CITY:  New York
;  STATE:  NY
;  COUNTRY:  USA
;  ZIP:  10036-2811
;  COMPUTER READABLE FORM:
;  MEDIUM TYPE:  Diskette
;  COMPUTER:  IBM Compatible
;  OPERATING SYSTEM:  Windows
;  SOFTWARE:  FastSEQ for Windows Version 2.0b
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;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/916,917
;     FILING DATE: 15-AUG-1997
;     CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 08/672,211
;     FILING DATE: 27-JUN-1996
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Abrams, Samuel B
;     REGISTRATION NUMBER: 30,605
;     REFERENCE/DOCKET NUMBER: 8549-0006-999
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 650-493-4935
;     TELEFAX: 650-493-5556
;     TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 14:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 1101 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: No. 5856132e
US-08-916-917-14
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Query Match      95.4%;  Score 5523.5;  DB 2;  Length 1101;
Best Local Similarity  95.2%;  Pred. No. 0;
Matches 1049;  Conservative  21;  Mismatches  31;  Indels  1;  Gaps  1;

Qy    1 MELENYEQPVVLREDNRRRRRMKPRSTAASLSMELIPIEFVLPTSQRNTKTPETALLH 60
Db    1 MELENYKQPVVLREDNCRRRRMKPRS-AASLSSMELIPIEFVLPTSQRKCKSPETALLH 59

Qy   61 VAGHGNVEQMKAQVWLRALETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLD 120
Db   60 VAGHGNVEQMKAQVWLRALETSVAADFYHRLGPHHFLLLYQKKGQWYEIYDKYQVVQTLD 119

Qy  121 CLRYWKVLHRSPGQIHVVQRHAPSEETLAPQRQLNALIGYDVTDVSNVHDDELEFTRRRL 180
Db  120 CLRYWKATHRSPGQIHLVQRHPPSEESQAFQRQLTALIGYDVTDVSNVHDDELEFTRRGL 179

Qy  181 VTPRMAEVAGRDPKLYAMHPWVTSKPLPEYLLKITNCVFIVIHRSTTSQTIKVSADDT 240
Db  180 VTPRMAEVASRDPKLYAMHPWVTSKPLPEYLWKKIANNCIFIVIHRSTTSQTIKVSPDDT 239

Qy  241 PGTIIQSFFTKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG 300
Db  240 PGAIIQSFFTKMAKKKSLMDIPESQSEQDFVLRVCGRDEYLVGETPIKNFQWVRHCLKNG 299

Qy  301 EEIHLVLDTPPDPALDEVRKEBWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK 360
Db  300 EEIHVVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK 359

Qy  361 FRVKIRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTSPKPFTEEVLMNVWLEFSIKI 420
Db  360 FRVKIRGIDIPVLPRNTDLTVFVEANIQHGQQVLCQRRTSPKPFTEEVLMNVWLEFSIKI 419

Qy  421 KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYVNLLLIDHRFLLRHGEY 480
Db  420 KDLPKGALLNLQIYCGKAPALSSKASAESPSSEESKGKVRLLYVNLLLIDHRFLLRRGEY 479

Qy  481 VLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKGHRPTDPPEG 540
Db  480 VLHMWQISCKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKGHQPTDPPEG 539

Qy  541 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQ 600
Db  540 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKHPKAYPKLFSSVKWGQ 599

Qy  601 QEIVAKTYQLLAAKREVWDQSALDVGLITMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 660
Db  600 QEIVAKTYQLLARREVWDQSALDVGLITMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 659

Qy  661 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY 720
Db  660 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY 719

Qy  721 LRGCGTAMLHDFTQQVQVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLP 780
Db  720 LRGCGTAMLHDFTQQVQVIEMLQKVTLDIKSLSAEKYDVSSQVISQLKQKLENLQNSQLP 779

Qy  781 QSFRVPYDPGLKAGALVIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ 840
Db  780 ESFRVPYDPGLKAGALAIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ 839

Qy  841 DMLILQILRIMESIWETESLDLCLLPYGCISTGDKIGMEIVKDATTIAKIQQSTVGNTG 900
Db  840 DMLILQILRIMESIWETESLDLCLLPYGCISTGDKIGMEIVKDATTIAKIQQSTVGNTG 899

Qy  901 AFKDEVLSHWLKEKCPIEKFQAAVERPVYSCAGYCVATFVLGIGDRHNDNIMISETGNL 960
Db  900 AFKDEVLNHWLKEKSPTEEKFQAAVERRVYSCAGYCVATFVLGIGDRHNDNIMITETGNL 959

Qy  961 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYALL 1020
Db  960 FHIDFGHILGNYKSFLGINKERVVPFVLTPDFLFVMGTSGKKTSPHFQKFQDICVKAYALAL 1019

Qy 1021 RHHTNLLILFSVMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW 1080
Db 1020 RHHTNLLILFSVMLMTGMPQLTSKEDIEYIRDALTVGKNEEDAKKYFLDQIEVCRDKGW 1079

Qy 1081 TVQFNWFLHLVLGIKQGEKHSA 1102
Db 1080 TVQFNWFLHLVLGIKQGEKHSA 1101
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RESULT 8
US-09-225-170-14
; Sequence 14, Application US/09225170
; Patent No. 6017763
; GENERAL INFORMATION:
;   APPLICANT: Stephens, Len
;   APPLICANT: Hawkins, Phillip Thomas
;   APPLICANT: Braselmann, Sylvia
;   TITLE OF INVENTION: G-BETA-GAMMA REGULATED
;   TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
;   NUMBER OF SEQUENCES: 14
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Pennie & Edmonds, LLP
;     STREET: 1155 Avenue of the Americas
;     CITY: New York
;     STATE: NY
;     COUNTRY: USA
;     ZIP: 10036-2811
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: Windows
;     SOFTWARE: FastSEQ for Windows Version 2.0b
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/225,170
;     FILING DATE:
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 08/916,917
;     FILING DATE: 15-AUG-1997
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Abrams, Samuel B
;     REGISTRATION NUMBER: 30,605
;     REFERENCE/DOCKET NUMBER: 8549-0006-999
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 650-493-4935
;     TELEFAX: 650-493-5556
;     TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 14:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 1101 amino acids
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                                                FILING DATE:  13 April 1993
                                           ;    ATTORNEY/AGENT INFORMATION:
                                           ;        NAME:  Pasqualini, Patricia A.
                                           ;        REGISTRATION NUMBER:  34,894
                                           ;        REFERENCE/DOCKET NUMBER:  LUD 5256
                                           ;    TELECOMMUNICATION INFORMATION:
                                           ;        TELEPHONE:  (212) 688-9200
                                           ;        TELEFAX:  (212) 838-3884
                                           ;    INFORMATION FOR SEQ ID NO: 37:
                                           ;    SEQUENCE CHARACTERISTICS:
                                           ;        LENGTH:  1069 amino acids
                                           ;        TYPE:  amino acid
                                           ;        STRANDEDNESS:  single
                                           ;        TOPOLOGY:  linear

US-08-162-081B-37

Query Match             25.3%;  Score 1465.5;  DB 2;  Length 1069;
Best Local Similarity   33.5%;  Pred. No. 1.6e-133;
Matches  382;  Conservative  204;  Mismatches  405;  Indels  149;  Gaps  39;

Qy   23  MKPRSTAASLSSMELIP---IEFVLPTSQRNTKTPETALLHVAGHGNVEQMKAQWLRA    78
Db    1  MPPRPSSGELWGIHLMPPRILVECLLPNGMIVI------LECLREATLITIKHELFKEA   53

Qy   79  LETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLDCLRYWKVLHRSPGQIHVV  138
Db   54  RKYPL-----HQLLQDESSYIFVSVTQEAEREFFDPETRRLCDLRLFQPF-----LKVI  102

Qy  139  QRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRLVTPRMAEVAGRD------  192
Db  103  EPVGNREEKI-LNREIGPAIGMPVCEFDMVKDPEVQDPRRNILNVCKEAVDLRDLNSPHS  161

Qy  193  PKLYAMHPWVTSKP-LPEYLLKKITNNCVFIV-----HRSTTSQTIKVSADDTPGTIL   245
Db  162  RAMVYYPPNVESSPELPKHIYNKLDKGQIIVIWVIVSPNNDKQKYTLKINHDCVPEQVI  221

Qy  246  QSFFTKMAKKKSLMDIPES------QNERDFVLRVCGDEYLVGETPIKNFQWVRQCLKN  299
Db  222  AEAIRK--KTRSMLLSSEQLKLCVLEYQQGKYIIKVCGCDEYFLEKYPLSQYKYIRSCIML  279

Qy  300  GEEIHLVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLT-----IHGKDHESVFTVSL  354
Db  280  GRMPNLML------MAKESLYSQLPM-DCFTMPSYSRISTATPYMNGE----TSTKSL   327

Qy  355  WDCDRKFRVK---------IRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTSPKPF  404
Db  328  WVINSALRIKILCATYVNVNIRDID---------KIYVRTGIYHGGEPLCDNVNTQRVP  377

Qy  405  TEEVLWNVWLEFSIKIKDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYYV  464
Db  378  CSNPRWNEWLNYDIYIPDLPRAARLCLSI-C----SVKGRKGA-------KEEHCPLAWG  425

Qy  465  NLLLIDHRFLLRHGEYVLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYC  524
Db  426  NINLPFDYTDTLVSGRMALNLWPVPHGLED--LLNPIGVT-GSNPNKE-TPCLELEFDWFS  481

Qy  525  HPIALPKHRPTPDPEGDRV-----------RAEMPNQLR--KQLEAIIATDPLN      565
Db  482  SVVKFPDMSVIEEHANWSVSREAGFSYSHAGLSNRLARDNELRENDKEQLRAICTRDPLS  541

Qy  566  PLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQQEIVAKTYQLLAKREWWDQSALDVG  625
Db  542  EITEQEKDFLWSRHYCVTIPBILPKLLLSVKWNSRDEVAQMYCL-----VKDWPPIKPB  596

Qy  626  LTMQLLDCNFSDENVRAIAVQKLES-LEDDDVLHYLLQLVQAVKFEYHDSALARFLLKR  684
Db  597  QAMELLDCNYPDPMVRGPAVRCLEKYLTDDKLSQYLIQLVQVLKYEQYLDNLLVRFLLKK  656

Qy  685  GLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAYLRGCGTAMLHDFTQQVQVIDMLQK  744
Db  657  ALTNQRIGHFFWHLKSEM-HNKTVSQRFGLLLESYCRACGMYIKH-LNRQVEAMEKLIN  714

Qy  745  VTIDIKSLSAEKYDVSSQVISQLKQKLENLQN---LNLPQSFRVPYDPGLKAGALVIEKC  801

Db  417  SESKGKVRLLYYVNLLLIDHRFLLRRGEYVLHMWQISGKGEDQSFNADKLTSATNPDKE   476
Qy  512  NSMSISILLDNYCHPIALPKGHRPTPDPEGDRVRAEMPNQLRKQLEAIIATDPLNPLTAED  571
Db  477  NSMSISILLDNYCHPIALPKGHQPTPDPEGDRVRAEMPNQLRKQLEAIIATDPLNPLTAED  536

Qy  572  KELLWHFRYESLKDPKAYPKLFSSVKWGQQEIVAKTYQLLAKREVWDQSALDVGLTMQLL  631
Db  537  KELLWHFRYESLKHPKAYPKLFSSVKWGQQEIVAKTYQLLARREVWDQSALDVGLTMQLL  596

Qy  632  DCNFSDENVRAIAVQKLESLEDDDVLHYLLQLVQAVKFEYHDSALARFLLKRGLRNKRI   691
Db  597  DCNFSDENVRAIAVQKLESLEDDDVLHYLLQLVQAVKFEYHDSALARFLLKRGLRNKRI   656

Qy  692  GHFLFWFLRSEIAQSRHYQQRFAVILEAYLRGCGTAMLHDFTQQVQVIDMLQKVTIDIKS  751
Db  657  GHFLFWFLRSEIAQSRHYQQRFAVILEAYLRGCGTAMLHDFTQQVQVIEMLQKVTLDIKS  716

Qy  752  LSAEKYDVSSQVISQLKQKLENLQNLNLPQSFRVPYDPGLKAGALVIEKCKVMASKKPL   811
Db  717  LSAEKYDVSSQVISQLKQKLENLQNSQLPESFRVPYDPGLKAGALAIEKCKVMASKKPL   776

Qy  812  WLEFKCADPTALSNETIGIIFKHGDDLRQDMLILQLIRIMESIWETESLDLCLLPYGCIS  871
Db  777  WLEFKCADPTALSNETIGIIFKHGDDLRQDMLILQLIRIMESIWETESLDLCLLPYGCIS  836

Qy  872  TGDKIGMIEIVKDATTIAKIQQSTVGNTGAFKDEVLSHWLKEKCPIEEKFQAAVERFVYS  931
Db  837  TGDKIGMIEIVKDATTIAKIQQSTVGNTGAFKDEVLNHWLKEKSPTEEKFQAAVERFVYS  896

Qy  932  CAGYCVATFVLGIGDRHNDNIMISETGNLFHIDFGHILGNYKSPLGINKERVPFVLTPDF  991
Db  897  CAGYCVATFVLGIGDRHNDNIMITETGNLFHIDFGHILGNYKSPLGINKERVPFVLTPDF  956

Qy  992  LFVMGTSGKKTSLHFQKFQDVCVKAYLALRHHTNLLIILFSMMLMTGMPQLTSKEDIEYI 1051
Db  957  LFVMGTSGKKTSPHFQKFQDICVKAYLALRHHTNLLIILFSMMLMTGMPQLTSKEDIEYI 1016

Qy 1052  RDALTVGKSEEDAKKYFLDQIEV 1074
Db 1017  RDALTVGKNEEDAKKYFLDQIEV 1039
```

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Best Local Similarity   33.5%;  Pred. No. 1.6e-133;
Matches 382;  Conservative 204;  Mismatches 405;  Indels 149;  Gaps 39;

Qy    23  MKPRSTAASLSSMELIP---IEFVLPTSQRNTKTPETALLHVAGHGNVEQMKAQVWLRA     78
             :. :   :  : ||   :     |:  |||  :
Db     1  MPPRPSSGELWGIHLMPPRILVECLLPNGMIVT------LECLREATLITIKHELFKEA     53

Qy    79  LETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLDCLRYWKVLHRSPGQIHVV    138
          ::. :  .            : ::.  .|.             |||       :.  LKVI
Db    54  RKYPL-----HQLLQDESSYIFVSVTQEAEREEFFDETRRLCDLRLFQPF------LKVI    102

Qy   139  QRHAPSEETLAFQRQLNALIGVDVTDVSNVHDDELEFTRRRIVTPRMAEVAGRD------    192
             . .     :..  . :  :|        :.  :.|  . :   ||
Db   103  EPVGNREEKI-LNREIGFAIGMPVCEFDMVKDPEVQDPRRNILNVCKEAVDLRDLNSPHS    161

Qy   193  PKLYAMHPWVTSKP-LPEYLLKKITNNCVFIVI------HRSTTSQTIKVSADDTPGTIL    245
           .: .   | . .|  ||   : ::..  .||||:.:..
Db   162  RAMVVYPPNVESSPELPKGHIYNKLDKGQIIVVIWIVISPNNDKQKYTLKINHDCVPEQVI   221

Qy   246  QSFFTKVMAKKKGLSMDIPES------QNERDFVLRVCGRDEVLVGETPIKNFQWVRQCLKN   299
                :: :         :..        ||  . ::.|  :    ::   .:  .::
Db   222  AEAIRK--KTRSMLLSSEQLKLCVLEYGKYILKVCGGDEYPLEKYPLSQYKYIRSCIML    279

Qy   300  GEEIHLVLDTPPDPALDEVRKBEWPLVDDCTGVTGYHEQLT---IHGKDHESVFTVSL     354
              . :||       : :.      ||            :.    ::: .:    TSTKSL
Db   280  GRMPNLML------MAKESLYSQLPM--DCFTMPSYSRRISTATPYMNGE---TSTKSL    327

Qy   355  WDCDRKFRVK----------IRGIDIPVLPRTADLTVFVEANIQYGQGQVLCQRRTSPKPF   404
          |  .  ::.            :. |:  .|        : .  :.||.|||      .:. VP
Db   328  WVINSALRIKILCATYVNVNIRDID----------KIYVRTGIYHGGEPLCDNVNTQRVP    377

Qy   405  TEBVLWNVWLEFSIKIKDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYYV   464
             :.   .|  .|  ||.|    : ||:|.: :     :      KEEHCPLAWG
Db   378  CSNPRWNEWLNYDIYIFPDLPRAARLCLSI-C------SVKGRKGA------           425

Qy   465  NLLLIDHRFLLRHGEYLHMWQLSGKEDQGSFNADKLTSATNPDKENSMSISILLDNYC    524
           :|: |. |::|||:||:::|   | ||           ||:   .:.      :.::
Db   426  NINLFDYTDTLVSGKMALNLWPVPHGLED--LLNPIGVT-GSNPNKE-TPCLELEFDWFS    481

Qy   525  HPIALPKHRPTPDPEGDRV-----------RAEMPNQLR----KQLBAIIATDPLN       565
           :|  .     |:. ||||.             |  |:|      |:|   :  :|  :
Db   482  SVVKFPDMSVIEHANWSVREAGFSYSHAGLSNRLARDNELRENDKEQLRAICTRDPLS    541

Qy   566  PLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQQEIVAKTYQLLAKREVWDQSALDVG   625
           :|.|:|: ||.||:.||.  |: .|||||.|||..|:||..:  |.     VKDWPIKPE
Db   542  EITEQEKDFLWSHRHYCVTIPEILPKLLSVKWNSRDEVAQMYCL-----VKDWPIKPE    596

Qy   626  LTMQLLDCNFSDENVRAIAVQKLES-LEDDDVLHYLLQLVQAVKFEYHDSALARFLLKR    684
           :|:.|||||:.| .|| .|||. :| ||||:.|.|:|||||.:|:.| |.|:.||||:
Db   597  QAMELLDCNYPDPMVRGFAVRCLEKYLTDDKLSQYLIQLVQVLKYQYLDNLLVRFLLKK    656

Qy   685  GLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAYLRGCGTAMLHDFTQQVQVIDMLQK   744
           .|.|.||..||.|:|:||: .:.:.||:||.:|||::|.||.|:|: |. |||. :::||
Db   657  ALTNQRIDRFFFWHLKSEM-HNKTVSQRFGLLLESYCRACGMYLKH-LNRQVEAMEKLIN   714

Qy   745  VTIDIKSLSAEKYDVSSQVISQLQKLENLQN--LNLPQSFRVPYDPGLKAGALVIEKC    801
            |.|:  |. |::  : .  :..|:. |.    ::.      :.||| |. |:|:|:|
Db   715  LT-DI--LKQEKKDETQKV--QMKFLVEQMRRPDFMDALQGFLSPLNPAHQLGNLRLEEC   769

Qy   802  KVMASKKKPLWLEFKCADPTALS-----NETIGIIFKHGDDLRQDMLILQILRIMESIW    855
           ::::|:|||||| :   . .: .      |.||:||.|||||||||| |||||||||.||
Db   770  RIMSSAKRPLWLNWE--NPDIMSELLFQNNE---IIFKNGDDLRQDMLTLQIIRIMENIW   824

Qy   856  ETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTGA--FKDEVLSHWLKE    913
           :.: |||.:|||||:|||| :|:|:|||:..|| :|  | :|  |   |::. |.:||||
Db   825  QNQGLDLRMLPYGCLSIGDCVGLIEVVRNSHTIMQI-QCKGGLKGALQFNSHTLHQWLKD   883

Qy   914  KCPIEBKFQAAVERFVVSCAGYCVATFVLGIGDRHNDNIMISETGNLFHIDFGHILGNYK    973
           |   | |::  |:.|..:|||||||||:|||||||||.||: .:|.|||||||||.|::|
Db   884  KNK-GEIYDAAIDLFTRSCAGYCVATFILGIGDRHNSNIMVKDDGQLFHIDFGHFLDHKK   942

Qy   974  SFLGINKERVPFVLTPDFLFVMGTSGKK--TSLHFQKFQDVCVKAYLALRHTNLLILF   1031
           |::|  |:|||||:| ||| |:  :.    ||||| ||||||||||:|:|: ||| ||
Db   943  KKFGYKRERVPFVLITQDFLIVISKGAQECTKTREFERFQEMCYKAYLAIRQHANLFINLF  1002

Qy  1032  SMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGWTVQFNWFLHLV  1091
           ||||.:||| | |::|:||||.:|::.|:|:||: |:::|:  ..| ||||:.:.||:||
Db  1003  SMMLGSGMPELQSFDDIAYIRKTLALDKTEQEALEYFMKQMNDAHHGGWTTKMDWIFHTI  1062
```

RESULT 12

US-08-780-872-37

US-08-780-872-37

Query Match 25.3%; Score 1465.5; DB 2; Length 1069;

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Qy   193  PKLYAMPWVTSKP-LPEYLLKKITNNCVFIVI-----HRSTTSQTIKVSADDTPGTIL   245
          :::|:|                                    :::|
Db   162  RAMYVYPPNVESSPELPKGIYNKLDKGQIIIVIWVIVSPNNDKQKYTLKINHDCVPEQVI 221

Qy   246  QSFFTKMAKKKSLMDIPBS-------QNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKN 299
Db   222  ABAIRK--KTRSMLLSSEQLKLCVLEYQGKYLKVCGCDEYFLEKYPLSQYYIRSCIML   279

Qy   300  GEEIHLVLDTPPDALDEVRKEEWPLVDDCTGVTGYHEQLT-----IHGKDHESVFTVSL  354
Db   280  GRMPNLML------MAKESLYSQLPM-DCFTMPSYSRRISTATPYMNGE----TSTKSL  327

Qy   355  WDCDRKFRVK---------IRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTSPKPF   404
Db   328  WVINSALRIKILCATYVNVNIRDID-------KIYVRTGIYHGGEPLCDNVNTQRVP    377

Qy   405  TEEVLWNVWLEFSIKIKDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYYV  464
Db   378  CSNPRWNEWLNYDIYIPDLPRAARLCLSI-C----SVKGRKGA-------KEEHCPLAWG  425

Qy   465  NLLLIDHRFLLRHGEYVLHMWOLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYC  524
Db   426  NINLFDYTDTLVSGKMALNLWPVPHGLED--LLNPIGVT-GSNPNKE-TPCLELEFDWFS  481

Qy   525  HPIALPKHRPTPDPEGDRV------------RAEMPNQLR---KQLEAIIATDPLN     565
Db   482  SVVKFPDMSVIEEHANWSVSREAGFSYSHAGLSNRLARDNELRENDKEQLRAICTRDPLS  541

Qy   566  PLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQQEIVAKTYQLLAKREVWDQSALDVG  625
Db   542  EITEQEKDFLWSHRHYCVTIPEILPKLLSVKWNSRDEVAQMYCL-----VKDWPPIKPB  596

Qy   626  LTMQLLDCNFSDENVRAIAVQKLES-LEDDDVLHYLLQLVQAVKPEPYHDSALARFLLKR  684
Db   597  QAMELLDCNYPDMVRGFAVRCLEKVLTDDKLSQYIQLVQVLKYEQYLDNLLVRFLLKK   656

Qy   685  GLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAYLRGCGTAMLHDFTQQVQVIDMLQK  744
Db   657  ALTNQRIGHFFFWHLKSEM-HNKTVSQRFGLLLESYCRACGMYLKH-LNRQVEAMEKLIN  714

Qy   745  VTIDIKSLSAEKYDVSSQVISOLKQKLENLQN---LNLPQSFRVPYDPGLKAGALVIEKC  801
Db   715  LT-DI--LKQEKKDETQKV--QMKFLVEBQMRRPDFMDALQGFLSPLNPAHQLGNLRIEEC 769

Qy   802  KVMASKKKPLWLEFKCADPTALS------NETIGIIFKHGDDLRQDMLILQILRIMESIW  855
Db   770  RIMSSAKRPLWLNWE--NPDIMSELLFQNNE---IIFKNGDDLRQDMLTLQIIRIMENIW  824

Qy   856  ETESLDLCLLPYGCISTGDKIGMEIVKDATTIAKIQQSTVGNTGA--FKDEVLSHWLKE  913
Db   825  QNQGLDLRMLPYGCLSIGDCVGLIEVVRNSHTIMQI-QCKGGLKGALQFNSHTLHQWLKD  883

Qy   914  KCPIEKFQAAVERFVVSCAGYCVATFVLGIGDRHNDNIMISETGNLFHIDFGHILGNYK   973
Db   884  KNK-GEIYDAAIDLFTRSCAGYCVATFILGIGDRHNSNIMVKDDGQLFHIDFGHFLDHKK  942

Qy   974  SFLGINKERVPFVLTPDFLFVNGTSGKK--TSLHFQKFQDVCVKAYLALRHHTNLLILLF  1031
Db   943  KKFGYKRERVPFVLTQDFLIVISKGAQECTKREFERFQEMCKYAYLAIRQHANLFINLF  1002

Qy   1032 SMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGWTVQFNWFLHLV 1091
Db   1003 SMMLGSGMPELQSFDDIAYIRKTLALDKTEQEALEYFMKQMNDAHHGGWTTKMDWIFHTI 1062
```

```
Query Match      25.3%;   Score 1465/5;   DB 3;   Length 1069;
Best Local Similarity   33.5%;   Pred. No. 1.6e-133;
Matches   382;  Conservative 204;  Mismatches 405;  Indels 149;  Gaps 39;

Qy   23   MKPRSTAASLSSMELIP---IEFVLPTSQRNTKTPETALLHVACHGNVEQMKAQVWLRA  78
Db   1    MPPRPSSGELWGIHLMPPRILVECLLPNGMIVT------LECLRBATLITIKIELFKEA  53

Qy   79   LETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLDCLRYWKVLHRSPGQIHVV  138
Db   54   RKYPL-----HQLLQDESSYIFVSVTQBABREEFFDETRRLCDLRLFQPF-----LKVI  102

Qy   139  QRHAPSEETLAFQRQLNALICYDVTDVSNVHDDELEFTRRRLVTPRMAEVAGRD------  192
Db   103  EPVGNREEKI-LNREIGFAIGMPVCEFDMVKDPEVQDFRRNILNVCKEAVDLRDLNSPHS  161
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Db   943  KKFGYKRERVPFVLTQDFLIVISKGAQECTKREFERFQEMCKYAYLAIRQHANLFINLF  1002
Qy   1032 SMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGWTVQFNWFLHLV 1091
Db   1003 SMMLGSGMPELQSFDDIAYIRKTLALDKTEQEALEYFMKQMNDAHHGGWTTKMDWIFHTI 1062
```

```
;   APPLICANT: Stefano; Gout, Ivan Tarasovitch
;   TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
;   TITLE OF INVENTION: THEIR PREPARATION AND USE
;   NUMBER OF SEQUENCES: 50
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Felfe & Lynch
;     STREET: 805 Third Avenue
;     CITY: New York
;     STATE: New York
;     COUNTRY: USA
;     ZIP: 10022
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
;   COMPUTER: IBM PS/2
;   OPERATING SYSTEM: PC-DOS
;   SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/162,081B
;   FILING DATE: February 7, 1994
;   CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: PCT/GB93/00761
;   FILING DATE: 13 April 1993
; ATTORNEY/AGENT INFORMATION:
;   NAME: Pasqualini, Patricia A.
;   REGISTRATION NUMBER: 34,894
;   REFERENCE/DOCKET NUMBER: LUD 5256
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212) 688-9200
;   TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 36:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 1080 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
; US-08-162-081B-36

Query Match             25.3%;  Score 1463.5;  DB 2;  Length 1080;
Best Local Similarity   33.3%;  Pred. No. 2.5e-133;
Matches  386;  Conservative  206;  Mismatches  406;  Indels  161;  Gaps  41;

Qy    23 MKPRSTAASLSSMELIP----IEFVLPTSQRNTKTPETALLHVAGHGNVEQMKAQVWLRA 78
                         | :: :|| ||||:|         | ::: ||
Db     1 MPPRPSSGELWGIHLMPPRILVECLLPNGMIVT------LECLREATLVTIKHELFKEA 53

Qy    79 LETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLDCLRYWKVLHRSPGQIHVV 138
                                   :| | ||
Db    54 RKYPL-----HQLLQDESSYIFVSVTQEAEREBFFDETRRLCDLRLFQPF------LKVI 102

Qy   139 QRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRLVTPRMAEVAGRD------ 192
             :: : ||      | || |   |  | ::
Db   103 EPVGNREEKI-LNRBIGFAIGMPVCEFDMVKDPEVQDFRRNILNVCKEAVDLRDLNSPHS 161

Qy   193 PKLIYAMHPWTSKP-LPEYLLKKITNNCVFIVI------HRSTTSQTIKVSADDTPGTIL 245
             | :| | : :|  ||  ::: |  ||
Db   162 RAMYVVPPHVESSPELPKHIYNKLDRGQIIVVIWVIVSPNNDKQKYTLKINHDCVPEQVI 221

Qy   246 QSFFTKMAKKKSLMDIPES-------QNERDFVLRVCGRDEYLVGETPIKNFQWRQCLKN 299
             ||        |: ||          || | | || ||||| ::
Db   222 AEAIRK--KTRSMLLSSEQLKLCVLEYQGKYILKVCGCDEYFLEKYPLSQYKYIRSCIML 279

Qy   300 GEEIHLVLDTPPDPALDEVRKE-----EWPLVDDCTGVTGHEQLT-----IHGKDHESVF 350
                 || || ||           :| |  ||| | || ::  ::
Db   280 GRM--------PNLKMWAKESLYSQLPM--DCFTMPSYSRRISTATPYMNGE----TS 323

Qy   351 TVSLWDCDRKFRVK-------IRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTS 400
             | |||  ||  |       | |:: |||  || :  :  | |:
Db   324 TKSLWVINRALRIKILCATYVNLNIRDID--------KIYVRTGIYHGGEPLCDNVNT 373

Qy   401 PKPFTEEVLNNVWLEFSIKIKDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQL 460
              : |  ::|  |  || | | |  ||:  |   |          :
Db   374 QRVPCSNPRNWEWLNVDIYIPDLPRAAARLCLSI-C----SVKGRKGA------KEEHCP 421

Qy   461 LYYVNLLLIDHRPLLRHGEYVLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILL 520
               :: | | : :  || ::: | ::||| ||
Db   422 LAWGNINLFDYTDTLVSGKMAlNLWPVPHGLED--LLNPIGVT-GSNPNKE-TPCLELEF 477

Qy   521 DNYCHPIALPKHRPTPDPEGDRV---------------RAEMPNQLR----KQLEAIIAT 561
             |  |  ||  |  |                       |  | |:      ||| | :
Db   478 DWFSSVVKFPDMSVIEEHANWSVSREAGFSYSHAGLSNRLARDNELRENDKSQLKAISTR 537

Qy   562 DPLNPLPAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQQEIVAKYQLLAKREVWDQSA 621
             ||    ||:|: ||  ||    ||| | ||| ||| ||||  | ||||| ||:
Db   538 DPLSEITEQEKDFLWSRHYCVTIPEILPKLLLSVKWNSRDEVAQMYCL-----VKDWPP 592

Qy   622 LDVGLTMQLLDCNFSDENVRAIAVQKLES-LBDDDVLHYLLQLVQAVKFEPYHDSALARF 680
             | |  | |||||| | | ||  |   |     | |||| ||||||: | ||   | | |
Db   593 IKPEQAMELLDCNYPDPMVRGFAVRCLEKYLTDDKLSQYLIQLVQVLKYEQYLDNLLVRF 652

Qy   681 LLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFPAVILEAYLRGCGTAMLHDFTQQVQID 740
             ||: | :|:||||| || ||||  |  || |  |   || ||| | |  |  :||| |
Db   653 LLKKALTNQRIGHFFWHLKSEM-HNKTVSQRFGLLLESYCRACGMYLKH-LNRQVEAME 710

Qy   741 MLQKVTIDIKSLSAEKYDVSSQVISQLQKLENLQN--LNLPQSFRVPYDPGLKAGALV 797
             :|: :  | :| |  | |      : |:|: |:||       || |  | | :| |||:
Db   711 KLINLT-DI--LKQERKDETQKV--QMKFLVEQMRRPDFMDALQGLLSPLNPAHQLGNLR 765

Qy   798 IEBCKVMASKKKPLWLEFKCADPTALS-------NETIGIIFKHGDDLRQDMLILQILRIM 851
             :| || ::|:|| |||   :                  |||| ||||||||| |||:|||
Db   766 LKECRIMSSAKRPlWLNWB---NPDIMSLLFQNNE---IIFKNGDDLRQDMLTLQIIRIM 820

Qy   852 ESIWETESLDLCLLPYGCISTGDKIGMEIVKDATTIAKIQQSTVGNTGA--FKDEVLSH 909
             | ||  | ||| :|||| | ||| :|:|||  | |  | |    | | |   :  : ||
Db   821 ENIWQNQGLDLRMLPYGCLSIGDCVGLIEVVRNSHTMQI-QCKGGLKGALQFNSHTLHQ 879

Qy   910 WLKEKCPIBEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNLPHIDFGHIL 969
             ||::| |  |:   :  ||| |||||||||| ||||||||:|||: : | ||||||||:|
Db   880 WLKDKNK-GEIYDAAIDLFTRSCAGYCVATFILGIGDRHNSNIMVKDDGQLPHIDFGHFL 938

Qy   970 GNYKSFLGINKERVPFVLTPDFLFVMGTSGKK--TSLHFQKFQDVCVKAYlALRHHTNLL 1027
              : :| || :||||||||| |||:| : | |    : |: |:: |||||||| :: :||
Db   939 DHKKKKFGYKRERVPFVLTQDFLIVISKGAQECKTKTREFERFQEMCKAYLAIRQHANLF 998

Qy  1028 IILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGWTVQFNWF 1087
             |:|||||| :||| |:  :|: :|| ||::|| :| |: || |: | :: || |: |:|
Db   999 INlFSMMLGSGMPELQSFDDIAVIRKTlALDKTEQEALEYFMKQMNDAHHGGWTTKMDWI 1058

Qy  1088 LHLV----LGIKQGEKHSA 1102
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Db  1059 FHTIKQHALNXKITEKMKA 1077


RESULT 15
US-08-780-872-36
; Sequence 36, Application US/08780872
; Patent No. 5846824
; GENERAL INFORMATION:
;   APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
;   APPLICANT: Bala, Waterfield, Michael Derek; Parker, Peter
;   APPLICANT: Joseph; Otsu, Masayuki; Panayotou, George; Volinia,
;   APPLICANT: Stefano; Gout, Ivan Tarasovitch
;   TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
;   TITLE OF INVENTION: THEIR PREPARATION AND USE
;   NUMBER OF SEQUENCES: 50
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Felfe & Lynch
;     STREET: 805 Third Avenue
;     CITY: New York
;     STATE: New York
;     COUNTRY: USA
;     ZIP: 10022
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
;   COMPUTER: IBM PS/2
;   OPERATING SYSTEM: PC-DOS
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     SOFTWARE:  Wordperfect
CURRENT APPLICATION DATA:
     APPLICATION NUMBER: US/08/780,872
     FILING DATE: 09-JAN-1997
     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
     APPLICATION NUMBER: 08/162,081
     FILING DATE:  February 7, 1994
     APPLICATION NUMBER: PCT/GB93/00761
     FILING DATE:  13 April 1993
ATTORNEY/AGENT INFORMATION:
     NAME:  Pasqualini, Patricia A.
     REGISTRATION NUMBER: 34,894
     REFERENCE/DOCKET NUMBER: LUD 5256
TELECOMMUNICATION INFORMATION:
     TELEPHONE:  (212) 688-9200
     TELEFAX:  (212) 838-3884
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
     LENGTH:  1080 amino acids
     TYPE:  amino acid
     STRANDEDNESS:  single
     TOPOLOGY:  linear
US-08-780-872-36

Query Match       25.3%;   Score 1463.5;  DB 2;   Length 1080;
Best Local Similarity   33.3%;   Pred. No. 2.5e-133;
Matches  386;   Conservative  206;  Mismatches  406;  Indels  161;  Gaps   41;
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Qy    23  MKPRSTAASLSSMELIP----IEBVLPTSQRNTKTPETALLHVAGHGNVEQMKAQVWLRA   78
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Db     1  MPPRPSSGELWGIHLMPPRIIVECLLPNGMIVT------LECLREATLVTIIKHELFKEA   53

Qy    79  LETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLDCLRYWKVLHRSPGQIHVV  138
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Db    54  RKYPL-----HQLLQDESSYIFVSVTQEAEREEFFDETRRLCDLRLFQPF-----LKVI  102

Qy   139  QRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRLVTPRMAEVAGRD------  192
              |   ::| |  :|::                 |::||:|:|:| :
Db   103  EPVGNREEKI-LNREIGFAIGMPVCEFDMVKDPEVQDFRRNILNVCKEAVDLRDLNSPHS  161

Qy   193  PKLYAVHPWVTSKP-LPEYLLKKITNNCVFVI-----HRSTTSQTIKVSADDTPGTIL  245
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Db   162  RAMYVYPPHVSSSPELPKHIYNKLDRGQIIVIWIVSPNNDKQKYTLKINHDCVPEQVI  221

Qy   246  QSFFTKWAKKKSLMDIPES--------QNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKQN  299
              :||    |::|:|          |:||::||:||:|| :|| |::||:||::|:
Db   222  AEAIRK--KTRSMLLSSEQLKLCVLEYQGKYILKVCGCDEYFLEKYPLSQYKYIRSCIML  279

Qy   300  GEEIHLVLDTPDPALDEVRKE----EWPLVDDCTGVTGYHEQLI-----IHGKDHESVF  350
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Db   280  GRM---------PNLKMMAXESLYSQLPM--DCFTMPSYSRRISTATPYMNGE----TS  323

Qy   351  TVSLWDCDRKFRVK---------IRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTS  400
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Db   324  TKSLWVINRALRIKILCATYVNLNIRDID--------KIYVRTGIYHGGEPLCDNVNT  373

Qy   401  PKPFTEEVLMNVWLEFSIKIKDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQL  460
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Db   374  QRVPCSNPRWNEWLNYDIYIPDLPRAARLCLSI-C------SVKGRKGA------KEEHCP  421

Qy   461  LYYVNLLLIDHRFLLRHGEYVLHMWQLSKGEDQGSFNADKLTSATNPDKENSMSISILL  520
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Db   422  LAWGNINLFDYTDTLVSGKMALNLWPVPHGLED--LLNPIGVT-GSNPNKE-TPCLELEF  477

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Db   478  DWFSSVVKFPDMSVIEEHANWSVSREAGFSYSHAGLSNRLARDNELRENDKEQLKAISTR  537

Qy   562  DPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQQEIVAKYQLLAKREVWDQSA  621
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Db   593  IKPEQAMELLDCNYPDPMVRGFPAVRCLEKYLTDDKLSQYLIQLVQVLKYEQYLDNLLVRF  652

Qy   681  LLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAYLRGCGTAMLHDFTQQVQVID  740
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Db   653  LLKKALTNQRIGHFFFWHLKSEM-HNKTVSQRFGLLLESYCRACGMYLKH-LNRQVEAME  710

Qy   741  MLQKVTIDIKSLSAEKYDVSSQVISQLKQLENLQN---LNLPQSFRVPYDPGLKAGALV  797
              ||:|:||||:|| ::||||::|:|||||:||:||    |::|:||:|| ||||:|:||
Db   711  KLINLT-DI--LKQERKDETQKV--QMKFLVEQMRRPDFMDALQGLLSPLNPAHQLGNLR  765

Qy   798  IEKCKVNASKKKPLWLEPKCADPTALS------NETIGIIFKHGDDLRQDMLILQILRIM  851
              ::::::  :|  :|:|| :: :::      :|| ||:|:|:||::|:|:||::|:||||
Db   766  LKECRIMSSAKRPLWLNWE--NPDIMSELLFQNNE---IIFKNGDDLRQDMLTLQIIRIM  820

Qy   852  ESTWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTGA--FKDEVLSH  909
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Db   821  ENIWQNQGJDLRMLPYGCLSIGDCVGLIEVVRNSHTIMQI-QCKGGLKGALQFNSHTLHQ  879

Qy   910  WLKEKCPIBEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNLFHIDFGHIL  969
              ||:|| | |:||  :   | ::||||||||:|||||||:|:|:|:  ||:|||||||||:
Db   880  WLKDKNK-GEIYDAAIDLFTRSCAGYCVATFILGIGDRHNSNIMVKDDGQLFHIDFGHFL  938

Qy   970  GNYKSFLGINKERVPFVLTPDELFVMGTSGKK--TSLHFQKFQDVCVKAYIALRHTNLL  1027
              ::  |:||::|||||||||:|  |: :: :    |:|:|:|::|::|:: |:|:|: |
Db   939  DHKKCKFGYKRERVPFVVLTQDFLIVISKGAQECKTREFERFQEMCYXAYLAIRQHANLF  998

Qy  1028  IILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGWTVQFNWF  1087
              |:|:|| :| |:||:|::|  ::|:| :|:|:::  :::||:| :|:: ||||: ||:|
Db   999  INLFSMMLGSGMPELQSFDDIAYIRKTLALDKTEQEALEYFMKQMNDAHHGGWTTKMDWI  1058

Qy  1088  LHLV----LGIKQGEKHSA  1102
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Search completed: February 15, 2004, 02:08:29
Job time : 35 secs

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                    GenCore version 5.1.6
          Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:     February 15, 2004, 02:05:12  ; Search time 80 Seconds
                                         (without alignments)
                                         2884.241 Million cell updates/sec

Title:           US-09-974-573-1
Perfect score:   5790
Sequence:        1 MELENYEQPVVLREDNRRRR.........QFNWFLHLVLGIKQGEKHSA 1102

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        801455 seqs, 20938283 residues

Total number of hits satisfying chosen parameters:        801455

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Published_Applications_AA:*
         1:  /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
         2:  /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	5790	100.0	1102	11	US-09-974-573-1	Sequence 1, Appli
2	5538	95.6	1103	12	US-10-334-143-4	Sequence 4, Appli
3	5523.5	95.4	1110	12	US-10-101-235A-4	Sequence 4, Appli
4	5298.5	91.5	1076	12	US-10-101-235A-6	Sequence 6, Appli
5	1460.5	25.2	1068	12	US-10-101-235A-8	Sequence 8, Appli
6	1351.5	23.3	1044	12	US-10-337-192-2	Sequence 2, Appli
7	1351.5	23.3	1044	14	US-10-027-591-2	Sequence 2, Appli
8	1349.5	23.3	1044	15	US-10-162-160-1	Sequence 1, Appli
9	1074	18.5	1686	14	US-10-092-219-2	Sequence 2, Appli
10	1034	17.9	1167	9	US-09-205-658-48	Sequence 48, Appli
11	1034	17.9	1167	9	US-09-844-353A-48	Sequence 48, Appl
12	1034	17.9	1167	12	US-09-963-693-48	Sequence 48, Appli
13	980	16.9	204	12	US-10-101-235A-2	Sequence 2, Appli
14	979	16.9	195	12	US-10-101-235A-9	Sequence 9, Appli
15	698.5	12.1	887	10	US-09-771-161A-192	Sequence 192, App

16	698.5	12.1	887	10	US-09-771-161A-193	Sequence 193, App
17	690.5	11.9	803	10	US-09-921-232-2	Sequence 2, Appli
18	690.5	11.9	803	10	US-09-921-330-2	Sequence 2, Appli
19	690.5	11.9	803	10	US-09-921-329-2	Sequence 2, Appli
20	679.5	11.7	928	12	US-10-369-493-3211	Sequence 3211, Ap
21	649.5	11.2	875	12	US-10-369-493-1795	Sequence 1795, Ap
22	646	11.2	873	12	US-10-369-493-5060	Sequence 5060, Ap
23	562.5	9.7	756	10	US-09-771-161A-101	Sequence 101, App
24	380	6.6	1900	10	US-09-801-368-390	Sequence 390, App
25	351.5	6.1	150	9	US-09-205-658-17	Sequence 17, Appl
26	351.5	6.1	150	9	US-09-844-353A-17	Sequence 17, Appl
27	351.5	6.1	150	12	US-09-963-693-17	Sequence 17, Appl
28	345.5	6.0	816	12	US-10-205-219-3	Sequence 3, Appl
29	321	5.5	817	10	US-09-976-165-28	Sequence 28, Appl
30	321	5.5	817	12	US-10-342-276-28	Sequence 28, Appl
31	321	5.5	829	10	US-09-976-165-31	Sequence 31, Appl
32	321	5.5	829	12	US-10-342-276-31	Sequence 31, Appl
33	282	4.9	508	10	US-09-771-161A-102	Sequence 102, App
34	277	4.8	1066	12	US-10-369-493-1948	Sequence 1948, Ap
35	274.5	4.7	604	12	US-10-369-493-6700	Sequence 6700, Ap
36	272	4.7	997	12	US-10-369-493-3593	Sequence 3593, Ap
37	255.5	4.4	113	9	US-09-205-658-18	Sequence 18, Appl
38	255.5	4.4	113	9	US-09-844-353A-18	Sequence 18, Appl
39	255.5	4.4	113	12	US-09-963-693-18	Sequence 18, Appl
40	252	4.4	51	9	US-09-866-761-48478	Sequence 48478, A
41	248	4.3	925	12	US-10-369-493-2281	Sequence 2281, Ap
42	232	4.0	4128	12	US-10-205-194-1	Sequence 1, Appli
43	215.5	3.7	1973	12	US-10-369-493-2380	Sequence 2380, Ap
44	215.5	3.7	2470	12	US-10-369-493-22191	Sequence 22191, A
45	210.5	3.6	2368	12	US-10-369-493-1468	Sequence 1468, Ap

ALIGNMENTS

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RESULT 1
US-09-974-573-1
; Sequence 1, Application US/09974573
; Publication No. US2003002344A1
; GENERAL INFORMATION:
;  APPLICANT: Williams, Roger
;  APPLICANT: Ried, Christian
;  APPLICANT: Walker, Edward H
;  APPLICANT: Stephens, Len
;  TITLE OF INVENTION: PHOSPHOINOSITIDE 3-KINASES
;  FILE REFERENCE: ONYX1048-US
;  CURRENT APPLICATION NUMBER: US/09/974,573
;  CURRENT FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: US 60/242,801
;  PRIOR FILING DATE: 2000-10-23
;  NUMBER OF SEQ ID NOS: 1
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;  LENGTH: 1102
;  TYPE: PRT
;  ORGANISM: Porcine PI3K
US-09-974-573-1

  Query Match             100.0%;  Score 5790;  DB 11;  Length 1102;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1102;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy       121 CLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRLNALIGYDVTDVSNVHDDELEFTRRRL 180
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Query Match             95.6%;  Score 5538;  DB 12;  Length 1103;
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Db    2 MELENYKQPVVLREDNCRRRRRMKPRSAAASLSSMELIPIPFVLPTSQRKCKSPETALLH  61

Qy   61 VAGHGNVEQMKAQVWLRALETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLD 120
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Qy  301 EEIHLVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK 360
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Db  301 EEIHLVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK 360

Qy  361 FRVKIRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTSPKPFTEEVLMNVWLEFSIKI 420
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 FRVKIRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTSPKPFTEEVLMNVWLEFSIKI 420

Qy  421 KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYYVNLLLIDHRFLLRHGEY 480
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYYVNLLLIDHRFLLRHGEY 480

Qy  481 VLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKHRPTPDPEG 540
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 VLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKHRPTPDPEG 540

Qy  541 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQ 600
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQ 600

Qy  601 QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 660
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 660

Qy  661 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY 720
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY 720

Qy  721 LRGCGTAMLHDFTQQVVQIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLP 780
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721 LRGCGTAMLHDFTQQVVQIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLP 780

Qy  781 QSFRVPYDPGLKAGALVIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ 840
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781 QSFRVPYDPGLKAGALVIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ 840

Qy  841 DMLIIQILRIMESIWETESLDLCLLPYGCISTGDKIGMEIVKDATTIAKIQQSTVGNTG  900
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841 DMLIIQILRIMESIWETESLDLCLLPYGCISTGDKIGMEIVKDATTIAKIQQSTVGNTG  900

Qy  901 AFKDEVLSHWLKEKCPIEEKPQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL 960
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901 AFKDEVLSHWLKEKCPIEEKPQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL 960

Qy  961 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLAL 1020
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLAL 1020

Qy 1021 RHHTNLLIILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW 1080
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021 RHHTNLLIILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW 1080

Qy 1081 TVQFNWFLHLVLGIKGQEKHSA 1102
        ||||||||||||||||||||||
Db 1081 TVQFNWFLHLVLGIKGQEKHSA 1102
```

RESULT 2
US-10-334-143-4

; APPLICANT: GRIGORIEV, IGOR VYACHESLAVOVICH
; APPLICANT: SUDARSANAM, SUCHA

```
Qy  361 FRVKIRGIDIPVLPRTADLTVFVEAANIQYGQQVLCQRRTSPKPFTEEVLWNVWLEFSIKI 420
        ||||||||||||| |||||||||||  ||||||||||||||||||||||||||||||||||
Db  360 FRVKIRGIDIPVLPRNTDLTVFVEANIQHGQQVLCQRRTSPKPFTEEVLWNVWLEFSIKI 419

Qy  421 KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYYVNLLLIDHRFLLRHGEY 480
        |||||||||||||||||||||| ||:||:|||:||||||:||||||||||||||||||:||
Db  420 KDLPKGALLNLQIYCGKAPALSSKASAESPSSESKGKVRLLYYVNLLLIDHRFLLRRGEY 479

Qy  481 VLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKHRPTPDPEG 540
        ||||||:|||||||||||||||||||||||||||||||||||||||||||||||:||||||
Db  480 VLHMWQISGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKHQPTPDPEG 539

Qy  541 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQ 600
        ||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db  540 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKHPKAYPKLFSSVKWGQ 599

Qy  601 QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 660
        |||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||
Db  600 QEIVAKTYQLLARREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 659

Qy  661 LQLVQAVKFEPYHDSALARFLLKRGLNKRIGHFLPWFLRSEIAQSRHYQQRPAVILEAY 720
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  660 LQLVQAVKFEPYHDSALARFLLKRGLNKRIGHFLPWFLRSEIAQSRHYQQRPAVILEAY 719

Qy  721 LRGCGTAMLHDFTQQVQVIDMLQKVTIDIKSLSAEKYDVSSQVISLQKLENLQNLNLP 780
        |||||||||||||||||||:|||||||:|||||||||||||||||||||||||||:|||
Db  720 LRGCGTAMLHDFTQQVQVIEMLQKVTLDIKSLSAEKYDVSSQVISLQKLENLQNSQLP 779

Qy  781 QSFRVPYDPGLKAGALVIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ 840
        :|||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||
Db  780 ESFRVPYDPGLKAGALAIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ 839

Qy  841 DMLILQILRIMESIWETESLDLCLLPYGCISTGDKIGMEIVKDATTIAKIQQSTVGNTG 900
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  840 DMLILQILRIMESIWETESLDLCLLPYGCISTGDKIGMEIVKDATTIAKIQQSTVGNTG 899

Qy  901 AFKDEVLSHWLKEKCPIEEKFQAAVERPVYSCAGYCVATFVLGIGDRHNDNIMISETGNL 960
        |||||||:|||||||:|:|||||||||||||||||||||||||||||||||||||:||||
Db  900 AFKDEVLNHWLKEKSPTEEKFQAAVERPVYSCAGYCVATFVLGIGDRHNDNIMITETGNL 959

Qy  961 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLAL 1020
        |||||||||||||||||||||||||||||||||||||||||||:||||||::|||||||||
Db  960 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSPHFQKFQDICVKAYLAL 1019

Qy 1021 RHHTNLLILFSWMLMTGMPQLTSKEDIEYIRDALTVGKSEBDAKKYFLDQIEVCRDKGW 1080
        ||||||||||||||||||||||||||||||||||||||:|::|||||||||||||||||
Db 1020 RHHTNLLILFSWMLMTGMPQLTSKEDIEYIRDALTVGKNEEDAKKYFLDQIEVCRDKGW 1079

Qy 1081 TVQPNWFLHLVLGIKQGEKHSA 1102
        ||||||||||||||||||||||
Db 1080 TVQPNWFLHLVLGIKQGEKHSA 1101
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Db  782 ESFRVPYDPGLKAGALAIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ 841
        :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  841 DMLILQILRIMESIWETESLDLCLLPYGCISTGDKIGMEIVKDATTIAKIQQSTVGNTG 900
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  842 DMLILQILRIMESIWETESLDLCLLPYGCISTGDKIGMEIVKDATTIAKIQQSTVGNTG 901

Qy  901 AFKDEVLSHWLKEKCPIEEKFQAAVERPVYSCAGYCVATFVLGIGDRHNDNIMISETGNL 960
        |||||||:|||||||:|:|||||||||||||||||||||||||||||||||||||:||||
Db  902 AFKDEVLNHWLKEKSPTEEKFQAAVERPVYSCAGYCVATFVLGIGDRHNDNIMITETGNL 961

Qy  961 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLAL 1020
        |||||||||||||||||||||||||||||||||||||||||||:||||||::|||||||||
Db  962 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSPHFQKFQDICVKAYLAL 1021

Qy 1021 RHHTNLLILFSWMLMTGMPQLTSKEDIEYIRDALTVGKSEBDAKKYFLDQIEVCRDKGW 1080
        ||||||||||||||||||||||||||||||||||||||:|::|||||||||||||||||
Db 1022 RHHTNLLILFSWMLMTGMPQLTSKEDIEYIRDALTVGKNEEDAKKYFLDQIEVCRDKGW 1081

Qy 1081 TVQPNWFLHLVLGIKQGEKHSA 1102
        ||||||||||||||||||||||
Db 1082 TVQPNWFLHLVLGIKQGEKHSA 1103
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US-10-101-235A-4

Query Match             95.4%;  Score 5523.5;  DB 12;  Length 1110;
Best Local Similarity   95.2%;  Pred. No. 0;
Matches 1049;  Conservative  21;  Mismatches  31;  Indels  1;  Gaps  1;

Qy    1 MELENYEQPVVLREDNRRRRRMKPRSTRAASLSSMELIPIEFVLPTSQRNTKIPETALLH 60
        ||||||:|||||||| |||||||||| :|||||||||||||||||||||||:  :||||||
Db    1 MELENYKQPVVLREDNCRRRRRMKPRS-AASLSSMELIPIEFVLPTSQRKCKSPETALLH 59

Qy   61 VAGHGNVEQMKAQVWLRALETSVSADFYHRLGPDHFLLLYQKKGQVWYEIYDKYQVVQTLD 120
        |||||||||||||||||||||||:|||||||||:||||||||||||||||||||||||||||
Db   60 VAGHGNVEQMKAQVWLRALETSVAADFYHRLGPHHFLLLYQKKGQVWYEIYDKYQVVQTLD 119

Qy  121 CLRYWKVLHRSPGQIHVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRL 180
        ||||||. :|||||||:.|||.|||| :.|||||:||||||||||||||||||||||| |
Db  120 CLRYWKATHRSPGQIHLVQRHPPSESESQAFQRQLTALIGYDVTDVSNVHDDELEFTRRGL 179

Qy  181 VTPRMAEVAGRDPKLYAMHPWVTSKPLPEYLLKKTNNCVFIVIHRSTTSQTIKVSADDT 240
        ||||||||.|||||||||||||||||||||:::||.|||:||||||||||||||||.|||
Db  180 VTPRMAEVASRDPKLYAMHPWVTSKPLPEYIWKKIANNCIFIVIHRSTTSQTIKVSPDDT 239

Qy  241 PGTIIQSFFTMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG 300
        ||.||||||||||||||||||||||.| :|||||||||||||||||||||||||:|||||
Db  240 PGAIIQSFFTMAKKKSLMDIPESQSEQDFVLRVCGRDEYLVGETPIKNFQWVRHCLKNG 299

Qy  301 EEIHLVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLMDCDRK 360
        ||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  300 EEIHVVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLMDCDRK 359
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RESULT 7
US-10-027-591-2
; Sequence 2, Application US/10027591
; Publication No. US20020161014A1
; GENERAL INFORMATION:
; APPLICANT: SADHU, Chanchal et al.
; TITLE OF INVENTION: INHIBITORS OF HUMAN PHOSPHATIDYLINOSITOL 3-KINASE DELTA
; FILE REFERENCE: 27866/36170C
; CURRENT APPLICATION NUMBER: US/10/027,591
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 09/841,341
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 60/199,655
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 60/238,057
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 2
; LENGTH: 1044
; TYPE: PRT
; ORGANISM: Human p110delta protein
US-10-027-591-2

Query Match   23.3%;   Score 1351.5;   DB 14;   Length 1044;
Best Local Similarity   32.5%;   Pred. No. 1.7e-113;
Matches 362;   Conservative 197;   Mismatches 401;   Indels 153;   Gaps 40;

Qy   38 IPIEFVLPTSQRNTKTPETALLH--VAGHGNVEQMKAQVWLRALETSVSADFYHRL-GPD   94
Db   20 VVVDFLLPTG--------VYLNFPVSRNANLSTIKQLLWHRAQYEPL----FHMLSGPE   66

Qy   95 HFLL-LYQKKGQWYEIYDKYQVVQTLDCLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRQ 153
Db   67 AYVFTCINQTAEQQELEDEQR--RLCDVQPFLPVL------RLVAREGDRVKKL-INSQ 116

Qy 154 LNALIGYDVTDVSNVHDDELEFTRRRLVTPRMAEVAGRDPKLYAMHPWVT-SKPL------ 207
Db 117 ISLLIGKGLHEFDSLCDPEVNDFRAKMC--QFCEEAAARRQQLGWEAWLQYSFPLQLEPS 174

Qy 208 ------PEYLLKKITNNCVFIVI--HRSTTSQTIKVSADDTPGTILQSFFTKMAK--KKSL 258
Db 175 AQTWGPGTL--RLPNRALLVNVKFEGSEESFTFQVSTKDVPLALMACALRKKATVFRQPL 232

Qy 259 MDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNGEEIHLVL---------- 307
Db 233 VEQPE-----DYTLQVNGRHEYLYGNYPLCQFQYICSCLHSGLITPHLTMVHSSSILAMRD 287

Qy 308 -DTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLMWDCDRKFRVK-I 365
Db 288 EQSNPAPQVQKPRAKPPP---------------TPAKKPSS---VSLWSLEQPPRIELI 328

Qy 366 RGIDIPVLPRTAD--LTVFVEANIQYGQQVLCQRRTSPK-PFTEEVLMNVWLEFSIKIKD 422
Db 329 QGSKV-----NADERMKLVVQAGLFHGNEMLCKITVSSSEVSVCSEPVWKQRLEFDINICD 383

Qy 423 LPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYVNLLLIDHRFLLRHGEYVL 482
Db 384 LPRMARLCFALYA----VIEKAKKARSTKKKSKKADCPIAWANLMLFDYKDQLKTGERCL 439

Qy 483 HMWQLSGKGEBDQGSFNADKLTSATNPDKENSMSISILLDNYC-HPIALP---------KH 532
Db 440 YMW--PSVPDEKGELLNPTGVTVRSNPNTDSAAALLICLPEVAPHFVYYPALEKILELGH 497

Qy 533 RPTPDPEGDRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKD-PKAYPK 591
Db 498 ------SECVHVTEEEQL--QLREILERRGSGELYEHEKDLVWKLRHEVQEHFPEALAR 548

Qy 592 LFSSVKWGGQQEHVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESL 651
Db 549 LLLIVTKWNKHEDVAQMLYLLCS---WPE--LPVLSALELLDFSPFDCHVGSFAIKSLRKL 603

Qy 652 EDDVLHYLLQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLPWFLRSEIAQSRHYQQ 711
Db 604 TDDELFQYLLQLVQVLKYESYLDCELTKFLLDRALANRKIGHFLFWFLHRSEM---HVPS 659

Qy 712 --RFAVILEAYLRGCGTAMLHDFTQQVQVIDMLQKVTIDIKSLSAEKYDVSSQVISQLK 768
Db 660 VALRFGLILEAYCRG-STHHMKVLMKQGEALSKL-KALNDFVLSSQKTP--------K 708

Qy 769 QKLENLQNLNLPQS--------FRVPVPDGLKAGALVIEKCKVMASKKKPLWLBFKCADP 820
Db 709 PQTKELMHLCMRQBEAYLEALSHLQSPLDPSTLLAEVCVEQCTFMDSKMKPLWIMY--SNE 766

Qy 821 TALSNETIGIIFKHGDDLRQDMLILQLRIMESIWETESLDLCLLPYGCISTGDKIGMIE 880
Db 767 EAGSGGSVGIIFKNGDDDLRQDMLTLQMIQLMDVLWKQEGLDLRMTPYGCLPTGDRTGLIE 826

Qy 881 IVKDATTIAKIQ--QSTVGNTGAFKDEVLSHWLKEKCPIEEKFQAAVERFVVSCAGYCVA 938
Db 827 VVLRSDTIANIQLNKSNMAATAAFNKDALLNWLKSKNP-GEALDRAIEEFTLSCAGYCVA 885

Qy 939 TFVLIGDRHNDNIMISETGNLFHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTS 998
Db 886 TYVLGIGDRHSDNIMIRESGQLFHIDFGHFLGNFKTKFGINRERVPFLTYDFVHVIQQG 945

Qy 999 GKKTLSLHFQKFQDVCVKAYLALRHHTNLLIILFSMMLMTGNPQLTSKEDIEYIRDALTVG 1058
Db 946 KTNNSEKFPERFRGYCERAYTILRRHGLLFLHLFALMRAAGLPELSCSCSKDIQYIKDSLALG 1005

Qy 1059 KSEEDAKKYFLDQIEVCRDKGWTVQFNWFLHLV 1091
Db 1006 KTEEEALKHFRVKFNEALRESWKTKVNWLAHNV 1038

RESULT 8
US-10-162-160-1
; Sequence 1, Application US/10162160
; Publication No. US20030099627A1
; GENERAL INFORMATION:
; APPLICANT: Van Haesebroeck, Bart
; APPLICANT: Waterfield, Michael D.
; TITLE OF INVENTION: No. US20030099627A1e1 Lipid Kinase
; FILE REFERENCE: 2332-1-002
; CURRENT APPLICATION NUMBER: US/10/162,160
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/194,640
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: 9611460.8
; PRIOR FILING DATE: 1996-06-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1044
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-162-160-1

Query Match   23.3%;   Score 1349.5;   DB 15;   Length 1044;
Best Local Similarity   32.5%;   Pred. No. 2.6e-113;
Matches 362;   Conservative 197;   Mismatches 401;   Indels 153;   Gaps 40;

Qy   38 IPIEFVLPTSQRNTKTPETALLH--VAGHGNVEQMKAQVWLRALETSVSADFYHRL-GPD   94
Db   20 VVVDFLLPTG--------VYLNFPVSRNANLSTIKQLLWHRAQYEPL----FHMLSGPE   66

Qy   95 HFLL-LYQKKGQWYEIYDKYQVVQTLDCLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRQ 153
Db   67 AYVFTCINQTAEQQELEDEQR--RLCDVQPFLPVL------RLVAREGDRVKKL-INSQ 116

Qy 154 LNALIGYDVTDVSNVHDDELEFTRRRLVTPRMAEVAGRDPKLYAMHPWVT-SKPL----- 207
Db 117 ISLLIGKGLHEFDSLCDPEVNDFRAKMC--QFCEEAAARRQQLGWEAWLQYSFPLQLEPS 174

Qy 208 -----PEYLLKKITNNCVFIVI--HRSTTSQTIKVSADDTPGTILQSFFTKMAK--KKSL 258

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;   CURRENT FILING DATE:  2002-03-07
;   PRIOR APPLICATION NUMBER: PCT/GB98//00244
;   PRIOR FILING DATE: 1998-01-27
;   PRIOR APPLICATION NUMBER: 09/355,160
;   PRIOR FILING DATE: 1999-10-01
;   PRIOR APPLICATION NUMBER: 9701652.1
;   PRIOR FILING DATE: 1997-01-28
;   NUMBER OF SEQ ID NOS: 11
;   SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 1686
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-092-219-2

Query Match         18.5%;       Score 1074;  DB 14;   Length 1686;
Best Local Similarity  28.9%;       Pred. No. 8.3e-88;
Matches 309;  Conservative 178;  Mismatches 343;  Indels 238;  Gaps 32;
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Db    175  AQTWGPGTL--RLPNRALLVNVKFEGSEESFTFQVSTKDVPLALMACALRKKATVFRQPL  232
                 ::                  :  ||||
Qy    194  KLYAMHPWVTSKPLPEYLLKKIT--NNCVFIVIHRSTSQTIKVSADDTPGTILQSFT  250

Qy    259  MDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNGEEIHLVL--------  307
                ::  ||    :::    : :     |||||      :         :|
Db    390  KLKTKFPYINHRTNPGYLLSPVTAQRNIC--------------GENASVKVSI-DIEGFQLPVTFT  440

Qy    233  VEQPE-----DYTLQVNGRHEYLYGSYPLCCQFQYICSCLHSGLTPHLTMVHSSSILAMRD  287
               :                   : ||        :|
Db    251  ------KMAKKSKSLMDIPESQNERD--FVLRVCGRDEYLVGETPIKNFQWVRQCLKNG  300

Qy    308  -DTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRKFPRVK-I  365
            ||||||  |||||||||||||                 ||   :  |:    |||: :||
Db    441  CDVSSTVEIIIMQALCWVHDDLNQVDVGSYVLKVCGQEEVLQNNHCLGSHEHIQNCRKWD  500

Qy    288  EQSNPAPQVQKPRAKPPP---------------IPAKKPSS---VSLWSLEQPFRIELI  328
               :  :::  :   :                    ||:||      :|||||:  :|
Db    301  EEIHLVL----------------------------DTPPPDPALDEVRKEEWPLVDDCTG------VT  333

Qy    366  RGIDIPVLPRTAD--LTVFVEANIQYGQQVLCQRRTSPK-PFTEEVLMNVWLEFSIKIKD  422
            ||:  :: :: ||   :::      :|||||||||         :  :   |:  :||
Db    501  TEIRIQLLITFSAMCQNLARTAEDDETPVD--------LNKHLYQIEKPCKEAMTRHPVEELLD  555

Qy    329  QGSKV-----NADERMKLVVQAGLFHGNEMLCKTVSSSEVSVCSEPVWKQRLBFDINICD  383
            ||:       ::    ::    :|||        || :  ::  :::  ||| :::|:
Db    334  GYHEQ------LTIHGKDH--------------------ESVFTVSLWDCDRKPRVKIRGIDIPVL  373

Qy    423  LPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYVNLLIDHRFLLRHGBEYVL  482
            ||:  : :|:    :: : :||  ||    : |||     :  |:  ::    :|| |
Db    556  SYHNQVELALQIENQHRAVDQVIKAVRKICSALDGVETLAITESVKKLK--RAVNLP-R  611

Qy    384  LPRMARLCFALYA-----VIEKAKKARSTKKKSKKADCPIAWANLMLFDYKDQLKTGERCL  439
            ||                                                     :
Db    374  PRTADLTVFV--------------------EANIQYGQQVLCQRRT--------------SP-  401

Qy    483  HMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNVC-HPIALP---------KH  532
            |:                                     :::                 :
Db    612  SKTADVTSLFGGEDTSRSSTRGSLNPENPVQVSINQLTAAIYDLLRLHANSGRSPTDCAQ  671

Qy    440  YMW--PSVPDEKGELLNPTG-TVRSNPNTDSAAALLICLPEVAPHVPYYPALEKILELGRH  497
                                                 :
Db    402  -----------------------------------------------------------  401

Qy    533  RPTPDPBEGDRVRAEMPNQLRKQLEAIIATDPLNPLITAEDKELLWHFRYESLKD-PKAYPK  591
              :  :                          :     : ::: :  ::  |||: |
Db    672  SSKSVKEAWTTTEQLQFTIFAAHGISSNWVSNYEKYYLICSLSHNGKDLFKPIQSKKVGT  731

Qy    498  ------SECVHVTEEQL--QLRElLERRGSGELYEHEKDLVWKLRHEVQEHFPEALAR  548
                      :::                :         ::   |   :|:
Db    402  -KPFTEEVLWNVWLEFSIKIKDLPKGALLNLQIY--CGKAPALSGKTSAEMPSPESKGKA  458

Qy    592  LFSSVKMGQQEIVAKTYQLLAKREVNDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESL  651
            |:                             :|: :::  ::   :
Db    732  YKNFFYLIKWDELIIFPIQISQLPLESYLHLTLFGILNQSSGSSPDNKQRKGPEALGK-  790

Qy    549  LLLVTKWNKHEDVAQMLYLLCS--WPE--LPVLSALELLDFSFPDCHVGSFAIKSLRKL  603
            |::   :   :: :::  :                 : :     |: ::  ::
Db    459  QLLYYVNLLIDHRFLLRHGEYVLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISI  518

Qy    652  EDDDVLHYLYLLQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQ  711
            |:::                : :        : ::    |||:         ::
Db    791  ------VSLPLCDFRRFLTCGTKLLYLWTSS----------HTNSVPGTV  824

Qy    712  ---RFAVILEAYLRGCGTAMLHDFTQQVQVIDMLQKVTIDIKSLSAEKYDVSSQVISQLK  768
                                :|   |: :           : ::   |:  ::  :||
Db    519  LLDNY-CHPIALPKGHRPTP--------DPEGDRVRAE------MPNQLRKQLEAIIATDPL  564

Qy    660  VALRFGLILEAYCRG-RTHMKVLMKQGEALSKL-KALNDFVKLSSQKTP---------K  708
            ||| :| ::|                  : ::                           :
Db    825  TKKGYVMERIVLQVDFPSPAFDIIYTTPQVDRSIIQQHNLETLENDIKGKLLDILHKDSS  884

Qy    769  QKLENL-QNLNLPQS-----------FRVPYDPGLKAGALVIEKCKVVASKKKPLWLEFKCADP  820
            |||    ||:                    :      :: :      :  ||| |||||:
Db    565  NPLTAEDXKELLWHFRYESLKDPKAYPKLFSSV---KWGQQBIVAKTYQLLAKREVWDQSA  621

Qy    709  PQTKELMHLCMRQEAYLEALSHLQSPLDPSTLLAEVCVEQCTFMDSKMKPLWIMY--SNE  766
            |||          : ::  : :::  ||  :   ::      :  ||||||:
Db    885  LGLSKEDKAFLWEKRYYCFKHPNCLPKILASAPNWKWGN--LAKTVSLLHQ---W-PA  936

Qy    821  TALSNETIGIIFKHGGDDLRQDMLIIQILRIMESIWETESLDLCLLPYGCISTGDKIGMIE  880
            |||        |   :: :::  :  :  ::::    : :  ::::
Db    622  LDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYLLQLVQAVKFEPYHDSALARFL  681

Qy    767  BAGSGGGSVGIIFKNGDLRQDMLTLQMIQLMDVLWKQEGLDRMTPYGCLPTGDRTGLIE  826
            || ||  |: |:|:||:||||||: ::::|: |  :  | :: ||||||: |||: |||
Db    937  LYPLIAIELLDSKFADQEVRSLAVTWIEAISDDELTDLLPQFVQALKYEIYLNSSLVQFL  996

Qy    881  IVKDATTIAKIQ--QSTVGNTGAFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAGYCVA  938
            ||                    :||::|     :|: :: ::     :  |  ||||||
Db    682  LKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAYLRGCGTAMLHDFTQQVQIDM  741

Qy    827  VVLRSDTIANIQLNKSNMAATAAFNKDALLNWLKKSKNP-GEALDRAIEEFTLSCAGYCVA  885
              ||::  | |:|   :::           : :            : | ::|||||||||
Db    997  LSRALGNIQIAHNLYWLLKDAL-HDVQFSTRYEHVLGALLSVGGKLREELLKQTKLVQL  1055

Qy    939  TFVLGIGDRHNDNIMISETGNLFHIDFGHILGNVKSFLGINKERVPFVLTPDELFVMGTS  998
            |:||||||:::|||: ||:|||||||||||:| |  |||::: |||::| ||:: :
Db    742  LQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLPQSFRVPYDPGLKAGALVIEKC  801

Qy    886  TYVLGIGDRHSDNIMIRESGQLFHIDFGHFLGNFKTKFGLNRERVPFIITYDFVHVIQQG  945
            || ||||||||||||||  |||||||||| ||:||:  ||||||||::| |||| ||: |
Db    1056 LGGVAEKVRQASGS----ARQVV-LQRSMERVQSFFQKNKCRLPLKPSLVAKELNIKSC  1109

Qy    999  GKKTSLHFQKFQDVCVKAYLALRHHTNLLIILFSMMLMTGMPQLTSKEDIEYIRDALTVG  1058
            |:|   |:|  | :|  :::   :: ::::::    |:   :: :    :: ::::
Db    802  KVMASKKKPLWLEFKCADPTALSNETIGIIFKHGGDDLRQDMLIQILRIMESIWETESLD  861

Qy    946  KTNNSEKFERFRGYCERAYTILRRGLLFLPLHLFALMRAAGLPELLSCSKDIQYLKDSLAIG  1005

Qy    1059 KSEEDAKKYFLDQIEVCRDKGWTVQFNWFLHLV  1091

Db    1006 KTEEEALKHFRVKFNEALRESWKIKVNWLAHNV  1038
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RESULT 9
US-10-092-219-2
; Sequence 2, Application US/10092219
; Publication No. US20020115114A1
; GENERAL INFORMATION:
;   APPLICANT: Domin, Jan
;   TITLE OF INVENTION: No. US20020115114A1e1 Lipid Kinase
;   FILE REFERENCE: 1064HG/50947
;   CURRENT APPLICATION NUMBER: US/10/092,219
```

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Db   1110 SFFSSNAVPLKVTMVNADPL---GEEINVMFKVGEDLRQDMLALQMIKIMDKINLKEGLD 1166
Qy    862 LCLLPYGCISTGTDGDKIGMIEIVKDATTIAKIQQSTVGNTGAFKDEVLSHWLKEKCPIEEKF 921
          |:||  ||| ||:|| ||||||||| |: :||||: ||| |: :  |  |:::|| |||
Db   1167 LRMVIFKCLSTGRDRGMVELVPASDTLRKIQVE-YGVTGSFKDKPLAEWLRKYNPSEEEY 1225
Qy    922 QAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNLFHIDFGHILGNYKSFLGINKE 981
          |  | ||:||||  ||||:|||| |||||||||| |||||||||| |||  | |||| |
Db   1226 EKASENFIYSCAGCCVATYVLGICDRHNDNIMLRSTGHMFHIDFGKFLGHAQMFGSFKRD 1285
Qy    982 RVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLALRHHTNLLIILPSMMLMTGMPQ 1041
          | ||:||  ::|| || | : |||:|||:  |: ||| |:  :::|||:|:::| |
Db   1286 RAPFFVLTSDMAYVI-NGGEKPTIRFQLFVDLCCQAYNLIRKQTNLFLNLLSLMIPSGLPE 1344
Qy   1042 LTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGWTVQFNWFLH 1089
          ||| :|::::|||| : |::::||:||| :|||  | ||:: ||| |
Db   1345 LTSIQDLKVVRDALQPQTTDAEATIFFTRLIESSLGSIAT-KFNFFIH 1391

Qy    369 DIPVLPRTADLTVFVEANIQYGQQVLQRRTSPKPFTEEVLMNVWL-EFSIKIKDLPKGA 427
          :: :  : : :  ::  :| ||  :                     : ::|:| ||    
Db    425 DFPA---DVDMYRIEFSVYVGTLTLASKSTI-KVNAQFAKWNKEMYTFDLYMKDMPPSA 480
Qy    428 LLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYYVNLLLIDHRFLLRHGEVLHMWQL- 487
                                          |:||  :||  ||:  ||: || :| |
Db    481 VLSIRVLYGK-----VGWVNMSLITDWRDELRQGQPLFHLW- 524
Qy    488 SGKGEDQGSFNADKLTSATNPDKEN----SMSISILLDNYCHPIALP---------KH 532
                                          :  :|:  |    :|| |
Db    525 ----------APFPTANRSRIGENGARIGTNAAVTIBISSYGGRVRMPSQGQYTYLVKH 573
Qy    533 R----PTPDPEGDRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKE---LLWHFRYESLKD 585
          |              |  : |        | :  |  |                      
Db    574 RSTWTETLNIMGDDYESCIRDPGYKKLQMLVKKHESGIVLEEDEQRHVWMWR-RYIQKQE 632
Qy    586 PKAYPKLFS-SVKWGQQEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIA 644
          |: |||:   ||  |  |:  :||  : |                 | :       |:
Db    633 PDLLIVLSLAFWTDRENFSELYVMLEK---WKPPSVAAALT--LLGKRCTDRVIRKFA 687
Qy    645 VQKLESLEDDDVLH-YLLQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHPLFWFLRSEI 703
          |||||:||||::: :::      |||     || ||:|||:|  |:|||||| |:|:||
Db    688 VEKLNEQLSPVTFHLFLFLPLIQALKYEPRAQSEVGMMLLTRALCDYRIGHRLFWLLRAEI 747
Qy    704 AQSR------HYQQRFAVILEAYLRGCGTAMLHDFTQQVQVIDMLQKVTIDIKLSLSAEKY 757
          | ||      ||  || : :     |  | |  :| |: |:                |:
Db    748 ARLRDCDLKSEEYRRISILLMEAYLRG-NEEHIKIITRQVDMVDELTRISTLVKGMPK--- 803
Qy    758 DVSS----QVISQLKQKLENLQNLNLPQSFRVPYDPGLKAGALVIEKCKVMASKKKPLWL 813
          |::     |:      |   |   |  ||         |:           : :| ||||
Db    804 DVATMKLRDELRSISHKMENMDS-----------PLDPVVKLGEMIIDKAIVLGSAKRPLML 854
Qy    814 EFKCADPTA-LSNETIGIIFKHGDDLRQDMLIIQLRIMESIWETESLDLCLLPYGCIST 872
          |||  ||   ||| || |:|| ||||||| :||  : |::|: :|  |||:|||| |
Db    855 HWKNKNPKSDLHLPFCAMIFKNGDDLRQDMLVLQVLEVMDNIWKAANIDCCLNPYAVLPM 914
Qy    873 GDKIGMIEIVKDATTIAKIQQST-VGNTG--AFKDEVLSHWLKEKCPIEE---------- 919
          | ||||||||||||||||||| :            :|    |||| :|
Db    915 GEMGIIEVVPNCKTIFEIQVGTGFMNTAVRSIDPSFMNKWIRKQCGIEDEKKKSKKDST 974
Qy    920 ------------KFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISTGNLFHID 964
                        |:|  | |||| ||  ||||::||| ||||||:|:::|  |||||
Db    975 KNPIEKKIDNTQAMKKYFESVDRFLYSCVGYSVATYIMGIKDRHSDNLMLTEDGKYVHID 1034
Qy    965 FGHILGNYKSFLGINKERVPFVLTPDFLFVM--GTSGKKTSLHFQKFQDVCVKAYLALRH 1022
          |||||||||| | ::||:||:| :||||:|   ||||||||||| ||:||:     | |
Db   1035 FGHILGHGKTKLGIQRDRQPFITEHMTVIRSGKSVDGNSHELQKFKTLCVEAYBVMWN 1094
Qy   1023 HTNLLILFSMMLMTGMPQLTSKEDIEVIRDALTV-GKSEEDAKKYFLDQIEVCRDKGWT 1081
          :::|:|:  ::|  |::|  | ||:|::  ||     |::|::|:|| :  |   || |
Db   1095 NRDLFVSLFTLMGMELPELSTKADLDHLKKTLFCNGESKEARKFFAGIYEBAFNGGSWS 1154
Qy   1082 VQFNWFLHV 1091
          | ||||:|
Db   1155 TKINWLFHAV 1164
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RESULT 10
US-09-205-658-48
; Sequence 48, Application US/09205658
; Patent No. US20010029617A1
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; APPLICANT: Ogg, Scott
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
; FILE REFERENCE: 00786/351004
; CURRENT APPLICATION NUMBER: US/09/205,658
; CURRENT FILING DATE: 1998-12-03
; EARLIER APPLICATION NUMBER: 08/857,076
; EARLIER FILING DATE: 1997-05-15
; EARLIER APPLICATION NUMBER: 08/888,534
; EARLIER FILING DATE: 1997-07-07
; EARLIER APPLICATION NUMBER: US98/10080
; EARLIER FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 1167
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-205-658-48

Query Match   17.9%; Score 1034; DB 9; Length 1167;
Best Local Similarity   27.2%; Pred. No. 2e-84;
Matches   313; Conservative 227; Mismatches 400; Indels 210; Gaps 44;

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Qy    78 ALETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLDCLRYWKVLHRSPGQIHV 137
         |:  :|| ||:|:|  :||:|| |  |:|  || | ::|| | ||||:||:| ||
Db       -------------------------------------------------------------
Qy    89 SLEIKLS-DFKHQL---FELIAPMKWGTYSVKPQDYVFRQLNNFGEIEVIFNDDQPLSK 143
         :::|::  |||||    |||| |  | |:|  ::|  ::|  |||||| |  :|  |:
Db   144 LELHGTFPMLFLYQPDGINRDKELMSDISHCLGYSLDKLEESLDEELRQFRASLWARTKK 203
Qy   138 VQRHAPSEETLAFQ---------RQLNALIGYDVTDVSNVHDDEL-EP------TRR 178
         :: |   :: || |         ||| |:|| |:||:|:||||  |         |||
Db   179 RLVT--------------PRMAEVAGRDPKLYAMHPWVTSKPLPEYLLKKI 215
Qy   204 TCLTRGLEGTSHYAFPEEQYLCVGESCPKDLESKVKAAKLSYQMFWRKK-------AEI 256
         : |                           |:                  || ||
Db   216 TNNCVFIVIHRSTTSQTIKVSADDTPGTILQSFFKMAKKKSLMDIPESQNERD--FVLR 273
Qy   257 NGVC------EKMMKIQIEFNPNETPKSLLHTFLYEMRK----LDVYDTDDPADEGWFLQ 306
                                      :|| |  | |:|     ||| |:|| |::|:
Db   274 VCGRDEYLVG-ETPIKNFQWVRQCLKN---GEEIH--LVLD--TPPDPALDE--VRKE 321
Qy   307 LAGRRTFVTNPDVKLTSYDGVRSELESYRCPGFVVRRQSIVLKDYCRPKLYEPHYVRAH 366
         ||| :|::::|:|:| | ||  | |   | ||::||||::||| :|| |||  :| |
Db   322 EWPLVDDCTGVTGYHEQLTIHGKDHESVFT--------VSLWDCDRKFRVK---IRGI 368
Qy   367 ERKLALDVLSVS--IDSTPKQSKNSDMVWTDFRPTASLKQVSLWDLDANLMIRPVNISGF 424
```

RESULT 11
US-09-844-353A-48
; Sequence 48, Application US/09844353A
; Patent No. US20020037588A1
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; APPLICANT: Kimura, Koutarou
; APPLICANT: Patterson, Garth
; APPLICANT: Ogg, Scott
; APPLICANT: Paradis, Suzanne
; APPLICANT: Tissenbaum, Heidi
; APPLICANT: Morris, Jason
; APPLICANT: Koweek, Allison
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
; FILE REFERENCE: 00786/351005

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; CURRENT APPLICATION NUMBER: US/09/844,353A
; CURRENT FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 08/857,076
; PRIOR FILING DATE: 1997-05-15
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 1167
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-844-353A-48

  Query Match        17.9%;   Score 1034;  DB 9;  Length 1167;
  Best Local Similarity  27.2%;  Pred. No. 2e-84;
  Matches  313;  Conservative 227;  Mismatches 400;  Indels 210;  Gaps  44;

Qy   78 ALETSVSADFYHRLGPDHFLLYQKKGQWYEIYDKYQVVQTLDCLRYWKVLHRSPGQIHV 137
                                                                        
Db   89 SLEIKLS-DFKHQL----FELIAPMKWGTYSVKPQDYVFRQLNNFGEIEVIFNDDQPLSK 143

Qy  138 VQRHAPSEETLAFQ-----------RQLNALIGYDVTDVSNVHDDEL-EF------TRR 178
                                                                        
Db  144 LELHGTFPMLFLYQPDGINRDKELMSDISHCLGYSLDKLEESLDEELRQFRASLWARTKK 203

Qy  179 RLVT-------------------PRMAEVAGRDPKLYAMHPWVTSKPLPEYLLKKI 215
                                                                        
Db  204 TCLTRGLEGTSHYAFPEEQYLCVGESCPKDLESKVKAAKLSYQMFWRKRK------AEI 256

Qy  216 TNNCVFIVIHRSTTSQTIKVSADDTPGTILQSFFTKVAKKKSLMDIPESQNERD--FVLR 273
                                                                        
Db  257 NGVC------EKMMKIQIEFNPNETPKSLLHTFLYEMRK---LDVYDTDDPADEGWFLQ 306

Qy  274 VCGRDEYLVG-ETPIKNFQWVRQCLKN----GEEIH--LVLD-TPPDPALDE--VRKE 321
                                                                        
Db  307 LAGRTTFVTNPDVKLTSYDGVRSELESYRCPGFVVRRQSVLVKDYCRPKPLYEPHYVRAH 366

Qy  322 EWPLVDDCTGVTGYHEQLTIHGKDHESVFT---------VSLWDCDRKFRVK---IRGI 368
                                                                        
Db  367 ERKLALDVLSVS--IDSTPKQSKNSDMVWTDFRPTASLKQVSLWDLDANLMIRPVNISGF 424

Qy  369 DIPVLPRTADITVFVEANIQYGQVQVLCQRRTSPKPFTEEVLMNVWL-EFSIKIKDLPKGA 427
                                                                        
Db  425 DFPA---DVDMYVRIEFSVVGTLTLASKSTT-KVNAQFAKWKNKEMYTFDLYMKDMPPSA 480

Qy  428 LLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYVNLLLIDHRFLLRHGEYYLHWQL 487
                                                                        
Db  481 VLSIRVLYGK---------VKLKSEEFE-----VGWVNMSLTDWRDELRQGQFLFHLW-- 524

Qy  488 SGKGEDQGGSFNADKLTSATNPDKEN--------SMSISILLDNYCHPIALP--------KH 532
                                                                        
Db  525 --------APEPTANRSRIGENGARIGTNAAVTIEISSYGGRVRMSQGGQYTYLVKH 573

Qy  533 R----PTPDPEGDRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKE---LLWHFRYESLKD 585
                                                                        
Db  574 RSTWTETLNIMGDDYESCIRDPGYKKLQMLVKKHESGIVLEEDEQRHVWMWR-RYIQKQE 632

Qy  586 PKAYPKLFS-SVKWGGQEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIA 644
                                                                        
Db  633 PDLLIVLSELAFVWTDRENFSELYYMLEK---WKPPSVAAALT--LLGKRCTDRVIRKFA 687

Qy  645 VQKLESLEDDDVLH-YLLQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEI 703
                                                                        
Db  688 VEKLNEQLSPVTFHLFILPLIQALKYEPRAQSEVGMMLLTRALCDYRIGHRLFWLLRAEI 747

Qy  704 AQSR------HYQQRFAVILEAYLRGCGTAMLHDFTQQVQVIDMLQKVTIDIKSLSAEKY 757
                                                                        
Db  748 ARLRDCDLKSEEYRRISLLMEAYLRG-NEBHIKIITRQVDMVDELTRISTLVKGMPK-- 803

Qy  758 DVSS----QVISQLKQKLENLQNLNLPQSFRVPYDPGLKAGALVIEKCKVMASKKKPLWL 813
                                                                        
Db  804 DVATMKLRDELRSTSHKMENMDS--------PLDPVYKLGEMIIDKAIVLGSAKRPLML 854

Qy  814 EFKCADPTA-LSNETIGIFPKHGDDLRQDMLILQLRIMESIWETESLDLCLLPYGCIST 872


Db  855 HWKNKNPKSDLHLPFCAMIFKNGDDLRQDMLVLQVLEVMDNIWKAANIDCCLNPYAVLPM 914

Qy  873 GDKIGMIEIVKDATTIAKIQQST-VGNTG--AFKDEVLSHWLKEKCPIEE-------- 919
                                                                        
Db  915 GEMGIIEVVPNCKTIFEIQVGTGFMNTAVRSIDPSFMNKWIRKQCGIEDEKKKSKKDST 974

Qy  920 -----------KFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNLFHID 964
                                                                        
Db  975 KNPIEKKIDNTQAMKKYPESVDRFLYSCVGYSVATYIMGIKDRHSDNLMLTBDGKYVHID 1034

Qy  965 FGHILGNYKSPLGINKERVPFVLTPDFLPVM-GTSGKKTSLHFQKFQDVCVKAYLALRH 1022
                                                                        
Db 1035 FGHILGHGKTKLGIQRDRQPFILTEHFMTVIRSGKSVDGNSHELQKFKTLCVEAYEVMWN 1094

Qy 1023 HTNLLIILFSMMLMTGMPQLTSKEDIEYIRDALTV-GKSEEDAKKYFLDQIFVCRDKGWT 1081
                                                                        
Db 1095 NRDLFVSLFTLMGMELPELSTKADLDHLKKTLFCNGESKEEARKFFAGIYEEAFNGSWS 1154

Qy 1082 VQFNWFLHLV 1091
                  
Db 1155 TKTNWLFHAV 1164


RESULT 12
US-09-963-693-48
; Sequence 48, Application US/09963693
; Publication No. US2003018364A1
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; APPLICANT: Ogg, Scott
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
; FILE REFERENCE: 00786/351004
; CURRENT APPLICATION NUMBER: US/09/963,693
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/205,658
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: 08/888,534
; PRIOR FILING DATE: 1997-07-07
; PRIOR APPLICATION NUMBER: US98/10080
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 1167
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-963-693-48

  Query Match        17.9%;   Score 1034;   Pred. No. 2e-84;  Length 1167;
  Best Local Similarity  27.2%;  Pred. No. 2e-84;
  Matches  313;  Conservative 227;  Mismatches 400;  Indels 210;  Gaps  44;

Qy   78 ALETSVSADFYHRLGPDHFLLYQKKGQWYEIYDKYQVVQTLDCLRYWKVLHRSPGQIHV 137
                                                                        
Db   89 SLEIKLS-DFKHQL----FELIAPMKWGTYSVKPQDYVFRQLNNFGEIEVIFNDDQPLSK 143

Qy  138 VQRHAPSEETLAFQ-----------RQLNALIGYDVTDVSNVHDDEL-EF------TRR 178
                                                                        
Db  144 LELHGTFPMLFLYQPDGINRDKELMSDISHCLGYSLDKLEESLDEELRQFRASLWARTKK 203

Qy  179 RLVT-------------------PRMAEVAGRDPKLYAMHPWVTSKPLPEYLLKKI 215
                                                                        
Db  204 TCLTRGLEGTSHYAFPEEQYLCVGESCPKDLESKVKAAKLSYQMFWRKRK------AEI 256

Qy  216 TNNCVFIVIHRSTTSQTIKVSADDTPGTILQSFFTKVAKKKSLMDIPESQNERD--FVLR 273
                                                                        
Db  257 NGVC------EKMMKIQIEFNPNETPKSLLHTFLYEMRK---LDVYDTDDPADEGWFLQ 306

Qy  274 VCGRDEYLVG-ETPIKNFQWVRQCLKN----GEEIH--LVLD-TPPDPALDE--VRKE 321
```

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Db    307 LAGRTTFVTNPDVKLTSYDGVRSELESYRCPGVVRRQSLIVLKDYCRPKPLYEPHYVRAH 366
           :   :    ::  ::   |||     |   ||
Qy    322 EWPLVDDCTGVTGYHEQLTIHGKDHESVFT--------VSLWDCDRKFRVK---IRGI 368
                |     |   ::      |||::   |||||::   |
Db    367 ERKLALDVLSVS--IDSTPKQSKNSDMWTDFRPTASLKQVSLWDLDANLMIRPVNISGF 424
                |:  ::   ||||||::      ::||::   |:|||
Qy    369 DIPVLPRTADLTVFVEANIQYGGQVLCQRRTSPKPFTEVLMNVWL-EFSIKIKDLPKGA 427
           ||:::   |  :|::|:|   :   |::|   :|:|   |:
Db    425 DFPA--DVDMYVRIEFSVYVGTITLASKSTT-KVNAQFAKWNKEMYTFDLYMKDMPPSA 480
           |||    |  |   ::|::||   :|||:|   |::|   |||
Qy    428 LLNLQIYCGKAPALSGKITSAEMPSPESKGKAQLLYYVNLLLIDHRFLLRHGEYLHMWQL 487
                ::| |||   |   ::||:   |   |::|||:   :|||
Db    481 VLSIRVLYGK--------VKLKSEEFE-----VGWVNMSLITDWRDELRQGQPLFHLM-- 524
           :|:   ||||        |||||||||       |   |::|:|:||:||
Qy    488 SGKGEDQGSFNADKLTSATNPDKEN-------SMSISILLDNYCHPIALP--------KH 532
           :||:|:|::   ||   :|   :|   :     ::|:|||||||||:       ||
Db    525 --------APEPTANRSRIGENGARIGTNAAVTIEISSYGGRVRMPSQQQYTYLVKH 573
                  ::| |:| |:|:|||||||::|||||||:|:::||:|::|::||||||
Qy    533 R----PTPDPEGDRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKE---LLWHFRYESLKD 585
           |    ||||:|||||||||||||||||||||||||||||||||      |:|||||:||
Db    574 RSTWTETLNIMGDDYESCIRDPGVYKKLQMLVKKHESGIVLEEDEQRHVWMWR-RYIQKQE 632
                :|   ::|||:|::::   ||::|::|||:::|||::|||   ||||| ||:|:|:|
Qy    586 PKAYPKLFS-SVKWGQQEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIA 644
           |||||||||  |||:||||||||||||||:||||||::|||||:|||::|:   ::|||
Db    633 PDLIVLSELAFVWTDRENFSELIYVMLEK--WKPPSVAAALI--LLGKRCTDRVIRKFA 687
           |:|:|:::|   |::||:|:||||:|::|:   ||||:|:||   |:|||:|||||||:|
Qy    645 VQKLESLEDDVLH-YLLQLVQAVKFEPYHDSALARFLLKRGIGHFLWFLRSEI 703
           ||||||||||:|  |||||||||||||||||||||||||||||:|||:|||:|
Db    688 VEKLNEQLSPVTFHLFILPLIQALKYEPRAQSEVGMMLJTRALCDYRIGHRLFWLLRAEI 747
               :|::|:| |||:|::|:|:|||:|:::::|:||::|:|::||:|||||||:||||:|
Qy    704 AQSR------HYQQRFAVILEAYLRGCGTAMLHDFTQQVQVIDMLQKVTIDIKSLSAEKY 757
           ||||      |:||||||||||:|||| |:|:|:|:::|::|::||||::||:|:|||::
Db    748 ARLRDCDLKSEYRRISLLMBAYLRG-NEEHIKIITRQVDMVDELITRISTLVKGMPK-- 803
                ||::|   ||:| |::||||||  |::||:|||:|:||||::|:::::|:|||||
Qy    758 DVSS---QVISQLKQKLENLQNLNLPQSPRVPYDPGLKAGALVIEKCKVMASKKKPLWL 813
               |:::|::||::||:|:|::|   |   ||:|:|::|||:::|:::::|:||:|
Db    804 DVATMKLRDELRSISHKMENMDS--------PLDPVYKLGEMIIDKAIVLGSSAKRPLML 854
           |:   |:|::|:::||::|::||         ||||:||::|||:|::||||:||:|||
Qy    814 EFKCADPTA-LSNETIGIIFKHGDDIRQDMLILQIIRIMESIWETESLDLCLLPYGCIST 872
           ||||||||   :|:|||:||:|||:|||||:::|::|:|:|::|:::|:|||||::|||
Db    855 HWKNKNPKSDDLHLPECAMIFNGDDLRQDMLVLQVLEVMDNIWKAANIDCCLNPYAVLPM 914
               ||:||::|::|:|||||||||:||||||:|||:|:|||::|||:||::||||||:|
Qy    873 GDKIGMEIVKDATTIAKIQQST-VGNTG--AFKDEVLSHWLKEKCPIEE---------- 919
           ||::||:::||||:|||:|||:   |||    |::||:|||||||:||
Db    915 GEMIGIIEVVPNCKTIFEIQVGTGFMNTAVRSIDPSFMNKWIRKQCGIEDEKKKSKKDST 974
           ||::|::|:|   ||:|::|:||:||:||::::||:|::|:|||:|:||:|||::|||||
Qy    920 --------KFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNLFHID 964
                    :||||:|||||:|:|||:|||||::|||||||::|::::|::|||||
Db    975 KNPIEKKIDNTQAMKKYFESVDRFLYHSCVGYSVATYIMGIKDRHSDNLMLJTEDGKYVHID 1034
           |||:|||:|||:|::||||||:||||||||||:|||::|:|||:|||:|:|:|:|||||||
Qy    965 FGHILGNYKSFLGINKERVPFVLTPDFLFVM--GTSGKKTSLHFCKFQDVCVKAYLALRH 1022
           |||:||||||:|:||||||:|:|||||||||   |:|||||:|||:||||||::||||||
Db   1035 FGHILGHGKTKLGIQRDRQPFILTEHFMTVIRSGKSVDGNSHELQKFKTLCVEAYEVMMN 1094
           |||:||:|||:||:|||:|:|:||::|:||:|||:|:|||:||||||||||||::|::::
Qy   1023 HTNLLILLFSMMLMTGMPQLTSKEDIEYIRDALTV-GKSEEDAKKYFLDQIEVCRDKGWT 1081
           |:|:|:|||:|:|:||||||:|:|||:|:||||||   |:||:||||||:|:||||:|||
Db   1095 NRDLFVSLFTMLGMELPELSTKADLDHLKKTLFCNGESKEEARKFFAGIYEEAFNGSWS 1154
           ||||||||:|||||:|||:|:|||:||||||:|||||:|::||||:|:||||:||:|||
Qy   1082 VQFNWFLHLV 1091
           ||:|||||:|
Db   1155 TKTNWLFHAV 1164
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RESULT 13
US-10-101-235A-2
; Sequence 2, Application US/10101235A
; Publication No. US20030182669A1
; GENERAL INFORMATION:
; APPLICANT: Rockman, Howard A.
; APPLICANT: Naga Prasad, Sathyamangla V.
; APPLICANT: Laporte, Stephane A.
; APPLICANT: Barak, Larry S.

US-10-101-235A-2

Query Match   16.9%; Score 980; DB 12; Length 204;
Best Local Similarity   93.2%; Pred. No. 8.5e-81;
Matches 193; Conservative   3; Mismatches   3; Indels   8; Gaps 2;

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Qy    521 DNYCHPIALPKHRPTPDPEGDRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRY 580
           |||:|||||:  :    ||||||||||||||||||||||||||||||
Db      6 DDDKHPIALPKHQPTPD--DRVRAEMPNQLRKQLEAIIATD-----TAEDKELLWHFRY 57
          
Qy    581 ESLKDPKAYPKLFSSVKWGQQEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENV 640
           |||:|||||||||||||||||||||||||||||:|||||||||||||||||||||||||
Db     58 ESLKHPKAYPKLFSSVKWGQQEIVAKTYQLLARREVWDQSALDVGLTMQLLDCNFSDENV 117

Qy    641 RAIAVQKLESLEDDDVLHYLLQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLWFWFLR 700
           |||||||||||||:|||||||||||||||||||||||||||||||||||:||||:|||||
Db    118 RAIAVQKLESLEDDDVLHYLLQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLWFWFLR 177

Qy    701 SEIAQSRHYQQRFAVILEAYLRGCGTA 727
           |||||||||||||||||||||||||||
Db    178 SEIAQSRHYQQRFAVILEAYLRGCGTA 204
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RESULT 14
US-10-101-235A-9
; Sequence 9, Application US/10101235A
; Publication No. US20030182669A1
; GENERAL INFORMATION:
; APPLICANT: Rockman, Howard A.
; APPLICANT: Naga Prasad, Sathyamangla V.
; APPLICANT: Laporte, Stephane A.
; APPLICANT: Barak, Larry S.

US-10-101-235A-9

Query Match   16.9%; Score 979; DB 12; Length 195;
Best Local Similarity   94.6%; Pred. No. 9.7e-81;
Matches 192; Conservative   2; Mismatches   2; Indels   1; Gaps 2;

```
Qy    525 HPIALPKHRPTPDPEGDRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLK 584
           |||||||:  |     ||||||||||||||||||||||||||||||||||||||||||||
Db      1 HPIALPKHQPTPD--DRVRAEMPNQLRKQLEAIIATD-----TAEDKELLWHFRYESLK 52

Qy    585 DPKAYPKLFSSVKWGQQEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIA 644
           |||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||
Db     53 HPKAYPKLFSSVKWGQQEIVAKTYQLLARREVWDQSALDVGLTMQLLDCNFSDENVRAIA 112

Qy    645 VQKLESLEDDDVLHYLLQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLWFWFLRSEIA 704
           ||||||||||:||||||||||||||||||||||||||||||||||:||||:|||||||||
Db    113 VQKLESLEDDDVLHYLLQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLWFWFLRSEIA 172

Qy    705 QSRHYQQRFAVILEAYLRGCGTA 727
           |||||||||||||||||||||||
Db    
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              ||||||||||||||||||||||
Db    173 QSRHYQQRFAVILEAYLRGCGTA 195
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RESULT 15
US-09-771-161A-192
; Sequence 192, Application US/09771161A
; Patent No. US2002011011A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 192
;   LENGTH: 887
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-771-161A-192

Query Match        12.1%;     Score 698.5;   DB 10;   Length 887;
Best Local Similarity    25.9%;     Pred. No. 5.2e-54;
Matches 224;    Conservative 146;    Mismatches 259;    Indels 237;    Gaps    30;

Qy    381 VFVEANIQYGQQVLCQRRTSPKFPTEEVLWNWLEFSIKIKDLPKGALLNLQIX----CG 436

Db     63 VFAE-----GKPSALPVRTSYKAFSTRWNWNEWLKLPVXYPDLPRNAQVALIIWDVVGPG 117

Qy    437 KAPALS---------------------------------------GKTSAEMPSPESKGKAQ 459

Db    118 KAVPVGGTTVSLFGKYGMSRQGMHDLKVWPNVEADGSEPTNTPGRTSSTLSEDQMSRLAK 177

Qy    460 LL------YYVNLLLIDHRFLLRHGEYVLH-------MWQLSG------KGEDQ------- 494

Db    178 LTKAHRQGHMVKVDWLD-RLTFREIEMINESVKRSSNFMYLMGGFRCVKCDDKEYGIVYY 236

Qy    495 --GSFNADKLTS---ATNPDKENSMSISILLDNYCHPIALPKH--------RPTPDP 538

Db    237 EKDGDESSPILTSFPLVKVPDPQ--MSLENLVESKHH-NLPRSLRSGPSDHDLKPYPSP 292

Qy    539 EGDRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKW 598

Db    293 ------RDQLKNIVSYPPSKPPTYEEQDLVWEFRYYLTNQDKALTKILTSVIW 339

Qy    599 GQQEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLH 658

Db    340 DLPQGAKQALALLGK---W--NPMDVEDSLELISSHYTNPTVRRYAVARLRQADDEDLLM 394

Qy    659 YLLQLVQAVKFEPYHD-------------------------------------------- 674

Db    395 YLSQIVQALKYENFDDIKNGLEPTKKDSQSSVSGNVSNSGINSAEIDSSQIITSPLFSVS 454

Qy    675 -------------SALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVI 716

Db    455 SPPPASKTKEVPDGENLEQDLCTFLISRASKNSTLANYLWYVIVE-CEDQDTQQRDPKT 513

Qy    717 LEAYLRGCGTAMLRDFTQQVQVIMLQKVTIDIKSLSAEKYDVSSQVISQL--------- 767

Db    514 HEMYLN-----VMRRFSQALLKGDKSVRV---MRSLLAQQTFVDRLVHLMKAVQRESGN 565

Qy    768 -KQKLENLQ-------NLNLPQSFRVPYDPGLKAGALVIEKCKVMASKKKPIWLEFKC 817

Db    566 RKKKNERLQALLGDNEKMMLSDVELIPLPLEPQVKIRGIIPETATLFKSALMPAQLFKT 625

Qy    818 ADPTALSNETIGIIPKHGDDLRQDMLILQLRIMESIWETESLDLCLLPYGCISTGDKIG 877
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Db    626 ED-----GGKYPVIFKHGDDLRQDLLQIISLMDKLLRKENLDLXLTPYKVLATSTKHG 680

Qy    878 MIEIVKDATTIAKIQQSTVGNTGAFKDEVLSHWLKEKCPIEK----FQAAVERFVYSCA 933

Db    681 FMQFIQ-SVPVAEV-LDTEGS--------IQNFFRKYAPSENGPNGISAEVMDTYVKSCA 730

Qy    934 GYCVATFVLGIGDRHNDNIMISETGNLFHIDFGHILGNYKSFL---GINKERVPFVLTP 989

Db    731 GYCVITYILGVGDRHLDNLVLTKGKLFHIDFGYILGRDPKPLPPPMKLNKE-------- 782

Qy    990 DFLFVMGTSGKKTSLHFQKFQDVCVKAYLALRHHTNLLILFSMMLMTGMPQLTSKED-- 1047

Db    783 ---MVEGMGGTQ-SEQYQEFRKQCYTAFLHLRRYSNLILNLFSLMVDPNIPDIALEPDKT 838

Qy   1048 IEYIRDALTVGKSEEDAKKYFLDQIE 1073

Db    839 VKKVQDFRLDLSDEEAVHYMQSLID 864
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Search completed: February 15, 2004, 02:10:05
Job time : 89 secs
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            GenCore version 5.1.6
      Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on:    February 15, 2004, 02:08:37 ; Search time 9655 Seconds
                                (without alignments)
                                4669.333 Million cell updates/sec

Title:          US-09-974-573-1
Perfect score:  5790
Sequence:       1 MELENYEQPVVLREDNRRRR.........QFNWFLHLVLGIKQGEKHSA 1102

Scoring table:  BLOSUM62
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                Ygapop  10.0 , Ygapext  0.5
                Fgapop   6.0 , Fgapext  7.0
                Delop    6.0 , Delext   7.0

Searched:       2888711 seqs, 2045813386 residues

Total number of hits satisfying chosen parameters:    5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09974573/runat_11022004_180013_18093/app_query.fasta_1.1287
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09974573_@CGN_1_16581 @runat_11022004_180013_18093 -NCPU=6 -ICPU=3
-NO_NMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database  :     GenEmbl:*
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           8:   gb_pl:*
           9:   gb_pr:*
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          12:   gb_sy:*
          13:   gb_un:*
          14:   gb_vi:*
          15:   em_ba:*
          16:   em_fun:*
          17:   em_hum:*
          18:   em_in:*
          19:   em_mu:*
          20:   em_om:*
          21:   em_or:*
          22:   em_ov:*
          23:   em_pat:*
          24:   em_ph:*
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          26:   em_ro:*
          27:   em_sts:*
          28:   em_un:*
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          29:   em_vi:*
          30:   em_htg_hum:*
          31:   em_htg_inv:*
          32:   em_htg_other:*
          33:   em_htg_mus:*
          34:   em_htg_pln:*
          35:   em_htg_rod:*
          36:   em_htg_mam:*
          37:   em_htg_vrt:*
          38:   em_sy:*
          39:   em_htgo_hum:*
          40:   em_htgo_mus:*
          41:   em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

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Result          %
No.     Score   Query   Length  DB      ID          Description
                Match
-------------------------------------------------------------------------
  1     5785    99.9    3808     4      SSP120       Y10743 S.scrofa mR
  2     5726    98.9    3808     6      AR026673     AR026673 Sequence
  3     5726    98.9    3808     6      AR026679     AR026679 Sequence
  4     5726    98.9    3808     6      AR029062     AR029062 Sequence
  5     5726    98.9    3808     6      AR033966     AR033966 Sequence
  6     5538    95.6    3860     9      BC035683     BC035683 Homo sapi
  7     5534    95.6    3410     9      AF327656     AF327656 Homo sapi
  8     5534    95.6    5162     6      AR026677     AR026677 Sequence
  9     5523.5  95.4    5397     9      AX327655     AX327655 Sequence
 10     5523.5  95.4    5397     9      HSIDEM       X83368 H.sapiens m
 11     5506    95.1    4725    10      MMU249280    AJ249280 Mus muscu
 12     5505    95.1    4330    10      BC051246     BC051246 Mus muscu
 13     5499.5  95.0    4137     6      A50265       A50265 Sequence 3
 14     5476.5  94.6    3342    10      AF208345     AF208345 Mus muscu
 15     5440    94.0    4134     6      A50263       A50263 Sequence 1
 16     3318    57.3   107527    9      AC005018     AC005018 Homo sapi
 17     3291    56.8   186349    2      AC073420     AC073420 Homo sapi
 18     3287    56.8    2080    10      MMU249413    AC249413 Mus muscu
 19     3286.5  56.8   146761    2      AC132894     AC132894 Mus muscu
 20     3286.5  56.8   164211    2      AC115801     AC115801 Mus muscu
 21     3286.5  56.8   198298    2      AC140314     AC140314 Mus muscu
 22     3280.5  56.7   221422    2      AC129663     AC129663 Rattus no
 23     1470.5  25.4    3452     5      AF001076     AF001076 Gallus ga
 24     1466.5  25.3    3424     9      AX327651     AX327651 Sequence
 25     1466.5  25.3    3424     9      HSPHI3K      Z29090 H.sapiens m
 26     1465.5  25.3    3207     4      BOVPHOS3KN   M93252 Bovine phop
 27     1465.5  25.3    3207     6      A75936       A75936 Sequence 36
 28     1465.5  25.3    3207     6      AR048987     AR048987 Sequence
 29     1465.5  25.3    3207     6      AR064288     AR064288 Sequence
 30     1465.5  25.3    3207     6      AR164681     AR164681 Sequence
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 32     1465.5  25.3    3498     6      A37232       A37232 Sequence 1
 33     1460.5  25.2    3240     6      AR048986     AR048986 Sequence
 34     1460.5  25.2    3240     6      AR064287     AR064287 Sequence
 35     1460.5  25.2    3240     6      AR164680     AR164680 Sequence
 36     1460.5  25.2    3412     6      A75939       A75939 Sequence 39
 37     1460.5  25.2    3412     6      AR048985     AR048985 Sequence
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 39     1460.5  25.2    3412     6      AR164679     AR164679 Sequence
 40     1450.5  25.1    3207    10      MMU03279     U03279 Mus musculu
 41     1450.5  25.1    3389    14      AF001075     AF001075 Avian sar
 42     1366    23.6   225277    2      AC129863     AC129863 Rattus no
 43     1362    23.5    3213    10      RNO012482    AJ012482 Rattus no
 44     1358    23.5    1921     3      AK113227     AK113227 Ciona int
 45     1354.5  23.4    3213     6      AR116356     AR116356 Sequence
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ALIGNMENTS

RESULT 1

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LOCUS       SSP120
DEFINITION  S.scrofa mRNA for p120-PI3K protein.
ACCESSION   Y10743                       3808 bp    mRNA    linear    MAM 12-MAY-1998
VERSION     Y10743.1  GI:3133115
KEYWORDS    p120-PI3K protein.
SOURCE      Sus scrofa (pig)
ORGANISM    Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1
AUTHORS     Stephens,L.R., Eguinoa,A., Erdjumen-Bromage,H., Lui,M., Cooke,F.,
            Coadwell,J., Smrcka,A., Thelen,M., Cadwallader,K., Tempst,P. and
            Hawkins,P.T.
TITLE       The G beta gamma sensitivity of a PI3K is dependent upon a tightly
            associated adaptor, p101
JOURNAL     Cell 89 (1), 105-114 (1997)
MEDLINE     97248491
PUBMED      9094719
REFERENCE   2
AUTHORS     Stephens,L.R.
TITLE       Direct Submission
JOURNAL     Submitted (23-JAN-1997) L.R. Stephens, Babraham Institute,
            Babraham, Cambridge, CB2 4AT, UK
REMARK      revised by [3]
REFERENCE   3  (bases 1 to 3808)
AUTHORS     Stephens,L.R.
TITLE       Direct Submission
JOURNAL     Submitted (24-APR-1998) L.R. Stephens, Babraham Institute,
            Babraham, Cambridge, CB2 4AT, UK
COMMENT     On May 15, 1998 this sequence version replaced gi:1935003.
FEATURES             Location/Qualifiers
     source          1..3808
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /db_xref="taxon:9823"
                     /dev_stage="adult"
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                     /protein_id="CAA71731.1"
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                     /function="catalytic subunit of G-beta-gamma-activated
                     PI3K"
                     /translation="MELENYEQPVVLREDNRRRRRRRMKPRSTAASLSSMELIPIEFVL
                     PTSQRNTKTPETALLHVAGHGNVEQMKAQVWLRALETSVSADFYHRLGPDHFLLLYQK
                     KGQWYEIYDKYQVVQTLDCLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRQLNALIGY
                     DVTDVSNVHDDELEFTRRRLVTPRMAEVAGRDPKLYAMHPWVTSKPLPEYLLKKITNN
                     CVFIVIHRSTTSQTIKVSADDTPGTILQSFFTKMAKKKSLMDIPESQNERDFVLRVCG
                     RDEYLVGETPIKNFQWVRQCLKNGEIHVVLDTPPDPALDEVRKEWPIVDDCTGVTG
                     YHEQLTIHGKDHESVPTVSLWDCDRKFRVKIRGIDIPVLPRTADLTVFVEANIQYGQQ
                     VLCQRRTSPKPFTEEVLMNVWLEFSIKIKDLPKGALLNLQIYCKAPALSGKITSRTNP
                     SPESKGKAQLLYYVNLLLIDHRFLRHGEYVLHMWQLSGKEDQGSFNADKLTSRTNP
                     DKENSMSISILLDNYCHPIALPKHRPTDPEGDRVRAEMPNQLRKQLEAIIATDPLNP
                     LTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGGQEIVAKTYQLLAKREVWDQSALDV
                     GLTMQLLDCNSDENVRAIAVQKLESLEDDDVLHYLLQLVQAVKFEPYHDSALARFLL
                     KRGLRNKRIGHFLFWFLRSEIAQSRHYQQRPAVILEAYLRGGGCTAMLHDFTQVQVID
                     MLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLPQSFRVPYDPGLKAGALVI
                     EKCKVMASKKKPLWLEFKCADPTALSNETGIIFPKHGDDLRQDMLILQILRIMESIWE
                     TESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTGAFKDEVLSHWLKEK
                     CPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNLFHIDFGHILGNY
                     KSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLALRHHTNLLIIL
                     FSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGWTVQFNWFL
                     HLVLGIKQGEKHSA"
BASE COUNT      1012 a    971 c    949 g    876 t
ORIGIN
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Alignment Scores:

Pred. No.:   0
Score: 5785.00
Percent Similarity: 99.91%
Best Local Similarity: 99.91%

Length: 3808
Matches: 1101
Conservative: 0
Mismatches: 1

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Query Match:    99.91%
DB:                  4

US-09-974-573-1 (1-1102) x SSP120 (1-3808)

Qy      1 MetGluLeuGluAsnTyrGluGlnProValValLeuArgGluAspAsnArgArgArgArg  20
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     89 ATGGAGCTTGAGAACTATGAACAGCCCGGTGGTGCTGAGAGAGGACAACGGCCGCAGGCGT 148

Qy     21 ArgArgMetLysProArgSerThrAlaAlaSerLeuSerSerMetGluLeuIleProIle  40
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    149 CGGAGGATGAAGCCCGAGCACGCAGCCGCCAGCTGTCCTCCATGGAGCTCATCCCCATC 208

Qy     41 GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeuLeuHis  60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    209 GAGTTTGTTTTGCCCACCAGCCAGCGCAACACCAAGACCCCCGAAACGGCACTGCTGCAC 268

Qy     61 ValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnValTrpLeuArgAlaLeuGlu  80
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    269 GTGGCCGGCCACGGCAATGTGGAGCAGATGAAGGCCCAGGTGTGGCTGCGCGCGCTGGAG 328

Qy     81 ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTyr 100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    329 ACGAGCGTGTCTGCGGACTTCACCACCGGCTCGGCCCCCGACCACTTCCTCCTGCTCTAC 388

Qy    101 GlnLysLysGlyGlnTrpTyrGluIleTyrAspLysTyrGlnValValGlnThrLeuAsp 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    389 CAGAAGAAGGGCCAGTGGTACGAGATCTATGACAAGTACCAGGTGGTGCAGACCCTGGAC 448

Qy    121 CysLeuArgTyrTrpLysValLeuHisArgSerProGlyGlnIleHisValValGlnArg 140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    449 TGCCTGCGCTACTGGAAGGTGTTGCACCGGAGCCCGGGCCAGATCCACGTGGTCCAGCGG 508

Qy    141 HisAlaProSerGluGluThrLeuAlaPheGlnArgGlnLeuAsnAlaLeuIleGlyTyr 160
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    509 CACGCGCCCTCCGAGGAGACCATTGGCCTTCCAGCGCCAGCTGAACGCCCTCATCGGCTAC 568

Qy    161 AspValThrAspValSerAsnValHisAspAspGluLeuGluPheThrArgArgArgLeu 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    569 GACGTCACCGACGTCAGCAACGTGCATGACGATGAGCTCGAGTTCACCCGGCGCCGCCTG 628

Qy    181 ValThrProArgMetAlaGluValAlaGlyArgAspProLysLeuTyrAlaMetHisPro 200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    629 GTCACCCCGCGCATGGCCGAGGTGGCCGGCCGAGACCCCAAGCTTTACGCCATGCACCCC 688

Qy    201 TrpValThrSerLysProLeuProGluTyrLeuLeuLysLysIleThrAsnAsnCysVal 220
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    689 TGGGTGACATCCAAGCCCCTGCCCGAGTACCTTCTGAAGAAGATCACTAACAACTGCGTC 748

Qy    221 PheIleValIleHisArgSerThrThrSerGlnThrIleLysValSerAlaAspAspThr 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    749 TTCATCGTCATTCACCGCAGCACCACCAGCCAGACCATCAAGGTCTCGGCCGATGACACC 808

Qy    241 ProGlyThrIleLeuGlnSerPhePheThrLysMetAlaLysLysLysSerLeuMetAsp 260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    809 CCAGGCACCATCCTGCAGAGCTTCTTCACCAAGATGGCCAAGAAGAAATCTCTGATGGAT 868

Qy    261 IleProGluSerGlnAsnGluArgAspPheValLeuArgValCysGlyArgAspGluTyr 280
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    869 ATCCCTGAAAGCCAGAACGAACGGGACTTTGTGCTGCGGGTCTGCGGCCGGGATGAGTAC 928

Qy    281 LeuValGlyGluThrProIleLysAsnPheGlnTrpValArgGlnCysLeuLysAsnGly 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    929 CTGGTGGGTGAGACGCCCATCAAGAACTTCCAGTGGGTGAGGCAGTGCCTCAAGAATGGG 988

Qy    301 GluIleHisLeuValLeuAspThrProProAspProAlaLeuAspGluValArgLysLys 320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    989 GAGGAGATTCACCTTGTCCTGGACACTCCTCCAGACCCCGGCACTGGACGAGGTGAGGAAG 1048

Qy    321 GluGluTrpProLeuValAspAspCysThrGlyValThrGlyTyrHisGluGlnLeuThr 340
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1049 GAAGAGTGGCCGCTGGTCGGTGGATGACTGCACCGGGAGTCACTGGCTACCACCAGCAGCTGACC 1108
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Indels: 0
Gaps: 0

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Qy   341 IleHisGlyLysAspHisGluSerValPheThrValSerLeuTrpAspCysAspArgLys 360
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1109 ATCCACGGCAAGGACCATGAAAGTGTTCACCGTGTCCCTGTGGGACTGTGACCGCAAG 1168

Qy   361 PheArgValLysIleArgGlyIleAspIleProValLeuProValThrAlaAspLeuThr 380
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1169 TTCAGGGTCAAAATCAGAGGCATTGATATCCCTGTCCTGCCCGGACCGCTCACCTCACG 1228

Qy   381 ValPheValGluAlaAsnIleGlnTyrGlyGlnValLeuCysValGlnArgArgThrSer 400
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1229 GTGTTTGTGGAGGCAAACATCCAGTATGGGCAGGTCCTTTGCCAAAGGAGGACCAGC 1288

Qy   401 ProLysProPheThrGluGluValLeuTrpAsnValTrpLeuGluPheSerIleLysIle 420
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1289 CCCAAACCCTTCACGGAGGAGGTGCTCTGGAACGTGTGGCTTGAGTTCAGTATTAAAATC 1348

Qy   421 LysAspLeuProLysGlyAlaLeuLeuAsnLeuGlnIleTyrCysGlyAlaProAla 440
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1349 AAAGACTTACCCAAAGGGGCTCTGCTGAACCTCCAGATCTACTGCGGCAAAGCTCCAGCA 1408

Qy   441 LeuSerGlyLysThrSerAlaGlyMetProSerProGluSerLysLysGlyAlaGlnLeu 460
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1409 CTGTCTGGCAAGACCTCTGCAGAGATGCCCAGTCCCGAGTCCAAAAAGGCAAAGCTCAGCTT 1468

Qy   461 LeuTyrTyrValAsnLeuLeuTyrLysAspHisArgPheLeuArgHisHisGlyGluTyr 480
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1469 CTGTACTATGTCAACCTATTGTATAAGGACCACCGCTTCCTCCGCCATCATGGCGAGTAT 1528

Qy   481 ValLeuHisMetTrpGlnLeuSerGlyLysGlyGlnGlySerPheAsnAlaAsp 500
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1529 GTGCTCCACATGTGGCAGTTATCCGGGAAGGGGCAAGGGAGCTTCAATGCCGAC 1588

Qy   501 LysLeuThrSerAlaThrAsnProAspLysGluAsnSerMetSerIleSerIleLeuLeu 520
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1589 AAGCTCACGTCGCGGACCAACCCCGACAAGGAGAACTCAATGTCTATCTCCATTCTTCTG 1648

Qy   521 AspAsnTyrCysHisProIleAlaLeuProLysHisArgProThrProAspProGluGly 540
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1649 GACAATTACTGCCACCCCATAGCCTTGCCTAAGCACCGGCCTACCCCTGACCCAGAAGGG 1708

Qy   541 AspArgValArgAlaGluMetProAsnGlnLeuArgLysGlnLeuGlnAlaIleIleAla 560
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1709 GACCGGGTTCGGGCAGAAATGCCCAATCAGCTTCGGAAGCAACTGCAGGCAATCATAGCC 1768

Qy   561 ThrAspProLeuAsnProLeuThrAlaGluLysAspLysLysGluLeuLeuTrpHisPheArgTyr 580
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1769 ACGGATCCGCTTAACCCACTCACAGCTGAGAAAGATGAGACTGCCTCTGGCATTTCAGATAT 1828

Qy   581 GluSerLeuLysAspProLysProLysProLeuProLeuPheSerSerValLysTrpGlyGln 600
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1829 GAAAGCCTGAAGGATCCCAAAGCGTATCCTAAGCCTCTTTAGCTCGGTGAAATGGGGACAG 1888

Qy   601 GlnGluValIleAlaLysGlyThrThrTyrArgArgGluIleGlyTrpAspGlnSer 620
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1889 CAAGAAGTTGTGGCCAAAGCATACCAATATTAGCCAAAGGGAGGTCTGGGATCAGAGT 1948

Qy   621 AlaLeuAspValGlyLeuThrMetGlnLeuLeuAspCysAsnPheSerAspGluAsnVal 640
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1949 GCTTTGGATGTGGGGTTAACCATGCAGCTCCTGGACTGCAACTTCTCGGATGAAAACGTG 2008

Qy   641 ArgAlaIleAlaValGlnLeuValGlnLeuGluSerLeuGlnAsnGluLeuHisTyrArgLeu 660
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2009 AGAGCCATTGCAGTCCAGCTGGTCCAGCTGGAGAGTCTGCAGAATGAACTGCATTACCTG 2068

Qy   661 LeuGlnLeuValGlnAlaValPheLysAspProLysPheHisAspAspAlaLeuArgArgPhe 680
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2069 CTCCAGCTGGTCCAGGCTGTGAAATTTGACCCATACCATGACGACGCACTAGCCAGATTT 2128

Qy   681 LeuLeuLysArgGlyLeuArgAsnLysArgIleGlyHisPheLeuPheTrpPheLeuArg 700
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2129 CTGCTGAAGCGTGGTTTAAGGAACAAGAGAATTGGTCACTTCCTGTTTTGGTTCCTTGAGA 2188

Qy   701 SerGlyIleAlaGlnSerArgArgHisTyrGlnAsnArgPheAlaValIleLeuGluAlaTyr 720
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Db  2189 AGTGAGATTGCCCAGTCTAGGCACTATCAGCAGGAGGTTTGCAGTGATCCTGGAGCCTAC 2248

Qy   721 LeuArgGlyCysGlyThrAlaMetLeuHisAspPheThrGlnGlnValGlnValIleAsp 740
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2249 CTGAGGGGCTGTGGCACAGCCATGCTGCACGACTTCACCCAGCAAGTCCAAGTAATTGAC 2308

Qy   741 MetLeuGlnLysValThrIleLysAspIleLysSerSerLeuSerAlaGluLysTyrAspValSer 760
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2309 ATGTTACAAAAAGTCACCATTGACATTAAATGCTCTCTGCTGAAAAGTATGACGTCAGT 2368

Qy   761 SerGlnValIleSerGlnLeuLysGlnLeuSerLeuGluAsnLeuGlnAsnLeuAsnLeuPro 780
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2369 TCCCAAGTTATTTCCCAACTTAAGCAAAAGCTTGAAAACCTACAGAATTTGAATCTCCCC 2428

Qy   781 GlnSerPheArgValProTyrAspProGlyLeuLysAlaGlyAlaLeuValIleGluLys 800
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2429 CAAAGCTTTAGAGTTCCCTATGATCCTGGACTGAAAGCCGGGGCACTGGTGATCGAAAAA 2488

Qy   801 CysLysLysValMetAlaSerLysLysProLeuGluTrpLeuGluPheLysTrpLeuGluCysAlaAspPro 820
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2489 TGTAAAGTGATGGCCTCCAAGAAGAAGCCCCTGGAGTTTAAAATGTCCGATCCT 2548

Qy   821 ThrAlaLeuSerAsnGluThrIleGlyIleLeuArgIleMetGluSerIleTrpGluThrGluSerLeu 840
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2549 ACGGCTCATCAAATGAAACAATTGGAATTATCTTTAAACACGGTGACGATCTGCGCCAA 2608

Qy   841 AspMetLeuLeuGlnIleLeuLeuArgIleMetGluSerIleTrpGluThrGluSerLeu 860
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2609 GACATGCTTATTTTACAGATTCTACGAATCATGGAGTCCATTTGGGAGACCGAATCTTTG 2668

Qy   861 AspLeuCysLeuGluProTyrGlyCysIleSerThrGlyLysLysIleGlyMetIleGlu 880
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2669 GATCTGTGCCTCCTGCCATATGGCTGTATTTCAACTGGTGACAAAATAGGAATGATCGAG 2728

Qy   881 IleValLysAspAlaThrThrIleAlaLysIleGlnGlnSerThrValGlyAsnThrGly 900
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2729 ATCGTGAAGGACGCGCACACCATCGCCAAAATCAGCAAGAGCACAGTGGGCAACACGGGT 2788

Qy   901 AlaPheLysAspGluValLeuSerHisTrpLeuLysSerProIleGluGluLys 920
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2789 GCCTTTAAAGATGAAGTCCTGAGTCACTGGCTCAAGAGAAAATGCCCATTGAAGAGAAAG 2848

Qy   921 PheGlnAlaAlaValGluArgPheValSerCysValAlaGlyTyrTyrCysValAlaAlaThrPhe 940
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2849 TTTCAGGCAGCTGTGGAGAGATTTGTTTATTCCTGTGTGGCCGGCTACTGTGTGGCAACCTTT 2908

Qy   941 ValLeuGlyIleGlyHisAspArgHisAsnAspAsnIleMetIleSerGluThrGlyLeuAsnLeu 960
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2909 GTTCTTGGAATAGGCCACGACAGACACAATGACAATATTATGATCTCAGAAACAGGAAATCTA 2968

Qy   961 PheHisIleAspProGlyHisIleLeuGluGlyTyrArgLysSerPheLeuGlyIleLeuAsnLys 980
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2969 TTTCATATTGATTTCGGACACATTCTTGGAATTACAAAAGTTCCTGGGCATTAATAAA 3028

Qy   981 GluArgValProLeuPheValMetGlyThrSerGlyLys 1000
             |||||||||||||||||||||||||||||||||||||||
Db  3029 GAGAGGGTGCCATTTGTGCTGGTGCATGGGGACTTCTGGAAAG 3088

Qy  1001 LysThrSerLeuHisPheGlnLysPheAspAspAlaValCysValLysValAlaThrLeuLeu 1020
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3089 AAGACAAGTCTACACTTCCAGAAATTTCAGGATGTCTGCGTCAAGGTCGCTGTACCTGG 3148

Qy  1021 ArgHisHisThrAsnLeuLeuIleIleLeuProSerMetMetThrGlyMetPro 1040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3149 CGTCATCACACAAACCTACTGATCATCCTCCCGAGTATGATGACAGGAATGCCC 3208

Qy  1041 GlnLeuThrSerLysGluAspProIleGluTyrIleArgAspAlaLeuThrValGlyLysSer 1060
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3209 CAGTTAACCAGCAAGGAGGACCCCATTGAATACATCCGAGATGCCCTGACAGTGGGCAAAGT 3268

Qy  1061 GluGluAspAlaLysLysTyrPheLeuAspGlnIleLeuValCysArgAspLysGlyLysGlyTrp 1080
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RESULT 2
AR026673
LOCUS   AR026673   3808 bp   DNA   linear   PAT 29-SEP-1999
DEFINITION Sequence 3 from patent US 5856132.
ACCESSION   AR026673
VERSION   AR026673.1 GI:5937513
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 3808)
  AUTHORS   Stephens,L., Hawkins,P.Thomas, and Braselmann,S.
  TITLE   G-beta-gamma regulated phosphatidylinositol-3' kinase
  JOURNAL   Patent: US 5856112-A 3 05-JAN-1999;
FEATURES   Location/Qualifiers
     source   1..3808
                     /organism="unknown"
BASE COUNT   1010 a   965 c   953 g   880 t
ORIGIN

Alignment Scores:

Pred. No.:   0
Score: 5726.00   Length: 3808
Percent Similarity: 99.46%   Matches: 1090
Best Local Similarity: 98.91%   Conservative: 6
Query Match: 98.89%   Mismatches: 6
                                           Indels: 0
DB: Gaps: 0

US-09-974-573-1 (1-1102) x AR026673 (1-3808)

Qy   1 MetGluLeuGluAsnTyrGluGlnProValValLeuProValLeuArgGluArgAspAsnArgArgArgArg   20
         ATGGAGCTGGAGAACTATGAACAGCCCGTGGTGCTGCCCGTGCTGAGAGAGAGAGACAACAGGAGGAGGAGG
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   89 ATGGAGCTGGAGAACTATGAACAGCCCGTGGTGCTGCCCGTGCTGAGAGAGAGAGACAACAGGAGGAGGAGG 148

Qy   21 ArgArgMetLysProArgSerThrAlaAlaSerLeuSerSerMetGluLeuIleProIle   40
         CGGAGGATGAAGCCGCGCAGCACGGCAGCCGCCAGCCTGTCCTCCATGGAGCTCATCCCCATC
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 149 CGGAGGATGAAGCCGCGCAGCACGGCAGCCGCCAGCCTGTCCTCCATGGAGCTCATCCCCATC 208

Qy   41 GluPheValLeuProThrSerGlnArgAsnThrLysThrProGlyThrAlaLeuLeuHis   60
         GAGTTTGTTCTGCCAACCTCTCAGAGGAATACGAAGACGCCCGGAACAGCACTGCTCCAC
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 209 GAGTTTGTTCTGCCAACCTCTCAGAGGAATACGAAGACGCCCGGAACAGCACTGCTCCAC 268

Qy   61 ValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnValTrpLeuArgAlaLeuGlu   80
         GTGGCCGGCCACGGCAATGTGGAGCAGATGAAGGCCCAGGTGTGGCTGCGCGGCCTGGAG
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 269 GTGGCCGGCCACGGCAATGTGGAGCAGATGAAGGCCCAGGTGTGGCTGCGCGGCCTGGAG 328

Qy   81 ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTyr   100
         ACGAGCGTTTCTGCTGACTTCTACCACCGGTTCGGCCCCGACCACTTCCTCCTGGTCTTC
         |||||||||||||||||::::|||||||||||||||||||||||||||||||||||||||
Db 329 ACGAGCGTTTCTGCTGACTATTACCACCGGTTCGGCCCCGACCACTTCCTCCTGGTCTTC 388

Qy 101 GlnLysLysGlyGlnTrpTyrGluIleTyrAspLysTyrGlnValValGlnThrLeuAsp   120
         CAGAAGAAGGGGCAGTGGTACGAGATCTATGACAAGTACCAGGTGGTCCAGACCCTGGAC
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Db 389 CAGAAGAAGGGGCAGTGGTACGAGATCTATGACAAGTACCAGGTGGTCCAGACCCTGGAC 448

Qy 121 CysLeuArgTyrTyrLeuGlyValLeuHisSerProGlyGlnIleHisValValGlnArg   140
         TGCCTGCGCTACTATCTGGGAGTTGTTCACAGCCCCGGGCAGATCCACGTGGTCCAGCGG
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 449 TGCCTGCGCTACTATCTGGGAGTTGTTCACAGCCCCGGGCAGATCCACGTGGTCCAGCGG 508

Qy 141 HisAlaProSerGluThrLeuAlaPheGlnArgGlnLeuAsnAlaLeuIleGlyTyr   160
         CACGCGCCCTCGGAGACATTGGCCTTCCAGCGCCAGCTCAACGCCCTCATCGGCTAC
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 509 CACGCGCCCTCGGAGACATTGGCCTTCCAGCGCCAGCTCAACGCCCTCATCGGCTAC 568

Qy 161 AspValThrAspValSerAsnValHisAspAspGluLeuGluPheThrArgArgArgLeu   180
         GACGTCACGGACGTCAGCAACGTGCATGATGACGAGCTGGAGTTCACGCGGCGGCGCCTG
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 629 GACGTCACGGACGTCAGCAACGTGCATGATGACGAGCTGGAGTTCACGCGGCGGCGCCTG 628

Qy 181 ValThrProArgMetAlaGluValAlaAlaGlyTyrAlaAspProLysLeuTyrAlaMetHisPro   200
         GTCACCCCGCGCATGGCCGAGGTGGCGGCCGGCTACGCCGACCCCAAGCTTACGGCCATGCACCCC
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 629 GTCACCCCGCGCATGGCCGAGGTGGCGGCCGGCTACGCCGACCCCAAGCTTACGGCCATGCACCCC 688

Qy 201 TrpValThrSerLysProLeuProGlyTyrLeuLeuLysLysIleThrAsnAsnCysVal   220
         TGGGTGACATCCAAGCCCCTCCCTGGTTACCTCCTGAAGAAGATCACTAACAACTGCGTC
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 689 TGGGTGACATCCAAGCCCCTCCCTGGTTACCTCCTGAAGAAGATCACTAACAACTGCGTC 748

Qy 221 PheIleValIleHisArgSerThrThrSerGlnThrIleLysSerAlaAspAspThr   240
         TTCATCGTCATTCACCGCAGCACCACCAGCCAGACCATCAAGGTTCGGCCGATGACACC
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 749 TTCATCGTCATTCACCGCAGCACCACCAGCCAGACCATCAAGGTTCGGCCGATGACACC 808

Qy 241 ProGlyThrIleLeuGlnSerPhePheThrLysLysMetAlaLysLysSerLeuMetAsp   260
         CCAGGCACCATCCTCCAGAGCTTCTTTACCAAGATGGCCAAGAAGAAATCCTCTGATGGAT
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 809 CCAGGCACCATCCTCCAGAGCTTCTTTACCAAGATGGCCAAGAAGAAATCCTCTGATGGAT 868

Qy 261 IleProGluSerGlnAsnGluValAspPheValLeuArgValCysGlyArgAspGluTyr   280
         ATCCCTGAAAGCCAGAACGAACGGGACTTTGTGCTGCGGGTGTGCGGCCGTGACGAGTAC
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 869 ATCCCTGAAAGCCAGAACGAACGGGACTTTGTGCTGCGGGTGTGCGGCCGTGACGAGTAC 928

Qy 281 LeuValGlyGluThrProIleLysAsnPheGlnTrpValArgGlnCysLeuLysAsnGly   300
         CTGGTGGGTGAGACGCCCATCAAAAATTTCCAGTGGGTGAGGCAGTGCCTGAAGAATGGG
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 929 CTGGTGGGTGAGACGCCCATCAAAAATTTCCAGTGGGTGAGGCAGTGCCTGAAGAATGGG 988

Qy 301 GluGluIleHisLeuValLeuAspThrProProAlaLeuAspProLeuValGlnArgLys   320
         GAGGAGATTCACCTTGTCCTGGACACTCCTCCAGCACCCCTGGACCCGCTGGTGCAGAGGAAG
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 989 GAGGAGATTCACCTTGTCCTGGACACTCCTCCAGCACCCCTGGACCCGCTGGTGCAGAGGAAG 1048

Qy 321 GluGluTrpProLeuValAspAspCysThrGlyValThrGlyTyrHisGluGlnLeuThr   340
         GAAGAGTGGCCCGTGGTGGATGACTGCACGGGAGTCACTGGCTACCACGAGCAGTTGACC
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1049 GAAGAGTGGCCCGTGGTGGATGACTGCACGGGAGTCACTGGCTACCACGAGCAGTTGACC 1108

Qy 341 IleHisGlyLysAspHisGluSerValPheThrValSerLeuTrpAspCysAspArgLys   360
         ATCCACGGCAAGGACCATGAAGTGTCTTTCACCGTGTCCCTGTGGGACTGTGACCGCAAG
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1109 ATCCACGGCAAGGACCATGAAGTGTCTTTCACCGTGTCCCTGTGGGACTGTGACCGCAAG 1168

Qy 361 PheArgValLysIleArgGlyIleGluAspIleProValLeuProArgThrAlaAspLeuThr   380
         TTCAGGGTCAAAATCAGAGGCATTGAAGATATCCCTGTCCTGCCCCGGACCGCTGACCTCACG
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1169 TTCAGGGTCAAAATCAGAGGCATTGAAGATATCCCTGTCCTGCCCCGGACCGCTGACCTCACG 1228

Qy 381 ValPheValGluAlaAsnIleGlnTyrGlyValGlnLeuGlnValArgArgSerThr   400
         GTGTTTGTGGAGGCAAACATCCAGTATGGGGTACAGCTGCAAGTGCGCAGAACCAGC
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1229 GTGTTTGTGGAGGCAAACATCCAGTATGGGGTACAGCTGCAAGTGCGCAGAACCAGC 1288

Qy 401 ProLysProPheThrGluGlnValTrpLeuValTrpLeuGluGlnIlePheLeuGluSerIle   420
         CCCAAACCCTTCACGGAGCAGGTGTGGCTTGTGTGGCTTGAGTTCAGTATTAAAATC
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1289 CCCAAACCCTTCACGGAGCAGGTGTGGCTTGTGTGGCTTGAGTTCAGTATTAAAATC 1348

Qy 421 LysAspProLysProLysLysGlyAlaAlaLeuAsnLeuTyrCysGlyLysAlaProAla   440
         AAAGACCCTAAACCCAAAAAGGGGCTCTGTGAACCTCCAGATTCACTGCGCAAAGCTCCAGCA
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1349 AAAGACCCTAAACCCAAAAAGGGGCTCTGTGAACCTCCAGATTCACTGCGCAAAGCTCCAGCA 1408

Qy 441 LeuSerGlyLysThrSerAlaGluMetProSerProGluLysGlyGlyLysLysAlaGlnLeu   460
         CTGTCTGGCAAGACCTCGCAGAGATGCCCAGTCCCAGAGTCCCAAAGGCAAAGGCAAAGCTCAGCTT
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1409 CTGTCTGGCAAGACCTCGCAGAGATGCCCAGTCCCAGAGTCCCAAAGGCAAAGGCAAAGCTCAGCTT 1468

Qy 461 LeuTyrTyrValAsnLeuLeuLeuIleAspHisArgPheLeuLeuArgHisGlyGluTyr   480
         CTGTACTATGTCAACCTATTGCTGATAGACCACCGGTTCCTCCTGCGCCATGGCGGAGTAT
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1469 CTGTACTATGTCAACCTATTGCTGATAGACCACCGGTTCCTCCTGCGCCATGGCGGAGTAT 1528

Qy 481 ValLeuHisMetTrpGlnLeuSerGlyLysGlnIleAspLysPheAsnAlaAsp   500
         GTGCTCCACATGTGGCAGTTATCCGGGAAGGGGAAGACCAAGGAGCTTCAATGCCGAC
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1529 GTGCTCCACATGTGGCAGTTATCCGGGAAGGGGAAGACCAAGGAGCTTCAATGCCGAC 1588

Qy 501 LysLeuThrSerAlaThrAsnProAspLysGlyAsnSerMetSerIleSerLeuLeuLeu   520
         AAGCTCACGTCGGCAACCAACCCGGACAAGGGAGGGACTCAAGTGCCAATGTCCATCTCCATTCTTCTG
         |||||::::|||||||||||||||||||||||||||||||||||:::::|||||||||||||||||||||
Db 1589 AAGCTCACGTCGGCAACCAACCCGGACAAGGGAGGGACTCAAGTGCCAATGTCCATCTCCATTCTTCTG 1648

Qy 521 AspAsnTyrCysHisProIleAlaLeuProLysHisArgProThrProAspProGluGly   540
         CACGGGCCCTCGGAGGAGACATTGGCCTTCCAGCGCGCCAGCGCCCTCAAGGCCCTCATCGGCTAC
         ...

Db 3269 GAGGAGGATGCTAAAAAGTATTTCTGGATCAGATTGAAGTTGCAGAGACAAAGGATGG 3328

Qy 1081 ThrValGlnPheAsnTrpPheLeuIleHisLeuValLeuGlyIleLeuLysGlyGlnLeuLysHis 1100
         ACCGTGCAGTTTAACTGGTTCTTACATCTTGTTCTTGGCATCAAAACAAGGGGAGAAGCAT
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3329 ACCGTGCAGTTTAACTGGTTCTTACATCTTGTTCTTGGCATCAAAACAAGGGGAGAAGCAT 3388

Qy 1101 SerAla 1102
         TCCGCA
         ||||||
Db 3389 TCCGCA 3394

Db 1649 GACAATTACTGCCACCCCATAGCCTTGCCTAAGGATCCGGCCTACCCCTGACCCAGAGGG 1708

Qy   541 AspArgValArgAlaGluMetProAsnGlnLeuArgLysGlnLeuLeuGluAlaIleIleAla 560
Db 1709 GACCGGGTTCGGGCAGAAATGCCCAATCAGCTTCGGAAGCAACTGCTGGAGGCAATCATAGCC 1768

Qy   561 ThrAspProLeuAsnProLeuThrAlaGluLysLysAspLysLeuTrpHisPheArgTyr 580
Db 1769 ACGGATCCGCTTAACCCACTCACAGCTGAGAAGAAAGACTGCTCTGGCATTCAGATAT 1828

Qy   581 GluSerLeuLysAspProLysAlaTyrProLysLeuPheSerSerValLysTrpGlyGln 600
Db 1829 GAAAGCCTGAAGGATCCCAAAGCGTATCCTAAGCTCTTTAGCTCCGTGAAATGGGGACAG 1888

Qy   601 GlnGluIleValAlaLysThrTyrGlnLeuLeuAlaLysArgGluValTrpAspGlnSer 620
Db 1889 CAAGAAATTGTGGCCAAAACATACCAATTATTAGCCAAAAGGGAGGTCTGGGATCAGAGT 1948

Qy   621 AlaLeuAspValGlyLeuThrMetGlnLeuLeuAspCysAsnPheSerAspGluAsnVal 640
Db 1949 GCTTTGGATGTGGGGTTAACCATGCAGCTCCTGGACTGCAACTTCTCCGATGAAAACGTG 2008

Qy   641 ArgAlaIleAlaValAlaGlnLysLeuGluSerLeuGluAspAspAspValLeuHisTyrLeu 660
Db 2009 AGAGCCATTGCAGTCGCACAGAAACTGGAGAGCCTGGAGGATGATGACGTGCTCCATTACCTG 2068

Qy   661 LeuGlnIleValGlnAlaValLysPheGluProTyrHisAspSerAlaLeuAlaArgPhe 680
Db 2069 CTCCAGCTGGTCCAGGCTGTGAAATTTGAACCATACCATGACAGTGCCCTAGCCAGATTT 2128

Qy   681 LeuLeuLysArgGlyLeuArgAsnLysArgIleGlyHisPheLeuPheTrpPheLeuArg 700
Db 2129 CTGCTGAAGCGTGGTTTAAGAAACAAGAGAATTGGTCACTTCTTGTTTTGGTTCTTGAGA 2188

Qy   701 SerGluIleAlaGlnSerArgHisTyrGlnGlnArgPheAlaValIleLeuGluAlaTyr 720
Db 2189 AGTGAGATTGCCCAGTCCAGTCGACTATCAGCAGGAGGTTTGCAGTGATCCTGGAAGCTAC 2248

Qy   721 LeuArgGlyCysGlyThrAlaMetLeuHisAspPheThrGlnGlnValGlnIleLeuAsp 740
Db 2249 CTGAGGGGCTGTGGCACAGCCATGCTGCACGACTTCACCCAGCAAGTCCAAGTAATTGAC 2308

Qy   741 MetLeuGlnLysValThrIleAspIleLysSerLeuSerAlaGluLysTyrAspValSer 760
Db 2309 ATGTTACAAAAAGTCACCATTGACATTAAATCGCTCTCTGCTGAAAAGTATGACGTCAGT 2368

Qy   761 SerGlnValIleSerGlnLeuLysLysGlnLeuLeuGluAsnLeuGlnAsnLeuAsnLeuPro 780
Db 2369 TCCCAAGTTATTTCCCAACTTAAGAAACAGCTTAAGGTCACTTCTAGGACAAAGCTTAACTACAGATTTGAATCTCCCC 2428

Qy   781 GlnSerPheArgValProTyrAspProProGlyLeuLysLysLeuAlaGlyValIleGluLysLys 800
Db 2429 CAAAGCTTTAGAGTTCCCTATGATCCTCCTGGACTGAAAAGCTGGGGCACTGGTGATCGAAAAA 2488

Qy   801 CysLysValMetAlaSerLysLysLysProLeuTrpLeuGluPheLysCysAlaAspProPro 820
Db 2489 TGTAAAGTGATGGCCTCCAAGAAGAGAGAGCCCCTGTGGCTTGAGTTTAAATGTGCCGATCCT 2548

Qy   821 ThrAlaLeuSerAsnGluThrIleGlyIleIleGluTyrIleGluPheLysGlyHisGlyAspLeuArgGln 840
Db 2549 ACGGCTCTCATCAAATGAAACAATTGGAATTATCTTTAAACACCGTGACGATCTGCGCCAA 2608

Qy   841 AspMetMetLeuGlnIleLeuGlnIleAspArgIleMetGluSerIleLeuTrpGluThrGluSerLeu 860
Db 2609 GACATGCTTATTTTACAGATTCTACGAATCATGGAGTCTATTTTGGGAGACCGAATCTTTG 2668

Qy   861 AspLeuCysSerLeuLeuProTyrGlyTyrGlyCysIleSerThrGlyLysAspValLysLysIleGlyMetIleGluGlu 880
Db 2669 GATCTGTGCTCCCTGCCATATGGCTGCATTTCAACTGGTGCAAAAGATATGGATGATGAG 2728

Qy   881 IleValLysAspAlaThrThrIleAlaLysIleLeuGlnIleSerThrValGlyAsnThrGly 900
Db 2729 ATCGTGAAGGACGCCACGACAATCGCCAAAAATTCAGCAAAGACCAGTGGGCAACACGGGT 2788

Qy   901 AlaPheLysAspGluValLeuSerHisTrpLeuLysGluLysCysProIleGluGluLys 920
Db 2789 GCCTTTAAGACAATGAAGTCCGAGTCACTGGCTCAAAGAAAAATGCCCTATTGAAGAAAAG 2848

Qy   921 PheGlnAlaAlaValGluArgPheValTyrSerCysAlaGlyThrCysValAlaThrPhe 940
Db 2849 TTTCAGGCAGCTGTGGAGAGATTTGTTTATTCCTGTGCCGGCTACTGTGTGGCAACCTTT 2908

Qy   941 ValLeuGlyIleGlyAspArgHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeu 960
Db 2909 GTTCTTGGAATAGGCGACAGACACAATGACAATATTATGATCTCAGAAACAGGAAATCTA 2968

Qy   961 PheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLys 980
Db 2969 TTTCATATTGATTTCGGACACATTCTGGGAAATTACAAAAGTTTCCTGGGCATTAATAAA 3028

Qy   981 GluArgValProPheValLeuThrProAspPheValMetGlyThrSerGlyLys 1000
Db 3029 GAGAGGGTGCCATTTGTCTAACCCAGACTTCCTGTTTGTGATGGGGACTTCTGGAAAG 3088

Qy 1001 LysThrSerLeuHisPheGlnLysAspValCysValLysAlaTyrLeuAlaLeu 1020
Db 3089 AAGACAAGTCTCACACTTCCAGAAATTTCAGGATGTGTGCGTCAAGGCTTACCTAGCCCTT 3148

Qy 1021 ArgHisHisThrAsnLeuLeuIleIleLeuPheSerMetMetThrGlyMetPro 1040
Db 3149 CGTCATCACACAAACCTACTGATCATCCTCTTCCCATGATGCTGATGACAGGAATGCC 3208

Qy 1041 GlnLeuThrSerLysGluGluIleGluTyrIleArgAspAlaLeuThrValGlyLysSer 1060
Db 3209 CAGTTAACCAGCAAAGAAGAAATTGAATACATTCGGGATGCCCTCACAGTGGGCAAAAGT 3268

Qy 1061 GluGluAspAlaLysLysTyrPheLeuAspGlnIleGluValCysArgAspLysGlyTrp 1080
Db 3269 GAGGAGGATGCTAAAAAGATATTTCTGGATCAGATTGAAGTTGCAGAGACAAAGGATGG 3328

Qy 1081 ThrValGlnPheAsnTrpPheLeuHisLeuValLeuGlyIleLysGluGlyLysHis 1100
Db 3329 ACCGTGCAGTTTAACTGGTTCTTACATCTTGTTCTTGGCATCAAACAAGGGGAGAAGCAT 3388

Qy 1101 SerAla 1102
Db 3389 CCCGCA 3394

Alignment Scores:

Pred. No.:	0	Length:	3808
Score:	5726.00	Matches:	1090
Percent Similarity:	99.46%	Conservative:	6
Best Local Similarity:	98.91%	Mismatches:	6
Query Match:	98.89%	Indels:	0
DB:	6	Gaps:	0

US-09-974-573-1 (1-1102) x AR026679 (1-3808)

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Qy    1  MetGluLeuLeuGlnAsnTyrGluGlnProValValLeuArgGluAspAsnArgArgArg   20
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   89  ATGGAGCTGGAGAACTATGAACAGCCCGTGGTGCTGAGAGAGGACAACCGCCGCAGCCGT  148

Qy   21  ArgArgMetLysProArgSerThrAlaAlaSerLeuSerMetGluLeuIleProIle     40
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  149  CGGAGGATGAAGCCCCGGAGCACGGCAGCCAGCCTGTCCATGGAGCTCATCCCCATC    208

Qy   41  GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeuLeuHis   60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  209  GAGTTTGTTTTGCCCACCAGCCAACAGAACACCAAGACCCCAGAAACGGCACTGCTGCAC  268

Qy   61  ValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnValTrpLeuArgAlaLeuGlu   80
            ||||||||||||||||||||||||::|:|||||||||||||||||||||||||||||||
Db  269  GTGGCCGGCCACGGCAATGTGGAGCAAATGAAGGCCCAGGTGTGGCTGCGCGCCCTGGAG  328

Qy   81  ThrSerValSerAlaAspPheTyrHisArgLeuGlyTyrProAspHisPheLeuLeuTyr  100
            ||||||||||||||||||||||||||||||||||||||||||||||||||:|:||::
Db  329  ACGAGCGTTTCTGCGGACTTCTACCACCGGTTCGGCTACCCGGACCACTTCCTGCTGTAC  388

Qy  101  GlnLysLysGlyGlyTrpTyrTyrGluIleTyrGlyLeuTyrGlnThrLeuAsp       120
            ||||||||||||||||||||||||||||||||||||||||||||::||::
Db  389  CAGAAGAAGGGGGGACTGGTGGTACCAGAGATCTATGACAAGTACCAGGTGTTGCAGACC  448

Qy  121  CysLeuArgGlyTyrTrpLysValLeuHisArgSerProGlyGlnIleHisValValGlnArg  140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  449  TGCCTGCGCTACTGGAAGGTGTTGCACCGGAGTCCAGGCCAGATCCACGTGGTCCAGCGG  508

Qy  141  HisAlaProSerGluGluThrGluLeuAlaPheGlnLeuArgGlnLeuAsnAlaAlaLeuAla  160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  509  CACGCGCCCTCGGAGGAGACAGAGCTGGCCTTCCAGCTGCGCCAGCTCAACGCCGCCCTA  568

Qy  161  AspValThrAspValSerArgAsnValHisAspAspArgGlnLeuGluGlyPheThrArgArgLeu  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  569  GACGTCACCGACGTCAGCAGGAACGTGCATGACGATGACCGGCAGCTGGAGTTCACGCGGCTG  628

Qy  181  AspAspArgValAlaGlyMetAlaGlyValAlaGlyAlaGlyMetProHisAspHisMetHisPro  200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  629  GACCGGGTTCCGGCGCCATGGCCCGGCCGAGGTCGGCCGGTTTACGCGCCATGCACCCC  688

Qy  201  TrpProLysThrSerGlyLysProLeuProGluLeuTyrArgLeuLeuValLysIleThrArgAsnCysVal  220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  689  TGGGGTGGACATCCAAGCCCCGAGTACCTTCGTTTCCTGGAAGATCACTAACAACTGCGTC  748

Qy  221  PheIleValIleHisArgSerThrThrSerGlnThrArgSerGlnGlnPheThrLysLysLysSerAlaAspAspThr  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  749  TTCATCGTCATTCACCGCAGCACCACCAGCCAGACCAGGTCTCAGCAGTTCCTGAAGAAAAGTCTGATGGAT  808

Qy  241  ProGlyThrIleLeuGlnSerPhePheThrPheSerArgMetAlaLysLysSerMetLeuSerMetAsp  260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  809  CCAGGCACCATCCTCCAGAGCTTCTTTACCAAGATGGCCAAGAAGAAATCTCTGATGGAT  868

Qy  261  IleGluProGluSerGlnAsnAsnLeuArgGlnAsnPheLysAsnTrpValLeuArgGlyValCysGlyGluTyr  280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  869  ATCCCTGAAAGCCAGAACAACCTCCGGCAGAACTTTAAGAACTGGGTGCTGCGCGGGGTAC  928

Qy  281  LeuValGlyTyrThrProIleLeuLysAsnPheGlnTrpValArgArgLeuGlyLeuLysLeuLysLeuTyrArgAsnGly  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  929  CTGGTGGGGTGAGACGCGCCATCAAAAAATTTCCAGTGGGTGCGGAGGCAGTGCCTCAAGAATGGG  988

Qy  301  GlnLeuIleHisLeuLeuValAspThrProProProAlaLeuAspGluValArgLys  320
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  989  GAGGAGATTCACCTTGTCGTGGACACTCCTCCTGGAATGTGTTTGGCTTGGAGGAGAAG  1048

Qy  321  GluGluTrpProLeuValAspAspCysThrGlyThrValThrPheGlyTyrHisGluGlnLeuThr  340
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1049  GAAGAGTGGCCGCTGGTGGATGACTGCACGGAGACTGTCACCTGGCTACCACGAGCAGCTGACC  1108

Qy  341  IleHisGlyLysAspHisGluSerValPheThrValSerLeuThrArgPheGlnArgPheAlaValIleLeuGlnAlaTyr  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1109  ATCCACGGCAAGGACCATGAAGTGTTCACCGTGTCCCTGTCCACCGGACTGTGACCCGCAAG  1168
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Qy  361  PheArgValLysIleArgGlyIleAspIleProValLeuProArgThrAlaAspLeuThr  380
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Db 1169  TTCAGGGTCAAAATCAGAGGGATTGATATCCCTGTCCTGCCCCGCACCGCTGACCTCACG  1228

Qy  381  ValPheValGluAlaAsnIleGlnTyrGlyGlnValLeuCysGlnArgArgThrSer    400
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1229  GTGTTTGTTGAGGCAAACATCCAGTATGGGCAGGTGCTGTGCCAAAGGAGAACCAGC   1288

Qy  401  ProLysProPheThrGluGluValGluLeuTrpAsnValPheLeuGluSerIleLysIle  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1289  CCCAAACCCTTCACGGAGGAGGTGGAGCTGTGGAACGTGTTCCTGGAGTCCATTAAAATC  1348

Qy  421  LysAspLeuProLysGlyTyrAlaLeuLeuAsnLeuGlnIleTyrCysGlyLysAlaProAla  440
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1349  AAAGACTTACCCAAAGGGGTCTGCTGAACCTCCAGATCTACTGCGGCAAAGCTCCAGCA  1408

Qy  441  LeuSerGlyLysThrSerAlaGluMetProSerProGluSerLysGlyLysAlaGlnLeu  460
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1409  CTGTCTGGCAAGACCTCTGCAGAGATGCCCAGTCCGGAAAGCAAAGGCAAAGCTCAGCTT  1468

Qy  461  LeuTyrTyrValThrValHisArgProGluLeuLeuLeuGlyLeuGlyLeuGlyGluTyr  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1469  CTGTACTACGTCACGGTGCACAGACCTGAGCTCCTCCTCGGCCTGGGCCTGGGAGAGTAT  1528

Qy  481  ValLeuHisMetTrpGlnLeuSerGlyGlyValAspGlyLysPheAsnAlaAsp       500
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1529  GTGCTCCACATGTGGCAGTTATCCGGAAGGCGAAGACCAGGAGCTTCAATGCCGAC    1588

Qy  501  LysLeuThrSerAlaThrAlaArgProGluLysAsnSerMetSerIleSerIleLeuLeu  520
            ||||||||||||||||||||||||||||||||||||||||:::||||::|||||||||||
Db 1589  AAGCTCACGTCGGGAACCACCCGGCACAAGGACCTCAATGTCCATCTCCATTCTTCTG  1648

Qy  521  AspAsnTyrCysHisProIleAlaAlaLeuProLysHisArgProThrProGluGluGly  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1649  GACAATTACTGCCACCCCATAGCCTTGCCTAAGATCGGCCTACCCCTGACCCCAGAAGGG  1708

Qy  541  AspAspArgValAlaAlaGlyMetProAsnGlnLeuAlaArgLysGlyLeuGlnLeuAlaIleIleAla  560
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1709  GACCGGGTTCCGGCGCAAGTGCCCAATCAGCTTCGGAAGCAACAAAGAACTGCTCTGCAGGCAATCATAGCC  1768

Qy  561  ThrAspProLeuAsnProLeuThrArgAlaGluAspValTyrProLeuSerGluLeuLeuTrpHisPheArgTyr  580
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1769  ACGGATCCGCTTAACCCACTCACAGCTGAAGACGTATCCCAAGCTCTTGAGTTCAGATAT  1828

Qy  581  GluSerLeuLysAspProLysAlaTyrProLeuValSerPheSerSerValLysTrpGlyGln  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1829  GAAAGCCTGAAAGATCCCAAAGCATACCCAAGGAGAGGAGTCTCTGGATGAAATGGGGACAGT  1888

Qy  601  GlnGluIleValAlaLysSerThrTyrGlnLeuLeuLeuAlaAlaArgGluValTrpAspGlnSer  620
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1889  CAAGAAATTGGTGGCCAAAACATACCAATTATTAGCACAAAGGGAGGTCTGGGATCCAGAGT  1948

Qy  621  AlaLeuAspLysValGlyLeuThrMetGlnLeuLeuLeuAspCysAsnPheSerGluAspGluAsnVal  640
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1949  GCTTTGGATGTGGGGTTAACGAGCTCCTGGACTCCGATGAAGAAACGTG  2008

Qy  641  ArgAlaIleAlaValGlnLeuLeuGluSerLeuGluLysHisTyrLeu  660
            ||||||||||||||||||||||||||||||||||||||||||||
Db 2009  AGAGCCATTGCAGTCCAGAAAACTGGAGGATGATGAGCTGCTCCATTACCTG  2068

Qy  661  LeuGlnLeuValGlnAlaValLeuProTyrHisGlnProTyrHisSerAlaLeuAlaArgPhe  680
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2069  CTCCAGCTGGTCCAGGCTGTGAAATTTGAACCATACCATGACAGTGCCCTAGCCAGATTT  2128

Qy  681  LeuLeuValArgGlyLeuArgAsnLysArgIleGlyHisPheLeuPheTrpPheArg  700
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2129  CTGCTGAAGCGTGGTTTAAGAAACAAGAGAATTGGTCACTTCTTGTTTTGGTTCTTGAGA  2188

Qy  701  SerGluIleLeuAlaGlnHisArgHisTyrGlnIleArgPheAlaValIleLeuGlnAlaTyr  720
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Db 2189  AGTGAGATTGCCCAGTGCCAGTTTGCGGCACTATCAGCAGAGGTTTGCAGTGATCCTGAAGCTAC  2248
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Qy  721  LeuArgGlyCysGlyThrAlaMetLeuHisAspPheThrGlnGlnValGlnValIleAsp  740
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Db 2249  CTGAGGGGCTGTGGCACAGCCATGCTGCACGACTTCACCCAGCAAGTCCAAGTAATTGAC 2308

Qy  741  MetLeuGlnLysValThrIleAspPheIleLeuSerLysAlaGluLysTyrAspValSer  760
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Db 2309  ATGTTACAAAAAGTCACCATTGACATTATCCTGTCTCTGCTGAAAAGTATGACGTCAGT  2368

Qy  761  SerGlnValIleSerGlnIleuLysGlnLeuGluAsnLeuAsnLeuAsnLeuAsnLeuPro  780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2369  TCCCAAGTTATTTCCCAACTTAAGCAAAAGCTTGAAAACTTACAGAAATTGAATCTCCCC 2428

Qy  781  GlnSerPheArgValProTyrArgProGlyLeuLysLysAlaGlyAlaLeuValIleGluLys  800
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Db 2429  CAAAGCTTTAGAGTTCCCTATGATCCTGGACTGAAGAAAGCCGGGGCACTGGTGATCGAAAAA 2488

Qy  801  CysLysLysValMetAlaSerLysLysLysLysProLeuTrpLeuGluPheLysCysAlaAspPro  820
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Db 2489  TGTAAAGTGATGGCCTCCAAGAAGAAGCCCCTGTGGCTTGAGTTTAAATGTGCCGATCCT 2548

Qy  821  ThrAlaLeuSerAsnGluThrIleGlyThrIleAlaLysLysPheLysHisGlyAspAspLeuArgGln  840
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Db 2549  ACGGCTCTATCAAATGAAACAATTGGAATTATCTTAAACACGGTGACGATCTGCGCCAA  2608

Qy  841  AspMetLeuIleLeuGlnIleLeuLeuArgIleMetGluSerIleLeuTrpGluThrGluSerLeu  860
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Qy  861  AspLeuCysLeuLeuProTyrGlyTyrCysIleSerThrGlyAspAspLysIleLeuSerIleIleGluGlu  880
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Db 2669  GATCTGTGCCCTCCTGCCATATGGCTGCATTTCAACTGGTGACAAAATAGGAATGATCGAG 2728

Qy  881  IleValLysLysAspAlaThrThrIleAlaLysLysIleAlaLysLysGlnIleSerThrValGlyAsnThrGly  900
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Db 2729  ATCGTGAAGAAGGACGCCACGACAATGCCAAAATTCAGCAAAGCACAGTGGCACACGGGT 2788

Qy  901  AlaPheLysAspGluValLeuSerHisGlnLeuSerTrpLeuLysSerGluGlyCysProIleGluGluLysLys  920
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Db 2789  GCCTTTAAAGATGAAGTCCTGAGTCACTGGCTCAAAGAAAAATGCCCTATTGAAGAAAAG 2848

Qy  921  PheGlnIleAlaAlaValGluArgPheValTyrSerCysAlaGlyTyrCysValAlaThrPhe  940
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Db 2849  TTTCAGGCAGCTGTGGAGAGATTTGTTTATTCCTGTGCCGGCTACTGTGTGGCAACCTTT 2908

Qy  941  ValLeuGlyIleGlyAspArgHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeu  960
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Db 2909  GTTCTCGGAATAGGCGACAGACAATGACAATATTATGATCTCAGAAACAGGAAATCTA  2968

Qy  961  PheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleLeuAsnLys  980
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Db 2969  TTTCATATTGATTTCGGACACATTCTTGGAAATTACAAAAGTTTCCTTGGCATTAATAAA 3028

Qy  981  GluArgValProPheLeuThrProPheLeuGluValMetGlyThrSerGlyLysLys 1000
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Db 3029  GAGAGGGTGCCATTTGTAACCCCAGACTTCCTGTTTGTGATGGGGACTTCTGGAAAG  3088

Qy 1001  LysThrSerLeuHisSerPheGlnLysPheGlnAsnLeuIleLeuProSerMetMetGlySerValValLysAlaTyrLeuAlaLeu 1020
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Db 3089  AAGACAAGTCTACACTTCCAGAAATTTCAGGATGTCTGCGTCAAGGCTTACCTAGCCCTT  3148

Qy 1021  ArgHisHisThrAsnLeuLeuIleLeuPheSerMetMetThrGlyMetPro 1040
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Db 3149  CGTCATCACCACAACCTACTGATCATCCTCTTCAGTATGATGACAGGAATGCCC  3208

Qy 1041  GlnLeuThrSerLysGluAspIleLeuGluThrValGlyTyrIleArgAspAlaLeuThrValGlyLysSer 1060
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Db 3209  CAGTTAACCAGCAAAGAAGACATTGAATACATTCGGATGCCCTCACAGTGGCAAAAGT  3268

Qy 1061  GluGluAspAlaAlaLysTyrPheLeuAspGlnIleGluAspValCysArgAspLysGlyTrp 1080
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Db 3269  GAGGAGGATGCTAAAAAGTATTTTCTGGATCAGATTGAAGATGTCAGAGACAAAGGATGG 3328

Qy 1081  ThrValGlnPheAsnTrpPheLeuHisLeuValLeuGlyIleLysGlnGlnGlyGluLysHis 1100
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Db 3329  ACCGTGCAGTTTAACTGGTTCTTACATCTTGTTCTTGGCATCAAACAAGGGGAGAAGCAT 3388

Qy 1101  SerAla 1102
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Db 3389  CCCGCA 3394
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RESULT 4
AR029062

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LOCUS       AR029062                3808 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 3 from patent US 5859201.
ACCESSION   AR029062
VERSION     AR029062.1  GI:5941035
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3808)
  AUTHORS   Stephens,L. and Hawkins,P.Thomas.
  TITLE     G-beta-gamma regulated phosphatidylinositol-3' kinase
  JOURNAL   Patent: US 5859201-A 3 12-JAN-1999;
FEATURES             Location/Qualifiers
     source          1..3808
                     /organism="unknown"
BASE COUNT     1010 a    965 c    953 g    880 t
ORIGIN
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Alignment Scores:
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Pred. No.:                          Length:       3808
Score:                      0       Matches:      5726.00
Percent Similarity:   99.46%        Conservative:    1090
Best Local Similarity: 98.91%       Mismatches:         6
Query Match:          98.89%        Indels:             6
DB:                                 Gaps:               0
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US-09-974-573-1 (1-1102) x AR029062 (1-3808)

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Qy    1  MetGluLeuGluAsnTyrGluGlnProValValLeuArgArgArgArgArgArg  20
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   89  ATGGAGCTGGAGAACTATGAACAGCCCGTGGTGCTGAGACGACAACCGCCAGGCGT 148

Qy   21  ArgArgMetLysProArgSerThrAlaAlaSerLeuSerSerMetGluLeuIleProIle  40
         |||||||||||||||||||||||||||||||||||||||||||||||||||:::::
Db  149  CGGAGGATGAAGCCGCGGAGCACGGCAGCCAGCCTGTCCTCCATGGAGCTCATCCCCATC 208

Qy   41  GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeuLeuHis  60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  209  GAGTTTGTTTTGCCAACCAGCCAGCGCAACACCAAGACCCCCGAAACGGCACTGCTGCAC 268

Qy   61  ValAlaGlyHisGlyAsnValGluGlnLysMetLysValAlaGlnGlnValTrpLeuArgAlaLeuGlu  80
         |||||||||||||||||||||||||||||||||||||::::|||||||||||||||||||
Db  269  GTGGCCGGCCACGGCAATGTGGAGCAGAAGATGAAGGTCGCCCAGGGTTGTTGGCGGCTGGAG 328

Qy   81  ThrSerValSerAlaAlaAspPheThrTyrHisArgLeuGlyLysProAspHisPheLeuLeuLeuTyr 100
         |||||||||||||||||||||||||||||||||||::::::
Db  329  ACGAGCGTTTCTGGACTTCTACCACCGGTTCGGCCGTTGTTGCTGCTGTTGCTGTTCCTGTCTTTC 388

Qy  101  GlnLysLysGlyGlnTrpTyrGlyIleLeuTyrArgValGlnValGlnIleThrLeuGlnAsp 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  389  CAGAAGAAGGGGGAGTGGTACGGAGTCATTGACAGAGTCAGTGTGCAGACCCTGGAC 448

Qy  121  CysLeuArgTyrTrpLysTrpTrpAspGlyLeuGlnIleHisValGlnIleArg 140
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db  449  TGCCTGCGCTACTGGAAGTGGTGGGACGGTTGCACCGGCAGATCCACGTGTCCAGCGG 508

Qy  141  HisAlaProSerGluGluThrLeuLeuAlaPheGlnArgGlnLeuAsnAlaLeuIleGlyTyr 160
         |||||||||||||||||||||||||||||||||||||||||||||||||||||:::::
Db  509  CACGCGCCCTCGGAGGAGACATTGGCCTTCAGCGGCCAGTCAAGCGCCCTCATCGGCTAC 568

Qy  161  AspValThrAspValSerAsnValHisAspGluGluSerValAsnGluProGlyAsnGlyArgLeu 180
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Db  569  GACGTCACCGACGTCAGCAACGTGCATGACGAGGAGAGTGTGAATGAGCCGGGCGCCCTG 628
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Qy  181  ValThrProArgMetAlaGluValAlaGlyTyrArgAspProLeuTyrAlaMetHisPro  200        Qy       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  1768
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||              Db  1709 GACCGGGTTCGGCAGAAATGCCAGAAGCAACTCAGCTTCGGAGGCAATCATAGCC  1768
Db  629  GTCACCCCGCGATGGCCGAGGTGGCCGGCCGGCAGCCCCAAGCTTACGCCATGCACCCC  688

Qy  201  TrpValThrSerLysProLeuProGluTyrLeuLysLysIleThrAsnAsnCysVal  220        Qy   561 ThrAspProLeuAsnProLeuThrLeuAlaGluAspLysLysGluLeuLysTrpHisArgTyr  580
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  689  TGGGTGACATCCAAGCCCCTCCCGAGTACCTTCTGAAGAAGATCACTAACAACTGCGTC  748        Db  1769 ACGGATCCGCTTAACCCACTTCAGCTGGCTGAAGACAAAGAACTGCTCTGGCATTTCAGATAT  1828

Qy  221  PheIleValIleHisArgSerThrThrSerGlnThrIleLysValSerAlaAspAspThr  240        Qy   581 GluSerLeuLysAspProLysProLysAlaTyrProLysLeuPheSerSerValLysTrpGlyGln  600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||              Db  1829 GAAAGCCTGAAGGATCCAAAGCGTATCCTAAGCTCTTTAGCTCGTCGTGAAATGGGGACAG  1888
Db  749  TTCATCGTCATTCACCGCAGCACCACCAGCCAATCCAAGGTCTCGGCGATGACACC  808

Qy  241  ProGlyThrIleLeuGlnSerPhePheThrLysMetAlaLysLysLysSerLeuMetAsp  260        Qy   601 GlnGlyIleValAlaLysThrTyrGlnLeuLeuAlaLysArgGluValValTrpAspGlnSer  620
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||              Db  1889 CAAGAAATTGTGGCCAAAACATACCAATTATTAGCCAAAAGGGAGGTCTGGGATCAGAGT  1948
Db  809  CCAGGCACCATCCTTCCAGAGCTTCTTTACCAAGATGGCCAAGAAGAAATCTCTGATGAT  868

Qy  261  IleProGluSerGlnAsnGlyArgAspPheValLeuGlyValCysGlyArgAspGluTyr  280        Qy   621 AlaLeuAspAspValGlyLeuThrMetGlnLeuLeuAspCysAsnPheSerAspGluAsnVal  640
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||              Db  1949 GCTTTGGATGTGGGTTAACCATGCAGCTCCTGGACTGCAACTTCTCGGATGAAAAACGTG  2008
Db  869  ATCCCTGAAAGCCAGAACGGACGGGACTTTGTGCTGCGCGTCTGCGGCCGGGATGAGTAC  928

Qy  281  LeuValGlyGluThrProIleLysAsnPheGlnTrpValArgGlnCysLeuLysAsnGly  300        Qy   641 ArgAlaIleAlaValGlnLysLeuGluSerLeuGluAspAspAlaValLeuHisTyrLeu  660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||              Db  2009 AGAGCCATTGCAGTGCAAAAACTGGAGAGCTTGGAGGATGATGCTGTCCTCCATTACCTG  2068
Db  929  CTGGTGGGGTGAGACGCCCATCAAAAATTTCAGTGGGTGAGGCAGTGCCTCAAGAATGGG  988

Qy  301  GluGluIleHisLeuValLeuAspThrProProAlaLeuAspGluValArgLys  320        Qy   661 LeuGlnLeuValGlnAlaValLysPheGluProTyrHisAspSerAlaLeuAlaArgPhe  680
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Db  989  GAGGAGATTCACCTTGTGCTGGACACTCCCCAGCAGCCCTGGACGAGGTGAGGAAG  1048

Qy  321  GluGluTrpProLeuValAspAlaAspCysThrValThrGlyTyrTyrHisGluLeuThr  340        Qy   681 LeuLeuLysArgGlyLeuArgAsnLysArgIleGlyHisPheLeuTrpPheLeuArg  700
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Db  1049 GAAGAGTGGCCGCTGGTGGATGACTGCACGGAGTCACTGGCTACCACGAGACGCTGACC  1108

Qy  341  IleHisGlyLysAspHisGluSerValPheThrValSerLeuTrpAspCysAspArgLys  360        Qy   701 SerGluIleAlaGlnSerArgHisTyrGlnArgPheAlaValIleLeuGluAlaTyr  720
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Qy  361  PheArgValLysIleAspIleProValLeuProValLeuCysGlnLeuValGluGlnThr  380        Qy   721 LeuArgGlyCysGlyThrAlaMetLeuHisAspPheThrGlnIleValIleAsp  740
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Qy  381  ValPheValGluValAlaAsnIleGlnThrTyrGlyTyrGlyLeuValGlnArgArgThrSer  400        Qy   741 MetLeuGlnLysValThrIleLysAspIleLysSerLeuSerLeuTyrAspValSer  760
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Db  1229 GTGTTTGTGGAGGTAGCAAATCCAGTATGGGCAGCAAGTCTTTGCCAAAGGAGAACCAGC  1288

Qy  401  ProLysProPheGluValLeuTrpAsnValTrpLeuGluPheSerIleLeuLysIle  420        Qy   761 SerGlyValIleSerGlnLeuGlnLysLeuGluLeuGlnLysLeuGluLeuAsnLeuAsnLeuPro  780
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Qy  421  LysAspLeuProLysProLysGlyLysLysLeuLeuAsnLeuGlnIleTyrCysLysLysAlaProAla  440        Qy   781 GlnSerPheArgValProTyrAspProGlyTyrLeuLysValAlaGlyAlaLeuValIleGluLys  800
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Qy  441  LeuSerGlyLysValThrSerArgAlaGluMetProSerProGluSerLysSerGlyLysLysAlaGlnLeu  460        Qy   801 CysLysValMetAlaSerLysLysLysProGluTrpProLeuTrpPheLysCysAlaAspPro  820
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Db  1409 CTGTCTGGCAAGACCTCTCGGGAGATGCCAAGTCCAGAGAGCAAAAGCGGAAAGCTCAGCTT  1468

Qy  461  LeuTyrTyrValAsnLeuLeuIleLeuAspHisArgPheLeuLeuIleGlyHisGlyTyrTyr  480        Qy   821 ThrAlaLeuSerAsnGluThrIleGlyIleIleGlyIleGluLeuGluProLeuHisGlyLysAspLeuArgGln  840
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Qy  501  LysLysThrSerAlaThrAsnProLysLysAspGluLysAsnSerMetSerIleSerSerIleLeuLeuLeu  520        Qy   861 AspLeuCysLeuLeuProTyrGlyCysIleSerThrGlyLysAspLysMetIleGlu  880
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RESULT 5
AR033966
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DEFINITION  Sequence 3 from patent US 5869271.
ACCESSION   AR033966
VERSION     AR033966.1   GI:5949571
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1  (bases 1 to 3808)
AUTHORS     Stephens,L. and Hawkins,P.Thomas.
TITLE       G-beta-gamma regulated phosphatidylinositol-3' kinase
JOURNAL     Patent: US 5869271-A 3 09-FEB-1999;
FEATURES             Location/Qualifiers
source          1..3808
                /organism="unknown"

BASE COUNT     1010 a    965 c    953 g    880 t
ORIGIN

Alignment Scores:
Pred. No.:          0
Score:              5726.00
Percent Similarity: 99.46%          Length:        3808
Best Local Similarity:              Matches:       1090
   98.91%                           Conservative:  6
   98.89%                           Mismatches:    6
Query Match:                        Indels:        0
DB:                 6               Gaps:          0

US-09-974-573-1 (1-1102) x AR033966 (1-3808)
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Qy   741  MetLeuGlnLysValThrIleAspIleLysSerLeuSerAlaGluLysTyrAspValSer   760
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Db  2309  ATGTTACAAAAGTCACCATTGATATCCTCTCTGCTGAAAAGTATGACGTCAGT        2368

Qy   761  SerGlnValIleSerGlnLeuLysLysLeuGluLeuAsnLeuGlnAsnLeuAsnLeuPro   780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2369  TCCCAAGTTATTTCCCAACTTAAGAAGCTTGAAACCTACAGAATTTGAATCTCCCC      2428

Qy   781  GlnSerPheArgValProTyrAspGlyLeuLysAlaGlyValAlaLeuValIleGluLys   800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2429  CAAAGCTTTAGAGTTCCTTATGATGGTCTGAAAGCTGGTGATCGAAAAA            2488

Qy   801  CysLysValMetAlaSerLysLysProGluTrpLeuTrpLysCysAlaAspPro        820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2489  TGTAAAGTGATGGCCTCCAAGAAGAGAGCCCCTGTGGCTTGAGTTTAAATGCCGATCCT   2548

Qy   821  ThrAlaLeuSerAsnGluThrIleGlyIleIleGlnIleLysGlyHisGlyGluGln     840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2549  ACGGCTCTATCAAATGAAACAATTGGAATTATCTTAAACACGGTGACGATCTGCGCCA    2608

Qy   841  AspMetLeuLeuGlnLeuLeuArgIleMetGluSerIleIleTrpGluThrGluSerLeu  860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2609  GACATGTCTTATTTTACAGATTCTACGAATCATGGAGTCCATTGGGAGACCAATCTTTG   2668

Qy   861  AspLeuCysLeuLeuProTyrGlyCysIleSerThrGlyAspLysIleGlyMetIleGlu  880
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Db  2669  GATCTGTGCCTCCTGCCATATGGCTGCATTTCAACTGGTGACAAAATAGGAATGATCGAG 2728

Qy   881  IleValLysAspAlaThrIleAlaLysIleGlnGlnSerThrValGlyAsnThrGly     900
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Db  2729  ATCGTGAAGGACGCCACGACCAGCAAATTCAGCAAAGCACAGTGGGCAACACGGGGT    2788

Qy   901  AlaPheLysAspGluLysSerHisTrpLeuLysGluLeuLysCysProIleGluGluLys  920
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Db  2789  GCCTTTAAAGATGAAGTCCTGAGTCCACTGGCTCAAAGAAAAATGCCCTATTGAAGAAAAG 2848

Qy   921  PheGlnAlaAlaAlaValGluArgPheValTyrSerCysValAlaGlyTyrCysValAlaThrPhe 940
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Db  2849  TTTCAGGCAGCTGTGGAGAGATTTGTTTATTCCTGCGTACTGTGTGGCAACCTTT      2908

Qy   941  ValLeuGlyTyrIleGlyAspAspArgHisAsnAspAsnIleMetIleSerGluThrGlyLysAsnLeu 960
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Qy   981  GluArgValProPheValLeuPheValMetGlyTyrThrSerGlyLys              1000
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Qy  1001  LysThrSerLeuHisPheGlnLysPheAspLysValCysValLysAlaTyrLeuAlaLeu  1020
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Qy  1021  ArgHisHisThrAsnLeuLeuIleLeuLeuPheSerMetMetLeuMetThrGlyMetPro  1040
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Qy  1041  GlnLeuThrSerLysGluAspPheIleGluTyrIleLysArgAspAlaLeuPheLysSer  1060
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Db  3209  CAGTTAACCAGCAAAGAGGACTTCATCGAGTACATCAAGAGAGATGCCCTCCACAGTGGCAAAAGT 3268

Qy  1061  GluGluAspAlaAlaLysTyrPheLeuAspGluValCysArgAspValGlyTrp        1080
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Db  3269  GAGGAGGATGCTAAAAAGTATTTTCTGGATGAGTTGCAGAGACAAAAGATGG         3328

Qy  1081  ThrValGlnPheAsnTrpPheLeuHisLeuValLeuGlyIleLysGlnGluLysHis     1100
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Qy   401  ProLysProGluThrGluValLeuPheAsnValTrpAsnValTrpPheSerIleLeuLysIle 420
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Qy   441  LeuSerGlyLysLeuThrSerAlaGluMetProSerProGluSerLysGlyGlyLysAlaGlyLeu 460
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Qy   481  ValLeuHisMetTrpGlnLeuSerGlyLysGlyGlnAspSerPheAsnAlaAlaAsp     500
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Db  1529  GTGCTCCACATGTGGCAGTTATCCGGAAGGGGGAAGACCAAGGGAGCTTCAATGCCGAC  1588

Qy   501  LysLeuThrSerAlaThrAsnProAspLysSerGluAsnSerMetSerIleLeuSerLeuLeu 520
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Qy   521  AspAsnTyrCysHisProIleAlaLeuProLysHisArgProThrProAspProGluGly  540
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Qy   541  AspArgValAlaArgAlaLeuMetProAsnLeuArgGlnLeuArgLysGlnLeuLeuGlnAlaIleIleAla 560
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Qy   561  ThrAspProLeuAsnProLeuThrAlaGluThrArgProTyrHisPheArgTyr        580
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Db  1769  ACGGATCCGCTTAACCCACTCACAGCTGAAGACAAAAGACTGCCTCTGGCATTTCAGATAT 1828

Qy   581  GluSerLeuLysAspProLysLeuAlaTyrProLysGlnAspSerValLysTrpGlyGln  600
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Qy   601  GlnGluIleValAlaAlaLysThrTyrGlnLeuValLeuAlaLysArgGlnValTrpAspGlnSer 620
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Qy   621  AlaLeuAspAspValGlyLeuThrMetGlnLeuLeuAspCysAsnPheSerAspGluAsnVal 640
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Db  1949  GCTTTGGATGGTGGGGTTAACCGAGCTCCTGGAGCTGCAACTTCTCGGATGAAAACGTG  2008

Qy   641  ArgAlaIleAlaValGlnLysLeuGluSerLeuGluAspAspAspGlyAspValLeuHisTyrLeu 660
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Db  2009  AGAGCCCATTGCAGTCCAGAACTGGAGAGCTTGGAGGATGATGACGGTGACCGTCCATTACCTG 2068

Qy   661  LeuGlnLeuValGlnAlaValPheGluProTyrArgGlnArgPheAlaValIleLeuLeuGluLysArgPhe 680
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Qy   681  LeuLeuLeuArgGlyLeuArgAsnLysArgIleGlyHisPheLeuPheLeuArg        700
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Qy   701  SerGluIleAlaGlnSerArgHisTyrGlnGlnArgPheAlaValIleLeuGluLeuAlaAlaTyr 720
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Db  2189  AGTGAGATTGCCCAGTCCAGCCACTATCAGCAGAGGTTTGCAGTGATCCTGGAAGCCTAC 2248

Qy   721  LeuArgGlyCysGlyThrAlaMetLeuHisLeuAspPheThrThrGlnGlnValIleAspAsp 740
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VERSION      BC035683.1  GI:23274229
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AUTHORS      Strausberg,R.
TITLE        Direct Submission
JOURNAL      Submitted (31-JUL-2002) National Institutes of Health, Mammalian
             Gene Collection (MGC), National Institutes of Health, Mammalian
             Sequencing Center (NISC),
             Gaithersburg, Maryland;
             Web site: http://www.nisc.nih.gov/
             Contact: nisc_mgc@nhgri.nih.gov
             Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
             Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
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             Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
             Madiro,Q., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
             McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
             Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
             Young,A., Zhang,L.-H. and Green,E.D.
REMARK       NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT      Contact: MGC help desk
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: National Institutes of Health Intramural
             Sequencing Center (NISC),
             Gaithersburg, Maryland;
             Web site: http://www.nisc.nih.gov/
             Contact: nisc_mgc@nhgri.nih.gov

             Clone distribution: MGC clone distribution information can be found
             through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
             Series: IRAK Plate: 79 Row: m Column: 11
             This clone was selected for full length sequencing because it
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ORIGIN

Alignment Scores:
Pred. No.:             0
Score:             5538.00
Percent Similarity:  97.10%
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US-09-974-573-1 (1-1102) x BC035683 (1-3860)

Qy     1 MetGluLeuGluAsnTyrLysGlnProValValLeuArgGluAspAsnArgArgArgArg   20
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Qy    21 ArgArgMetLysProArgSerThrAlaAlaSerLeuSerMetGluLeuIleProIle   40
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Qy    41 GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeuLeuHis   60
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Qy    61 ValAlaGlyHisGlyAsnValGluAspGlnMetLysAlaGlnValTrpLeuArgAlaLeuGlu   80
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Qy    81 ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuTyr  100
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Qy   181 ValThrProArgMetAlaGluValAlaGlyArgAspProLysLeuTyrAlaMetHisPro  200
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Qy   221 PheIleValIleHisArgSerThrSerGlnThrIleLysValSerAlaAspAspThr  240
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Qy   241 ProGlyThrIleLeuGlnSerPheThrLysMetAlaLeuLysLysSerLeuMetAsp 260
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Qy   301 GluGluHisLeuValLeuAspThrProAspProAlaLeuAspGluValArgLys 320
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Db  1734 ACTGACCCTAACCCCTTCACACGAGCAGAGGTTTCTGGCTTTTCTCAGAGCGTTAAGTGGGGACACTTCAGATAC 1793

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         |||||||||||||||||||||||||||:  :||||||||||||||||||||||||||
Db  1794 GAAAGCCCTTAAGGACCCCAAAAAGCCAAAGATCATTCCCACAGCATATTTGGAATGGGGACAG 1853

Qy   601 GlnGluIleIleValAlaLeuLysThrTyrGlnLeuLeuAlaLysArgGluLysValArgGluLysTrpAspGlnSer 620
```

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Db  1854 CAAGAAATTGTGGCCAAAACATACCAATGTTGGCCAGAGGGAGTCTGGGATCAAAGT 1913
         |||||||||||||||||||||||||||||||||||||:::||||||||||||||||||

Qy   621 AlaLeuAspValGlyLeuThrMetGlnLeuLeuAspCysAsnPheSerAspGluAsnVal 640
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1914 GCTTTGGATGTTGGGTTAACAATGCAGCTCCTGGACTGCAACTTCTCAGATGAAAATGTA 1973

Qy   641 ArgAlaIleAlaValGlnLysLeuGluSerLeuGluAspAspAspValLeuHisTyrLeu 660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1974 AGAGCCATTGCAGTTCAGAAACTTGAGAGCCTTGGAGGACCATGATGTTCTGCATTACCTT 2033

Qy   661 LeuGlnLeuValGlnAlaValLysPheGluProTyrHisAspSerAlaLeuAlaArgPhe 680
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2034 CTACAATTGGTCCAGGCTGTGAAATTTGAACCATACCATGATAGTGCCCTTGCCAGATTT 2093

Qy   681 LeuLeuLysArgGlyLeuArgAsnLysArgIleGlyHisPheLeuPheTrpPheLeuArg 700
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2094 CTGCTCAAGCGTGGTTTAAGAACAAAAAGAATTGGTCACTTTTGTTTTGTTTCTTGAGA 2153

Qy   701 SerGluIleAlaGlnSerArgHisTyrGlnValArgPheAlaValIleLeuGluAlaTyr 720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2154 AGTGAGATAGCCCAGTCCAGACACTATCAGGACAGAGTTCGCTGTGATTCTGGAAGCCTAT 2213

Qy   721 LeuArgGlyGlyThrAlaMetLeuHisAspPheThrGlnGlnValGlnIleValIleAsp 740
         ||||||||||||||||||||||||||||||||||||||||:::||||||||||||||||||
Db  2214 CTGAGGGGCTGTGGCACAGCCATGCTGCACGACTTTACCCAAAGTAATGCAGT 2273

Qy   741 MetLeuGlnLysValThrIleAspIleArgIleLeuSerLeuSerAlaGluLysTyrAspValSer 760
         ||||||||||||||||||:  :|||||||||||||||||||||||||||||||||||||
Db  2274 ATGTTACAAAAGGTCACCCTTGATATTAAATCGCTCTCTGCTGAAAAGTATGACGTCAGT 2333

Qy   761 SerGlnValIleSerGlnLeuLysGlnLeuLysLeuGluGlnAsnLeuGlnAsnLeuAsnLeuPro 780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2334 TCCCAAGTTATTTCACAACTTAAACAAAGCTTGAAAACCTGCAGAATTCTCAACTCCCC 2393

Qy   781 GlnSerPheArgValProTyrAspProGlyLeuLysLysAlaGlyAlaLeuValIleGluGluLys 800
         |||:::|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2394 GAAAAGCTTTAGAGTTCCATATGATCCTGGACTGAAAGCAGGAGCCCTGGCAATTGAAAAA 2453

Qy   801 CysLysLysValMetAlaSerLysLysAspLysLysAlaAlaAspProPro 820
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2454 TGTAAAGTAATGGCCTCCAAGAAAAAAACCACATGGCTTGAGTTTAAATGTGCCGATCCT 2513

Qy   821 ThrAlaLeuSerAsnGluThrIleGlyTyrIleIlePheLysHisGlyAspSerLeuArgGln 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   841 AspMetLeuIleLeuGlnIleLeuArgIleMetGluSerIleTrpGluThrGluSerLeu 860
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Db  2574 GACATGTTAATTCTACAGATTCTTAGGATTATGGGAGACTGAATTCTTTG 2633

Qy   861 AspLeuCysLeuLeuProTyrTyrGlyCysIleSerSerThrGlyTyrAspLysHisGlyMetIleGlu 880
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2634 GATCTATGCCTCCTGCCATATGGTTGCATTTCAACTGGTGACAAAATAGGAATGATCGAG 2693

Qy   881 IleValLysAspAlaThrArgIleLysIleGlnLysSerThrValGlyAsnThrGly 900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2694 ATTGTGAAAGACGCCACGAGAATTAAAATTCAGCAAAGCACAGTGGGCAACACGGGA 2753

Qy   901 AlaPheLysAspGluValLeuSerHisTrpLeuLysSerCysProIleGluGluLys 920
         ||||||||||||||||||||||||||:  :|||||||||||||||||||||||||||
Db  2754 GCATTTAAAGATGAAGTCCTGAATCACTGGCTCAAAGAAAAATCCCTACTGGAGAAAAG 2813

Qy   921 PheGlnAlaAlaValAlaGluPheValTyrSerCysValAlaGlyThrPhe 940
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2814 TTTCAGGCAGCAGTGGCAGAGTTTGTTTATTCCTGTGTGGCAGGTACGTTTGGCAACCTTT 2873

Qy   941 ValLeuGlyTyrIleGlyAspArgHisAsnAspMetIleSerGluHisArgLysAsnLeu 960
         |||||||||||||||||||||||||:::|||||||||||||||||||||||||||||||
Db  2874 GTTCTTGGATATATAGGGGCGACAGACAGAATGACAATATATGATCACCGAGACAGAACCTA 2933

Qy   961 PheHisIleAspPheGlyHisPheLeuLeuHisTyrLysTyrLysAsnTyrLysSerIleAsnLys 980
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Qy  1021  ArgHisHisThrAsnLeuLeuIleIleLeuPheSerMetMetLeuThrGlyMetPro  1040             CIFIVIHRSTTSQTIKVSPDDTPGAILQSFFTKWAKKKSLMDIPESQSEQDFVLRVCG
          |||||||||| |||||||||||||||||||||||  ||||||||||||| |:::||                     RDEYLVGETPIKNFQWVRHCLKNGBEIHVVLDTPPDPALDEVRKEEWPLVDDCTGVTG
Db   3114  CGTCATCACACAAACCTACTGATCATCCTGTTTCTCCATGATGCTGATGACAGGAATGCC  3173            YHEQLTIHGQHDESVFTVSLWDCDRKFRVKIRGIDIPVLPRNTDLTVFVEANIQHGQQ
                                                                                    VLCQRRTSRKPFTEEVLMNVWLEFSIKKDLPKGALANLQIYCGKAPALSSKASAESP
Qy  1041  GlnLeuThrSerLysGluAspIleGluTyrIleArgAspAlaLeuTrpValGlyLysSer  1060           SSESKGKVRLLYYVNLLIIDHRFLLRRGEYVLHMWQISGKGEDQQSFNADKLTSATNP
          |||||||||||||||||| ||||||:||||||||||||||  |:::||                             DKENMSISILLDNYCHPIALPKGHQPTPDPEGDRVRAEMPNQLRKQLERIIATDPLNP
Db   3174  CAGTTAACAAGAAGAGACAACATTGAATATATCCGGGATGCCCTCACAGTGGGGAAAAT  3233            LTADKDELLWHFRYESLKHPKAYPKLFSSVKWGQQEIVAKTYQLLARREVWDQSALDV
                                                                                    GLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYLLQLVQAVKFEPYHDSALARFLL
Qy  1061  GluGluAspAlaLysLysTyrPheLeuAspIleGlnLeuGluValCysArgAspLysGlyTrp  1080        KRGLRNKRICHFLFLFWLFRSSIAQSRHYQAGTALAYLEAYLRGCGTAMLHDFTQQVVIE
          |||||||||||||||||||||   |||||||||||||||||||||||||||||                         MLQKVTLDIKSLSAEKYDVSSQVISQLKQKLENLQNSQLPESFRVPYPDGLKAGALAI
Db   3234  GAGGAGGATGCTAAAAAGTATTTTCTTGATCAGATCGAAGTTTGCAGAGACAAAGGATGG  3293            EKCKVMASKKKPLMLEFKCADPTALSNEIIGIIFKHGDDLRQDMLILQIRIMESIWE
                                                                                    TESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTGAFKDEVLNHWLKEK
Qy  1081  ThrValGlnPheAsnTrpPheLeuHisLeuValLeuGlyIleLysGlnGlyLeuHis  1100             SPTEEKFQAAVERPFVLTPDFLFVMGTSGKKTSPHFQKFQDICVKAYLALRHHTNLLIIL
          |||||||||||| ||| ||||||||||||||||||||||||||| |||:::||                         KSFIGINKRVPFVLTPDFLFVMGTSGKKTSPHFQKFQDICVKAYLALRHHTNLLIIL
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                                                                                    HLVLGIKQGEKHSA"
Qy  1101  SerAla  1102
          ||||||
Db   3354  TCAGCC  3359

BASE COUNT     950 a    861 c    849 g    750 t
ORIGIN

Alignment Scores:
RESULT 7                                                           Pred. No.:           0               Length:         3410
AF327656                                                           Score:           5534.00             Matches:        1049
LOCUS       AF327656     3410 bp    mRNA    linear    PRI 31-JAN-2001  Percent Similarity:  97.10%     Conservative:     21
DEFINITION  Homo sapiens phosphoinositide-3-kinase gamma catalytic subunit  Best Local Similarity:  95.19%    Mismatches:       32
            (PI3CG) mRNA, complete cds.                            Query Match:         95.58%          Indels:           0
ACCESSION   AF327656                                               DB:                  9               Gaps:             0
VERSION     AF327656.1   GI:12620870
KEYWORDS    .                                                      US-09-974-573-1 (1-1102) x AF327656 (1-3410)
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens                                           Qy    1  MetGluLeuGluAsnTyrGlyGlnProValValLeuArgGluAspAsnArgArgArg  20
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;           |||||||||||||||||||||||||||:|:||||||||||||||| |
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.    Db    1  ATGGAGTTGGAGAACTATAAACAGCCCGTGGTGCTGAGAGAGGACAACTGCCGAAGGCGC  60
REFERENCE   1  (bases 1 to 3410)
  AUTHORS   Stoyanov,B., Volinia,S., Hanck,T., Rubio,I., Loubtchenkov,M.,   Qy   21  ArgArgMetLysProArgSerThrAlaAlaAlaSerLeuSerSerMetGluLeuIleProIle  40
            Malek,D., Stoyanov,S., Vanhaesebrock,B., Dhand,R., Nurnberg,B.,            |||||||||||||||||||||||||||||||||||||||||||||||||||
            Gierschik,P., Seedorf,K., Hsuan,J.J., Waterfield,M.D. and    Db   61  CGGAGGATGAAGCCGCGCAGTGCTCGGCCAGCCGTCGTCCTCCATGGAGCTCATCCCCATC  120
            Wetzker,R.
  TITLE     Cloning and characterization of a G protein-activated human   Qy   41  GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluHisAlaLeuLeuHis  60
            phosphoinositide-3 kinase                                                 |||||||||||||||||||||||||||:|||||||||||||||||| |
  JOURNAL   Science 269 (5224), 690-693 (1995)                      Db  121  GAGTTCGTGCTGCCCACCAGCCAGCGCAAATGCAAGAGCCCAAATGCAAGAGCCCAAAT  180
  MEDLINE   95350661
   PUBMED   7624799                                                 Qy   61  ValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnValTrpLeuArgAlaLeuGlu  80
REFERENCE   2  (bases 1 to 3410)                                              |||||||||||||||||||||||||||||||||||||||||||||
  AUTHORS   Michalke,M., Schaefer,M., Stoyanov,B., Wetzker,R. and Nuernberg,B.  Db  181  GTGGCCGGCCACGGCAACGTGGAGCAGATGAAGGCCCAGGTGTGGCTGCGAGCGCTGGAG  240
  TITLE     Regulation of a G-protein-activated phosphoinositide-3-kinase
  JOURNAL   Unpublished                                            Qy   81  ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisHisPheLeuLeuLeuTyr  100
REFERENCE   3  (bases 1 to 3410)                                              |||||||||||||||||||||||||||||||||||||||||||||||||
  AUTHORS   Michalke,M., Schaefer,M., Stoyanov,B., Wetzker,R. and Nuernberg,B.  Db  241  ACCAGCGTGTCGGCGGACTTCTACCACCGGCTGGGACCCGATCACTTCCTCCTGCTCTAT  300
  TITLE     Direct Submission
  JOURNAL   Submitted (11-DEC-2000) Department of Pharmacology, Freie   Qy  101  GlnLysGlyGlnTrpTyrGluIleTyrAspArgLysTyrGlnValValGlnThrLeuAsp  120
            Universitaet Berlin, Thielallee 67-73, Berlin 14195, Germany            ||||||||||||||||||||||||||||||||||||||||||||||||||
FEATURES             Location/Qualifiers                           Db  301  CAGAAGGAGGGCCAGTGGTACGAGATCTACGACAGAAGTACCAGGTGGTGCAGACTCTGGAC  360
     source          1..3410
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                     /mol_type="mRNA"                                         ||||||||||||||||||||||||||||||||||||||||||||||||||
                     /db_xref="taxon:9606"                          Db  361  TGCCTGCGCTACTGGAAGGCCACGCACCGGAGCCCGGGCCAGATCCACGTGGTGCAGCGG  420
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     gene            1..3410                                                  ||||||||||||||||||||||:::||
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Qy    1 MetGluLeuGluAsnTyrGluGlnProValLeuProValLeuAspAsnArgGluArgArgArg   20
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   84 ATGGAGCTGGAGAACTATAAACAGCCCGTGGTGCTGCCGGTGCTGGAGACGAGAGGAGGGGC 2760
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Qy   21 ArgArgMetLysProArgSerThrAlaAlaSerLeuSerMetGluLeuIleProIle         40
          | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  144 CGGAGGATGAAGCCGCGAGTGCTGCGGCCAGCCTGTCTTCCATGGAGCTCATCCCAATC     2820
                                                                          203

Qy   41 GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeuLeuHis      60
          | | | | | | | | | | | | | | | : : : | | | | | | | | | | |
Db  204 GAGTTCGTGCTGCCCACCAGCCAGCGAAATGCAAGAGCCCGAAACGGCGCTGCTGCAC       2880
                                                                          263

Qy   61 ValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnValTrpLeuArgAlaLeuGlu      80
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  264 GTGGCCGGCCACGGCAACGTGGAGCAGATGAAGGCCCAGGTGTGGCTGCGAGCGCTGGAG     2940
                                                                          323

Qy   81 ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTyr     100
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  324 ACCAGCGTGCGCGGCGACTTCTACCACCGGCTGGGACCCGACCACTTCCTCCTGCTCTAT     3000
                                                                          383

Qy  101 GlnLysLysGlyGlnTrpTyrGluIleTyrAspLysTyrGlnValValGlnThrLeuAla Leu 120
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  384 CAGAAGAAGGGCCAGTGGTACGAGATCTACGACAAGTACCAGGTGGTGCAGACTCTGGAC     3060
                                                                          443

Qy  121 CysLeuArgTyrTrpLysTyrValLeuHisArgSerProGlyGlnIleHisValValGlnArg 140
          | | | | | | | | | | | | | | | | | | | | | | | |
Db  444 TGCCTGCGCTACTGGAAGGCCACCACGGCAGCCAGCGAGTCCCAGGCGG                 3120
                                                                          503

Qy  141 HisAlaProSerGluThrLysLysGlnSerValHisAlaLeuIleGlyTyr             160
          | | | | | | | | : : : |
Db  504 CACCCCGCCCCTTCCGAGGTCCCAAGTCAGGCGGATGCCCTCACGGCGTCAGTGGCTAT     3180
                                                                          563

Qy  161 AspValThrAspValSerAsnValHisAspAspGluValSerArgAspLeuArgLeu        180
          | | | | | | | | | | | | | | | | | |
Db  564 GACGTCACTGACGTCAGCAACGTGCACGACGATGAGGTTCACGCCCGCTGCCTTG          3240
                                                                          623

Qy  181 ValThrProArgMetAlaGluValAlaAlaGlyArgAspProLysLeuTyrAlaMetHisPro 200
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  624 GTGACCCCGCGCATGGCAGAGGTGGCCGCAGGCCGCGACCCCAAGCTCTACGCCATGCACCCG 3300
                                                                          683

Qy  201 TrpValThrSerLysProLeuProGluTyrLeuLeuLysIleThrAsnAsnCysVal        220
          | | | | | | | | | | | | | | | | | | | : : : |
Db  684 TGGGTGACGTCCAAGCCCCTCCCGGAGTACCTGTTGAAGAAGATTGCCAACAACTGCATC     743

Qy  221 PheValIleIleHisArgSerThrSerGlnThrIleLysValSerAlaAspAspThr        240
          | | | | | | | | | | | | | | | | | | | | | | |
Db  744 TTCATGTCATTCACCCGCAGCACCAGCCAGACCATTAAGGTCTCACCCGACGACACC       803

Qy  241 ProGlyTyrThrLeuGlnSerPhePheThrLysMetAlaLysLysLysSerLeuMetAsp     260
          | | | | | | | | | | | | | | | | | | | | | | |
Db  804 CCCGGCGCCATCCTGCAGAGCTTCTTCACCAAGATGGCCAAGAAGAAATCTCTGATGGAT     863

Qy  261 IleProGluSerGlnAsnGluArgAspValLeuArgValCysGlyArgAspGluTyr        280
          | | | | | : : : | : | : |
Db  864 ATTCCCGAAAGCCAAAGCGACAGGATTTTGTGCGTCTGTGGGCCGGGATGAGTAC         923

Qy  281 LeuValGlyGluThrProLeuGluLysAsnProGlnPheAsnTrpValArgGlnCysLysAsnGly 300
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  924 CTGGTGGGCGAAACGCCCATCAAAAACTTCCAGTGGGTGAGGCACTGCCTCAAGAACGGA     983

Qy  301 GluGluLeuHisLeuValLeuAspThrProProAspProAlaLeuArgGluValArgLys    320
          | | | | | | : : : | | | | | | | | | | | | | | | | | | | |
Db  984 GAAGAGATTCACGTGGTACTGGACACGCCTCCAGACCCCGCCTTAGAGGAGGTGAGGAAG   1043

Qy  321 GluGluTrpProLeuValAspAspCysThrGlyTyrThrGlyLeuTyrHisGluLeuThr    340
          | | | | | | | | | | | | | | | | | | | | | | | |
Db 1044 GAAGAGTGGCCGCTGGTGGACGACTGCACGGAGTCACCGGCTACCATGAGCAGTTACC    1103

Qy  341 IleHisGlyLysAspHisGluSerValPheThrValSerLeuTrpAspCysAspArgLys   360
          | | | | | | | | | | | | | | | | | | | | | | : : : |
Db 1104 ATCCACGGCAAGGACCACGAGAGTGTGTTCACCGTGTCCCTGTGGGACTGCGACCGGCAAG 1163
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Qy  901 AlaPheLysAspLysGluValLeuSerHisHisTrpLeuLysLysCysProIleGluGluLys 920
          | | | | | | | | | | | | : : : |
Db 2701 GCATTTAAAGATGAAGTCCTGAATCACTGGCTCAAAGAAAAATCCCTACTGAAGAAAAAG 2760

Qy  921 PheGlnAlaAlaValAlaGluArgPheValTyrSerCysAlaGlyTyrCysValAlaThrPhe 940
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2761 TTTCAGGCAGCAGTTGCAGAGATTGTTTATTCCTGCGCAGGCTACTGTGTGGCAACCTTT 2820

Qy  941 ValLeuGlyValIleGlyGlyAspAlaArgHisAsnAspAspAsnIleMetIleSerGluThrGlyIleAsnLeu 960
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2821 GTTCTTGGAATAGGCGACAGACAACATGACATATTATGATCACCGAGACAGAGAAACCTA 2880

Qy  961 PheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLys 980
          | | | | | | | | | | | | | | | | | | | | | | | | | : | | | |
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Qy  981 GluArgValProPheValLeuThrProAspPheLeuPheValMetGlyThrSerGlyLys 1000
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2941 GAGAGAGTGCCATTTGTCCTAACCCCTGACTTCCTCTTTGTGATGGGAACTTCTGGAAAG 3000

Qy 1001 LysThrSerLeuHisPheGlnLysLysProAspValCysValLysAlaTyrLeuAlaLeuAlaLeu 1020
          | | | | | | | | | : : : | | | | | | | | | | | | | | | | | |
Db 3001 AAGACAAGCCCACACTTCCAGAAATTCAGGACATCTGTGTTAAGGCTTATCTAGCCCTT 3060

Qy 1021 ArgHisHisAsnLeuLeuIleLeuPheSerMetMetLeuMetThrGlyMetPro 1040
          | : | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 3061 CGTCATCACAACCTACTGATCATCCGTTCCATGATGCTGATGACAGGAATGCCC 3120

Qy 1041 GlnLeuThrSerLysLeuGlnProValHisArgIleArgAspAspAlaLeuThrValGlyTyrLysSer 1060
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Db 3121 CAGTTAACAAGCAAAGAAGCAGAAGACATTGAATATATACCGGATGACCCTCACAGTGGGAAAAAT 3180

Qy 1061 GluGluValAsnAlaLysSerTyrPheLeuAspLeuIleGluGluValCysArgAspGlyGlyTrp 1080
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Qy 1101 SerAla 1102
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Db 3301 TCAGCC 3306
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RESULT 8
AR026677

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LOCUS       AR026677                5162 bp    DNA        linear   PAT 29-SEP-1999
DEFINITION  Sequence 13 from patent US 5856132.
ACCESSION   AR026677
VERSION     AR026677.1  GI:5937517
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 5162)
  AUTHORS   Stephens,L., Hawkins,P.Thomas. and Braselmann,S.
  TITLE     G-beta-gamma regulated phosphatidylinositol-3' kinase
  JOURNAL   Patent: US 5856132-A 13 05-JAN-1999;
FEATURES             Location/Qualifiers
  source           1..5162
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BASE COUNT    1471 a   1173 c   1149 g   1367 t    2 others
ORIGIN
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Alignment Scores:

Pred. No.:	0
Score:	5534.00
Percent Similarity:	97.10%
Best Local Similarity:	95.19%
Query Match:	95.58%

Length:	5162
Matches:	1049
Conservative:	21
Mismatches:	32
Indels:	0
Gaps:	0
	6

US-09-974-573-1 (1-1102) x AR026677 (1-5162)

Qy   361 PheArgValLysIleArgGlyIleAspIleProValLeuProArgThrAlaAspLeuThr   380
Db 1164 TTCAGGGTCAAGATCAGAGGCATTGATATCCCGCTGCTCGGAACACCGGACCTCACA   1223

Qy   381 ValPheValGluAlaAsnIleGlnTyrGlyGlnValLeuCysGlnArgThrSer   400
Db 1224 GTTTTTCGTAGAGGCAAACATCCAGTACGGGCAACAGAGTCCTTGCCAAAGGAGAGACCAGC 1283

Qy   401 ProLysProThrGluPheGluValLeuTrpLeuAsnValTrpLeuGluPheSerIleLysIle 420
Db 1284 CCCAAACCCTTCACAGAGGAGGTGCTGTGGAATGTGTGGCTTGAGTTCAGTATCAAAATC   1343

Qy   421 LysAspLeuProLysGlyLysAlaLeuLeuAsnLeuGlnIleTyrCysGlyLysAlaProAla 440
Db 1344 AAAGACTTGCCAAAGGGCTTCTACTAACTCCAGATCTACTGCGTAAAGCTCCAGCA   1403

Qy   441 LeuSerGlyLysThrSerAlaGluMetProSerProGluSerLysGlyGlyLysAlaGlnLeu 460
Db 1404 CTGTCCAGCAAGGCCTCTGCAGAGTCCCCAGTTCTGAGTCCAAGGCAAAGTTCCGGCTT   1463

Qy   461 LeuTyrTyrValAsnLeuLeuIleLeuIleAspHisArgPheLeuLeuArgHisGlyGluTyr 480
Db 1464 CTCTATTATGTGAACCTGCTGTCTGCTGATAGACACCGTTTCCTCCTGCGCCGTCATGGAGAATAC 1523

Qy   481 ValLeuHisMetTrpGlnLeuSerGlyGlyGluAspGlyGlySerPheAsnAlaAsp   500
Db 1524 GTCCTCCACATGTGGCAGATATCTGGGAAGGAGGACCAAGGAAGCTTCAATGCTGAC   1583

Qy   501 LysLeuThrSerLeuThrAsnProAspLysSerMetSerIleSerLeuLeuLeu   520
Db 1584 AAACTCACGTCTCGAACTAACCCAGACAAGAGAACTCAATGTCCATTCTCCATTCTTCTG 1643

Qy   521 AspAsnTyrCysHisProIleAlaLeuProLysLeuProAspHisProAspProGluGly   540
Db 1644 GACAATTACTGCCACCCGATAGCCCTGCCTAAGCTCCTAGCATCAGCCCCACCCGACCCGGAAGGG 1703

Qy   541 AspArgArgValAlaGluMetProAsnGlnLeuArgLysArgLysAlaIleIleIleAla   560
Db 1704 GACCGGCGGTTCGAGCAGAGAAATGCCCAACCAGCTCGCAAGCAATTGGAGGCGGATCATAGCC 1763

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Db 1764 ACTGATCCACTTAACCCTCTCACAGAGGACAAGGACAAGAATTGCTCTGGCATTTTAGATAC 1823

Qy   581 GluSerLeuLysAspProLysAlaTyrProLysLeuPheSerSerValLysTrpGlyGln   600
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Qy   601 GlnGluIleLeuValAlaLysThrTyrGlnLeuValAlaLysArgGluValTrpAspGlnSer 620
Db 1884 CAAGAAATTGTGGCCAAAACATACCAATTGTTGGCCAAAGGGAAGTCTGGGATCAAAGT   1943

Qy   621 AlaLeuAspValGlyLeuThrMetGlnLeuLeuAspCysAsnPheSerAspGluAsnVal   640
Db 1944 GCTTTGGATGTTGGGTTAACAATGCAGCTCCTCGACTGCAACTTCTCAGATGAAAATGTA 2003

Qy   641 ArgAlaLeuAlaValGlnLysGlyLeuGlnSerLeuGluSerAspAspValLeuHisTyrLeu 660
Db 2004 AGAGCCATTGCAGTTCAGTCAGGAACTCGGAGAGCTTGGAGGACGATGGTTCTCGCATTACCTT 2063

Qy   661 LeuGlnLeuValGlnAlaAlaValLysAspProTyrHisAspSerAlaLeuAlaLysArgPhe 680
Db 2064 CTACAAATTGGTCACAGGCTGTGAAATTTGAACATACCATACCAATAGCGCCCTTTGCCAGATTT 2123

Qy   681 LeuLeuLysArgGlyLeuArgAsnLysGluAspIlePheValAspGlnValAlaGluLysGlyTrp 700
Db 2124 CTGCTGAAGCGTGGTTTAAGAAACAAAGAAGATATTTTCGTTGATCAGGTTGCAGAGAAAGGATGG 2183

Qy   701 SerGluIleAlaGlnGlnSerArgHisSerTyrGlnArgPheAlaValIleLeuGluValAlaTyr 720
Db 2184 AGTGAGATAGCCCAGTCCAGACACTCATCAGCAGAGGTTCGCTGTATCTGTGAATTCTGGAAGCCTAT 2243

Qy   721 LeuArgGlyCysGlyThrAlaMetLeuHisAspPheThrGlnIlenValIleGlnValIleAsp 740

Db 2244 CTGAGGGGCTGTGGCACAGCTGCCATGCTGCGACTTACCCAACAGTCCAAGTAATCGAG   2303

Qy   741 MetLeuGlnLysValThrLeuAspIleLysSerGluSerAlaGluValTyrAspValSer   760
Db 2304 ATGTTACAAAGGTCACCCTGATATTATAAATCGTCTCTGCTGAAAGTATGACGTCAGT   2363

Qy   761 SerGlnValIleSerGlnLeuLeuGlyGlnLeuLysLeuGlnAsnLeuAsnLeuAsnLeuPro 780
Db 2364 TCCCAAGTTATTTCACAACTAAACAAAAGCTTGAAAACCTGAACAATTCTCAACTCCCC   2423

Qy   781 GlnSerPheArgValProTyrArgAspProGlyLeuLysLeuAlaGlyAlaLeuValIleGluGlyLys 800
Db 2424 GAAAGCTTTAGAGTTCCAATGATCCTGGACTGAAAGACGCTGCAATTGAAAA   2483

Qy   801 CysLysValMetAlaSerLysLysLysProGluTrpLeuPheLysCysGlyAlaAspPro   820
Db 2484 TGTAAAGTAATGGCCTCCAAGAAAAAAACCACTATGGCTTGAGTTTAAATGTGCCGATCCT 2543

Qy   821 ThrAlaLeuSerAsnGluThrIleGlyIleIleIleHisGlyAspAspLeuArgGln   840
Db 2544 ACAGCCCTATCAAATGAAACAATTGGAATTATCTTAAACATGGTGATGATCTGCCAA   2603

Qy   841 AspMetLeuIleLeuGlnIleLeuLeuArgIleMetGluSerIleGluTrpGluThrGluSerLeu 860
Db 2604 GACATGCTTATTTTACAGATTCTACGAGTCATGGAGTCTATTGGAGACTGAATCTTTG   2663

Qy   861 AspLeuCysLeuLeuProTyrGlyTyrCysIleSerThrGlyAspLysIleIleGlyMetIleGlu 880
Db 2664 GATCTATGCCTCCTGCCATATGGTTGCATTTCAACTGGTGACAAAATAGGAATGATGGAG 2723

Qy   881 IleValLysAspAlaThrIleAlaLysIleIleGlnGlnInSerThrValGlyAsnThrGly   900
Db 2724 ATTGTGAAACGACGCCAGCAACAATTGCCAAAATTCAGACAAGCACAGTGGGCAACACGGGA 2783

Qy   901 AlaPheLysAspGluValLeuSerHisTrpLeuLysCysCysProIleGluGluLys   920
Db 2784 GCATTTAAAGATGAAGTCCTGAATCACTGGCTCAAAGAAAATCCCCTACTGAGGAAAAAG 2843

Qy   921 PheGlnAlaAlaValGluArgPheValTyrSerCysAlaGlyTyrTyrCysValAlaThrPhe 940
Db 2844 TTTCAGGCAGCAGTGGAGAGATTTGTTTATTCCTGTGCAGGCTACTGTGTGGCAACCTTT 2903

Qy   941 ValLeuGlyIleGlyAlaValGluAspArgHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeu 960
Db 2904 GTTCTTGGAATAGGCGCAGTGGAAGATCGTCACAATGATAATATTATGATCAGCAGGAAACCTA 2963

Qy   961 PheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLys   980
Db 2964 TTTCATATTGACTTCGGGCACATTCTTGGGAATTACAAAAGTTTCTTGGGCATTAATAAA   3023

Qy   981 GluArgValProPheValLeuThrProAspPheLeuPheValMetGlyThrSerGlyLys 1000
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Qy 1001 LysThrSerLeuHisPheGlnLysPheGlnAspValLysLeuAlaTyrArgLeuAlaLeu 1020
Db 3084 AAGACAAGCCCACACTTCAGAAATTTCAGGACATCTGTGTTAAGGCTTATCGACTAGCCCTT 3143

Qy 1021 ArgHisHisThrAsnLeuLeuIleLeuLeuPheSerMetMetLeuMetThrGlyMetPro 1040
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Qy 1041 GlnLeuThrSerLysGluAspProIleGluTyrIleLeuArgGlnGlyIleLeuGluValGlyLeuSer 1060
Db 3204 CAGTTAACAAGCAAAGAAGACCCAATTGAATATATCCCGGATGCCCTCACAGTGGGGAAAAAAT 3263

Qy 1061 GluGluAspAlaLysLysTyrPheLeuAspAlaLeuLeuValCysArgAspPheGlyTyrTrp 1080
Db 3264 GAGGAGGATGCTAAAAAGTATTTTCTTGATGCAGTTGCAGAGAAAGGATGG   3323

Qy 1081 ThrValGlnPheAsnTrpPheLeuHisLeuValLeuGlyIleLysLeuGlnGluHis   1100

Db   3324 ACTGTGCAGTTTAATTGGTTCTCACATCTTGTTCTTCTTGCGCATCAAACAAGGAGAAACAT 3383

Qy   1101 SerAla 1102
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Db   3384 TCAGCC 3389

RESULT 9
AX327655
LOCUS   AX327655   5397 bp   DNA   linear   PAT 07-JAN-2002
DEFINITION Sequence 9 from Patent WO0185986.
ACCESSION   AX327655
VERSION   AX327655.1 GI:18097985
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Sadhu,C.
  TITLE   Phosphatidyl inositol 3-kinase delta binding partner
  JOURNAL   Patent: WO 0185986-A 9 15-NOV-2001;
            ICOS CORPORATION (US)
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                     KENSMSISILLDNYCHPIALPKHQTPDPEGDRVRAEMPNQLRKQLEAIIATDPINPL
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BASE COUNT   1534 a   1224 c   1207 g   1432 t
ORIGIN

Alignment Scores:
Pred. No.:   0   5397
Score: 5523.50
Percent Similarity: 97.10%   Matches: 5049
Best Local Similarity: 95.19%   Conservative: 21
Query Match: 95.40%   Mismatches: 31
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DB: Gaps: 1

US-09-974-573-1 (1-1102) x AX327655 (1-5397)

Qy   1 MetGluLeuGluAsnTyrLysGlnProValValLeuArgGluAspAsnArgArgArg Arg 20
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Qy   21 ArgArgMetLysProArgSerThrAlaAlaSerLeuSerSerMetGluLeuIleProIle 40
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Db   384 CGGAGGATGAAGCCACGGAGT---GCTGCCAGCGTGCTGTCTCCATGGAGCTTCATCCCCATC 440

Qy   41 GluPheValLeuProThrSerGlnArgCysLysSerProGluThrAlaLeuLeuLeuHis 60
                 |||||| :|||||||||||||||||||||||:::|||:|||||||||||||||||||
Db   441 GAGTTCGTGCTGCCCACCAGCCAGCGCAAATGCAAGAGCCCGGAGACGGCTCTGCTGCAC 500

Qy   61 ValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnValTrpLeuArgAlaLeuGlu 80
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Qy   81 ThrSerValSerAlaAspPheTyrHisArgLeuGlyProHisHisPheLeuLeuLeuTyr 100
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Qy   101 GlnLysLysGlyGlnTrpTyrGluIleTyrAspLysTyrGlnValValGlnThrLeuAsp 120
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Db   621 CAGAAGAAGGGGCAGTGGTACGAGATCTACGACAAGTACCAGGTGGTGCAGACTCTGGAC 680

Qy   121 CysLeuArgTyrTrpLysAlaThrHisArgSerProGlyGlnIleHisLeuValGlnArg 140
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Qy   141 HisAlaProSerGluGluThrLeuAlaPheGlnArgGlnLeuAsnAlaLeuIleGlyTyr 160
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Qy   161 AspValThrAspValSerAsnValHisAspAspLeuGluLeuGluPheThrArgArgLeu 180
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Db   801 GACGTCACTGACGTCAGCAACGTGCACGACGATGGACTTGAGTTCGAGTTCACGCGCGCTTG 860

Qy   181 ValThrProArgMetAlaGluValAlaGlyArgAspProLysLeuTyrAlaMetHisPro 200
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   861 GTGACCCCGCGCATGGCGGAGGTGGCCGGCCGAGACCCCAAGCTCTACGCCATGCACCCG 920

Qy   201 TrpValThrSerLysProLeuProGluTyrLeuTrpLysLysIleThrAsnAsnCysVal 220
                 ||||||||||||||||||||||||||||||||||||||||||||||||||::: |||||
Db   921 TGGGTGACGTCCAAGCCCCTCCCGGAGTACCTGTGGAAGAAGATTGCCAACAACTGCATC 980

Qy   221 PheIleIleHisArgSerThrThrSerGlnThrIleLysValSerProAspAspThr 240
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Db   981 TTCATCGTCATTCACCGGAGCACCACCAGCCAGACCATCAAGGTCTCACCGGACGACACC 1040

Qy   241 ProGlyThrIleLeuGlnSerPhePheThrLysMetAlaLysLysLysSerLeuMetAsp 260
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Db   1041 CCCGGCGCCATCCTGCAGAGCTTCTTCACCAAGATGGCCAAGAAGAAATCTCTGATGGAT 1100

Qy   261 IleProGluSerGlnSerGluGlnAspPheValLeuArgValCysGlyArgAspGluTyr 280
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Db   1101 ATTCCCGAAAGCCAAAGCGAACAGGATTTTGTGCTGCGCGTGTGCGGGATGGAGTAC 1160

Qy   281 LeuValGlyGluThrProIleLysAsnPheGlnTrpValArgGlnCysLeuLysAsnGly 300
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Db   1161 CTGGTGGGGGAAACGCCCATCAAAAACTTCCAGTGGGTGCGGCACTGCCTCAAGAACGGA 1220

Qy   301 GluGluIleHisLeuValLeuAspThrProProAspAlaLeuAspGluValArgLys 320
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Db   1221 GAAGAGATTCACGTGCTACTGGACACGCCTCCAGACGCCCTGGACGAGGTGAGGAAG 1280

Qy   321 GluGluTrpProLeuValAspAspCysThrGlyValThrGlyTyrHisGluGlnLeuThr 340
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Db   1281 GAAGAGTGGCCGCTGGTGGACGACTGCACGGGAGTCACCGGCTACCATGAGCAGCTTACC 1340

Qy   341 IleHisGlyLysAspHisGluSerValPheThrValSerLeuMetAspCysAspArgLys 360
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Db   1341 ATCCACGGCAAGGACCACGAGAGTGTGTTCACGGTGTCGCTGATGGACTGCGACCGCAAG 1400

Qy   361 PheArgValLysIleArgGlyIleAspIleProValLeuProArgThrAlaAspLeuThr 380
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Db   1401 TTCAGGGTGAAGATCAGAGGCATTGATATCCCCGTCCTGCCCCGGAACACCGACCTCACA 1460

Qy   381 ValPheValGluAlaAsnIleGlnTyrGlyGlnGlnValLeuCysGlnArgArgThrSer 400
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Qy   401  ProLysProThrGluValLeuTrpLeuPheAsnTrpLeuPheSerIleLysIle  420
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Db  1521  CCCAAGCCTTCACAGAGGAGGTGCTGTGGAATGTGGCTTCAGTTCAGTCAAAATC  1580

Qy   421  LysAspLeuProLysGlyAlaLeuLeuAsnLeuGlnIleTyrCysGlyLysAlaProAla  440
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Db  1581  AAAGACTTGCCCAAGGGGCTCTTACTGAACCTCCAGATCTACTGCGGTAAAGCTCCAGCA  1640

Qy   441  LeuSerGlyLysThrSerAlaGluMetProSerProGluSerLysGlyLysAlaGlnLeu  460
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Db  1641  CTGTCCAGCAAGGCCCTCTGCCAGGTGCCCAGTTCTGAGTCCAAAGGCAAAGTTCGGCTT  1700

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Qy   481  ValLeuHisMetTrpGlnLeuSerGlyLysGlyGlyAspPheSerPheAsnAlaAsp  500
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Qy   501  LysLeuThrSerAlaThrAsnProAspLysGluAsnSerMetSerIleLeuLeu  520
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Qy   541  AspArgValArgAlaAlaGluMetProAsnGlnLeuArgLysGlnLeuAlaIleIleAla  560
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Qy   561  ThrAspProLeuAsnProLeuThrAlaGluAspLysLysGluLeuGluHisPheArgTyr  580
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Qy   601  GlnGluIleValAlaLysThrTyrGlnIleLeuLeuAlaLysArgGluValTrpAspGlnSer  620
          |||||||||||||||||||||::::|||||||||||||||||||||||
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Qy   621  AlaLeuAspAspValGlyLeuThrMetGlyLeuAspCysAsnPheSerArgAspGluAsnVal  640
          |||||||||||||||||||||||||||||||||||||||||||
Db  2181  GCTTTGGATGTTGGTGTGGGTTAACAACTGCAGCTCCTGAGACTGCAACTTCTCCAGATGAAAATGTA  2240

Qy   641  ArgAlaAlaValAlaGlnLysGluLeuGluSerLeuGluAspAspAspSerValLeuHisTyrLeu  660
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Db  2241  AGAGCCGCAGTTGCAGTGCAGAAAGAGCTTGGAGAGCTTGGAGGATGATGTTCTGCATTACCTT  2300

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Qy   681  LeuLeuLeuLysArgGlyLeuArgAsnLysArgIleGlyIleGlyArgHisTyrGlnHisArgPheLeuTrpLeuArg  700
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Qy   701  SerGluIleAlaGlnSerArgHisTyrGlnLeuArgPheAlaValIleLeuGlnLeuAlaTyr  720
          ||||||||||||||||||||||||||||||||::::|||||||||||||||||||||||
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Qy   721  LeuArgGlyCysGlyThrAlaMetLeuHisGlnInGlnInValGlnAsnValIleLeuAsp  740
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Db  2481  CTGAGGGGCTGTGGCACAGCCATGCTGCACCAGTCCCAACAAGTCCAACTAATCGAG  2540

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Qy   761  SerGlnValIleSerGlnLeuLysGlnLeuGluAsnLeuGlnAsnLeuAsnLeuPro  780
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Db  2601  TCCCAAGTTATTTCACACTTAAACAAAAGCTTGAAAACCTGCAGAATTCTCAACTCCCC  2660

Qy   781  GlnSerPheArgValProTyrAspProGlyLeuLysAlaLeuAlaGlyAlaLeuIleGluLys  800
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Db  2661  GAAAGCTTTAGAGTTCCAATATGATCCTGGACTCAAAGCGCTGGCAGGAGCGCTGGCAATTGAAAAA  2720

Qy   801  CysLysValMetAlaSerLysLysProLeuPheLysGluCysLysAlaAspPro  820
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Qy   821  ThrAlaLeuSerAsnGluThrArgIleGlyTyrIleIlePheHisGlyTyrAspAspArgGln  840
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Qy   841  AspMetLeuIleLeuGlnIleLeuLeuArgIleMetGluSerIleTrpGlnThrGluSerLeu  860
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Db  2841  GACATGCTTATTTTACAGATTCTACGAATCATGGAGTCTATTTGGCAGACTGAATCTTTG  2900

Qy   861  AspLeuCysLeuLeuProTyrGlyCysValIleSerThrGlyAspAspLysMetIleGlu  880
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Qy   881  IleValLysAspAlaThrThrIleAlaAlaLysIleGlyGlnSerThrValGlyTyrAsnThrGly  900
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Db  2961  ATTGTGAAAGACGCGCCACGACAATTGCCAAAATTCAGCAAGCACCAGTGGCCAACACGGGA  3020

Qy   901  AlaPheLysAspGluValLeuSerHisTrpLeuTyrGluLysProIleGluGluLeuLys  920
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Db  3021  GCATTTAAAGATGAAGTCCTGAATCACTCGGCTCAAAGAAAAATCCCCTACTGAAGAAAAG  3080

Qy   921  PheGlnAlaAlaValGlyArgPheValSerCysSerAlaGlyTyrCysValAlaThrPhe  940
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Db  3081  TTTCAGGCAGCAGTGGGAGAGTTCGTTATCTGTGCAGCTGGCTACTGTGTGGCAACCTTT  3140

Qy   941  ValLeuGlyTyrIleGlyAspArgHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeu  960
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Qy   961  PheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleIleAsnLys  980
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Qy   981  GluArgValProPheValLeuPheProAspPheLeuGluMetGlyThrSerGlyLysLys  1000
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Qy   1041 GlnLeuThrSerLysGluAspGlyIleGluThrValIleGluArgAspAlaLeuThrLeuGlyLysSer  1060
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Qy   1101 SerAla  1102
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Db  3621  TCAGCC  3626
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RESULT 10

HSIDEM

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LOCUS       HSIDEM            5397 bp    mRNA      linear   PRI 07-OCT-1996
DEFINITION  H.sapiens mRNA for phosphatidylinositol 3 kinase gamma.
ACCESSION   X83368
VERSION     X83368.1  GI:1507821
KEYWORDS    phosphatidylinositol 3-kinase.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Stoyanov,B., Volinia,S., Hanck,T., Rubio,I., Loubtchenkov,M.,
            Malek,D., Stoyanova,S., Vanhaesebroeck,B., Dhand,R., Nuernberg,B.,
            Gierschik,P., Seedorf,K., Hsuan,J.J., Waterfield,M.D. and
            Wetzker,R.
TITLE       Cloning and characterization of a G protein-activated human
            phosphoinositide-3 kinase
JOURNAL     Science 269 (5224), 690-693 (1995)
MEDLINE     95350661
PUBMED      7624799
REFERENCE   2
AUTHORS     Waterfield,M.D.
TITLE       Direct Submission
JOURNAL     Submitted (08-DEC-1994) M.D. Waterfield, Ludwig-Inst. for Cancer
            Research, Courtauld Building, 91 Riding House Street, London, W1P
            8BT, UK
REMARK      Revised by [3]
REFERENCE   3  (bases 1 to 5397)
AUTHORS     Waterfield,M.D.
TITLE       Direct Submission
JOURNAL     Submitted (23-AUG-1996) M.D. Waterfield, Ludwig-Inst. for Cancer
            Research, Courtauld Building, 91 Riding House Street, London, W1P
            8BT, UK
COMMENT     On Aug 26, 1996 this sequence version replaced gi:940513.
            X83368 is homologous to M93252.
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                     /cell_line="U937"
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                     RGLRNKRIGHFLFWFLRSBIAQSRHYQQRFAVILEAYLRGCCTAMLHDFTQQVQVIEM
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BASE COUNT     1534 a   1224 c   1207 g   1432 t
ORIGIN
Alignment Scores:
Pred. No.:
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Score: 5523.50   Matches: 1049
Percent Similarity: 97.10%   Conservative: 21
Best Local Similarity: 95.19%   Mismatches: 31
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US-09-974-573-1 (1-1102) x HSIDEM (1-5397)

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Qy     1 MetGluLeuGluAsnTyrGluGlnProValValLeuArgGluAspAsnArgArgArgArg 20
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Qy    21 ArgArgMetLysProArgSerThrAlaAlaSerLeuSerSerMetGluLeuIleProIle 40
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Qy    41 GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeuLeuHis 60
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Qy    81 ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTyr 100
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Qy   101 GlnLysLysGlyGlnTrpTyrGluIleTyrAspLysTyrGlnValValGlnThrLeuAsp 120
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Qy   121 CysLeuArgTyrTrpLysValThrHisArgSerProGlyGlnIleHisValValGlnArg 140
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Qy   141 HisAlaProSerGluGluThrLeuAlaPheGlnArgGlnLeuAsnAlaLeuIleGlyTyr 160
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Qy   201 TrpValThrSerLysProLeuProGluTyrLeuLeuLysLysIleThrAsnAsnCysVal 220
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Qy   221 PheIleValIleHisArgSerThrThrSerGlnThrIleLysValSerAlaAspAspThr 240
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Qy   241 ProGlyThrIleLeuGlnSerPhePheThrLysMetAlaLysLysLysSerLeuMetAsp 260
Db  1041 CCCGGCGGCCATCCTGCAGAGCTTCTTCACCAAGATGGCCAAGAAGAAATCTCTGATGGAT 1100

Qy   261 IleProGluSerGlnAsnGluAspPheValLeuArgValCysGlyValCysTyrAspGluTyr 280
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Qy   281 LeuValGlyGluThrProIleLysAsnProGlnTrpValArgGlnCysLeuLysAsnGly 300
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Qy   301 GluIleIleHisLeuValLeuAspThrProProAspProAlaLeuAspGluValArgLys 320
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Qy   321 GluGluTrpProLeuValAspAspCysThrGlyValThrGlyTyrHisGluGlnLeuThr 340
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Length:   5397
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(This page contains a two-column nucleotide/protein sequence alignment. Each block shows a query (Qy) translated/DNA line, a match-bar line, and a database (Db) DNA line, with flanking residue/position numbers. The content is too dense for reliable character-by-character transcription; the legible block position markers are listed below.)

Left column (Qy/Db blocks, positions):

Qy	Db
341 / 1281	1340
361 / 1341	1400
381 / 1401	1460
401 / 1461	1520
421 / 1521	1580
441 / 1581	1640
461 / 1641	1700
481 / 1701	1760
501 / 1761	1820
521 / 1821	1880
541 / 1881	1940
561 / 1941	2000
581 / 2001	2060
601 / 2061	2120
621 / 2121	2180
641 / 2181	2240
661 / 2241	2300
681 / 2301	2360

Right column (Qy/Db blocks, positions):

Qy	Db
701 / 2361	2420
721 / 2421	2480
741 / 2481	2540
761 / 2541	2600
781 / 2601	2660
801 / 2661	2720
821 / 2721	2780
841 / 2781	2840
861 / 2841	2900
881 / 2901	2960
901 / 2961	3020
921 / 3021	3080
941 / 3081	3140
961 / 3141	3200
981 / 3201	3260
1001 / 3261	3320
1021 / 3321	3380
1041 / 3381	3440
1061 / 3441	3500

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Qy   1081 ThrValGlnPheAsnTrpPheLeuHisLeuValLeuGlyIleLysGlnGlyLysHis 1100
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Db   3561 ACTGTGCAGTTTAATTGGTTTCTACATCTTGTTCTTGGCATCAAACAAGGAGAAACAT 3620

Qy   1101 SerAla 1102
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Db   3621 TCAGCC 3626

RESULT 11
MMU249280
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DEFINITION  Mus musculus mRNA for phosphoinositide 3-kinase gamma (PI3Kg1
            gene).
ACCESSION   AJ249280
VERSION     AJ249280.1  GI:7668042
KEYWORDS    phosphoinositide 3-kinase gamma; PI3Kg1 gene.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Hirsch,E., Wymann,M.P., Patrucco,E., Tolosano,E.,
            Bulgarelli-Leva,G., Marengo,S., Rocchi,M. and Altruda,F.
  TITLE     Analysis of the murine phosphoinositide 3-kinase gamma gene
  JOURNAL   Gene 256 (1-2), 69-81 (2000)
  MEDLINE   20509993
  PUBMED    11054537
REFERENCE   2  (bases 1 to 4725)
  AUTHORS   Wymann,M.P.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-AUG-1999) Wymann M.P., Inst. Biochemistry, University
            of Fribourg, Rue du Musee 5, Fribourg CH-1700, SWITZERLAND
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Percent Similarity:            97.10%                    Conservative:        31
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Query Match:                   95.09%                    Indels:               0
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BASE COUNT   1251 a   1194 c   1134 g   1146 t
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US-09-974-573-1 (1-1102) x MMU249280 (1-4725)

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Qy    21 ArgArgMetLysProArgSerThrAlaAlaGlySerLeuSerMetGluLeuIleProIle   40
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Qy    81 ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTyr  100
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Qy   121 CysLeuArgTyrTrpLysValLeuHisArgSerProGlyGlnIleHisValValGlnArg  140
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Qy   161 AspValThrAspValSerAsnValHisAspAspGluLeuGluPheThrArgArgArgLeu  180
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Db   802 GACGTCACTGACATCAGCAATGTGCACGATGAGCTAGAGTTCACTCGCCGCCGTCTG 861

Qy   181 ValThrProArgMetAlaGluValAlaGlyArgAspAlaLysLeuTyrAlaMetHisPro  200
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Qy   201 TrpValThrSerLysProLeuProAspTyrLeuSerLysLysIleThrAsnAsnCysVal  220
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Db   922 TGGGTAACGTCCAAACCTCTCCCAGATACCTGTCAAAAAGATTGCCAACAACTGCGTCATC 981

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Db   982 TTCATCGTCATCCACCGCGGTACCACCAGCCAAACCATCAAGGTCTCCGCAGATGATACT 1041

Qy   241 ProGlyThrIleLeuGlnSerPhePheThrLysMetAlaLysLysLysSerLeuMetAsp  260
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Db  1042 CCTGGTACCATCCTTCAGAGCTTCTTCACCAAGATGGCCAAGAAGAAGTCCCTAATGAAT 1101

Qy   261 IleProGluSerGlnAsnGluArgAspPheValLeuArgValCysGlyArgAspGluTyr  280
         ||||||::::|||||||||||||||||||||||||||||||||||||||||||||||||
Db  1102 ATCCCAGAAAGTCAAAGTGAGCAGAGATTTTGTATTGCGGGTTTGTGGGCCGGATGAGTAC 1161

Qy   281 LeuValGlyGluThrProLeuLysAsnPheGlnTrpValArgGlnCysLeuLysAsnGly  300
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Db  1162 |||||||||||||||||||||||||||||||||||||: :|||||||||||||||||||
         CTGGTGGGTGAAACACCCCTCAAAAATTTCCAGTGGGTGGAGGAGTGCTGTCAGAACGGA 1221
Qy   301 GluGluIleHisLeuValLeuAspThrProAspProAlaLeuAspGluValArgLys 320
         GATGAAAATACACCTGGTGCTGACACGGCTCCAGACCCCAGCCCTTGATGAGGTGAGGAAG 1281
Db  1222 

Qy   321 GluGluTrpProLeuValAspAspCysThrGlyValThrGlyTyrHisGlnLeuThr 340
         GAGAAATGGCCGCTGGTAGATGATGATTGCACCGGCTACCACGGCTACCACCAGCTGACC 1341
Db  1282 

Qy   341 IleHisGlyTyrLysAspHisGluSerValPheThrValSerLeuTrpAspCysArgLys 360
         ATCCATGGCTACAAGGACCACGAGAGTGTCTTCACAGTGTCTTTGTGGGACTGCCGGAAAG 1401
Db  1342 

Qy   361 PheArgValLysIleArgIleTyrIleAspIleProValLeuProArgThrAlaAspLeuThr 380
         TTCAGGGTGAAGATCAGAGATTCAGATATCCCTGTCCTCCGGAACACCGACCTCACT 1461
Db  1402 

Qy   381 ValPheValGluValAlaAsnIleGlnTyrGlyGlnIleValLeuCysGlnArgArgThrSer 400
         GTGTTTGTGGAAGGAAGCCAACATCCAGCGGCAACAAGTCTCTGCCAAAGGAGAACCAGC 1521
Db  1462 

Qy   401 ProLysProPheThrGluGluValLeuTrpAsnValTrpLeuGluPheSerIleLysIle 420
         CCTAAGCCCTTCGCAGAGAGGTACTCTGGAATGTGGCTGGAGTTTGGCATCAAAATC 1581
Db  1522 

Qy   421 LysAspLeuProLysGlyValAlaLeuAsnLeuGlnIleTyrCysGlyLysLysAlaProAla 440
         AAAGACTTGCCCAAAGGGGTCTTATTGAACCTACAGATCTACTGCGGCAAAACCCCATCA 1641
Db  1582 

Qy   441 LeuSerGlyLysThrSerAlaGluMetProSerProGlySerLysSerGlyLysLysAsnGlnLeu 460
         CTGTCCAGGAAGACTTCTGCAGAGACTCCGAGTCCAGGCTCCCAAGAGCCCAGCTT 1701
Db  1642 

Qy   461 LeuTyrTyrTyrValAsnLeuLeuLeuIleAspHisArgPheLeuLeuArgHisGlyGluTyr 480
         CTCTATTACTGTGTAAATCTGCTGTTAATAGAGCACCGTTTCCTCCTGCACCGGGAGACTAT 1761
Db  1702 

Qy   481 ValLeuHisMetTrpGlnLeuSerGlyLysGlyLysGluAspGlnGlySerPheAsnAlaAsp 500
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Db  1762 

Qy   501 LysLeuThrSerAlaThrAlaThrAsnProAspLysValAsnSerMetSerIleSerIleLeuLeu 520
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Db  1822 

Qy   521 AspAsnAsnTyrCysHisProIleAlaThrAlaTyrProLysGlnHisArgProThrProGluGly 540
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Db  1882 

Qy   541 AspArgValArgAlaArgMetProAsnGlnLeuArgLysValGlnLeuGlyAlaIleIleAla 560
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Db  1942 

Qy   561 ThrAspProLeuAsnProLeuThrArgAlaGluLysLysGluLeuLeuTrpHisPheArgTyr 580
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Db  2002 

Qy   581 GluSerLeuLysAspProLysAlaTyrProLysLeuPheSerSerValLysTrpGlyGln 600
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Db  2062 

Qy   601 GlnGlyIleValAlaLysThrArgTyrGlnLeuIleLeuAlaLysArgGluValArgIleAspAspPheGlnSer 620
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Qy   621 AlaLeuAspValGlyTyrLeuThrMetGlnLeuLeuAspAspCysSerAspProPheGluSerAsnVal 640
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Qy   641 ArgAlaIleAlaValAlaGlnLysLeuGluSerLeuGluAspAspAspProValAspHisTyrLeu 660
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Qy   661 LeuGlnLeuValGlnAlaValAspThrProAspProAlaLeuAspGluValArgPhe 680
         CTCCAGCTGGTACAGGCTGTGAAATTTGACCGTACCACGACAGTGCGCTGGCCAGATTC 2361
Db  2302 

Qy   681 LeuLeuLeuArgGlyLeuArgAsnLysArgIleGlyPheIleGlyHisGlnPheLeuTrpPhePheLeuArg 700
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Db  2362 

Qy   701 SerGluIleAlaGlnSerArgHisTyrGlnGlnArgPheAlaValIleLeuValAlaTyr 720
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Db  2422 

Qy   721 LeuArgGlyCysGlyThrHisAlaMetLeuHisAspThrGlnGlnValIleValIleAsp 740
         CTGCGAGGCTGTGGCACAGCCATGTTGCAGGACTTCACACAGCAGGTCATTGGTGATTGAG 2541
Db  2482 

Qy   741 MetLeuGlnLysValThrIleAspIleLysSerLeuSerLeuArgGluLysTyrAspValSer 760
         ATGTTACAGAAAGTCACCATTGATATTAAATCGCTTCGGCAGAAGAAGTATGACGTCAGT 2601
Db  2542 

Qy   761 SerGlnValIleSerGlnLeuLeuLysGluGlnAsnLeuGlnAsnLeuAsnLeuPro 780
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Db  2602 

Qy   781 GlnSerPheArgValProTyrAspProGlyLeuLysAlaGlyAlaLeuValIleLeuGluLys 800
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Db  2662 

Qy   801 CysLysLysValMetAlaSerLysLysLysProLeuPheLysLysCysLysAlaAspPro 820
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Qy   821 ThrAlaLeuSerArgAsnGluThrGlyLysThrIleGlyIleIleGlyTyrAspAspLeuArgArgGln 840
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Qy   841 AspMetLeuIleLeuGlnIleLeuAsnArgIleMetGluSerIleTrpGluThrGluSerLeu 860
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Qy   861 AspLeuCysLeuLeuProTyrGlyCysIleSerThrGlyAspLysLysMetIleGlu 880
         GACCTGTGCCTTCTGCCTTACGGTTGCATCTCAACTGGTGACAAAATAGGAATGATCGAG 2961
Db  2902 

Qy   881 IleValLysAspAlaThrThrIleAlaLysIleIleGlnIleAsnThrGlyValGlyAsnThrGly 900
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Db  3022 

Qy   921 PheGlnAlaAlaValGluArgPheValSerCysAlaGlyTyrTyrSerAlaGlyTyrTyrCysValAlaThrPhe 940
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Qy   941 ValLeuGlyIleGlyAspAspArgHisArgAsnAsnAspAsnIleMetIleSerGluArgThrGlyAsnLeu 960
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Qy   981 GluArgValProPheValLeuThrProAspPheLeuPheValMetGlyThrSerGlyTyrLysLys 1000
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Db  3262 

Qy  1001 LysThrSerLeuHisPheGlnLysPheGlnAspAspAspAspProValCysValLysTyrLeuAlaLeu 1020
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Qy   1021  ArgHisHisThrAsnLeuLeuIleIleLeuPheSerMetMetGlyMetPro  1040
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Qy   1041  GlnLeuThrSerLysGluArgAspAlaLeuTyrIleArgAspAlaLeuThrValGlyLysSer  1060
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Qy   1061  GluGluAspAlaLysLysTyrPheLeuAspGlnIleGluValCysArgAspLysGlyTrp  1080
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Db   3502  GAGGAGGACGCGTAAGAAATATTTCCTTGACCAGATCGAAGTCTGCAGACAAAGGATGG  3561

Qy   1081  ThrValGlnPheAsnTrpPheLeuHisLeuValLeuGlyIleLysGlnGlnGluGlyLysHis  1100
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Qy   1101  SerAla 1102
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Db   3622  TCCGCT 3627
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RESULT 12
BC051246
LOCUS       BC051246               4330 bp    mRNA    linear    ROD 22-APR-2003
DEFINITION  Mus musculus phosphoinositide-3-kinase, catalytic, gamma
            polypeptide, mRNA (cDNA clone MGC:58890 IMAGE:6514979), complete
            cds.
ACCESSION   BC051246
VERSION     BC051246.1  GI:30048085
KEYWORDS    MGC.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 4330)
AUTHORS     Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
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            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
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            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
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            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE       Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE     22388257
PUBMED      12477932
REFERENCE   2  (bases 1 to 4330)
AUTHORS     Strausberg,R.
TITLE       Direct Submission
JOURNAL     Submitted (18-APR-2003) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
REMARK      NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
```

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            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
            Akhter,N., Ayle,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
            Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
            Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
            McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
            Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
            Young,A., Zhang,L.-H. and Green,E.D.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 108 Row: o Column: 22
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 9937983.
FEATURES             Location/Qualifiers
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                     /clone="MGC:58890 IMAGE:6514979"
                     /tissue_type="Mammary tumor. MMTV-LTR/INT3 model. 5 month
                     old mouse. Taken by biopsy."
                     /clone_lib="NCI_CGAP_Mam2"
                     /lab_host="DH10B"
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                     /note="synonyms: PI3Kgamma, p110gamma, 5830428L06Rik"
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                     /db_xref="LocusID:30955"
                     /translation="MELENYEQPVLREDNLRRRRMKPRSAAGSLSSMELIPIEFVL
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                     DVTDISNVHDDELEFTRRRLVTPRMAEVAGRDAKLYAMHPWVTSKPLPDYLSKKIANN
                     CIFIVIHRGTSQTTKVSADDTPGTILQSFTKVAKKKSLMNISSQSEQDFVLRVCG
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                     YHEQLTIHGKDHESVFTVSLWDCDRKFRVKIRGIDIPVLPRNTDLTVFSANIOHGQQ
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BASE COUNT   1168 a   1088 c   1041 g   1033 t
ORIGIN

Alignment Scores:
Pred. No.:                           0            Length:          4330
Score:                          5505.00           Matches:         1039
Percent Similarity:              97.10%           Conservative:      31
Best Local Similarity:           94.28%           Mismatches:        32
Query Match:                     95.08%           Indels:             0
DB:                                  10            Gaps:               0

US-09-974-573-1 (1-1102) x BC051246 (1-4330)
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Qy   1 MetGluLeuGluAsnTyrGluGlnProValValLeuArgGluAspAsnArgArgArgArg   20
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Db   62 ATGGAGCTGGAGAACTATGAACAACCGGTGGTTCTAAGAGAGGACAACCTCCGCCGGCGC 121

Qy   21 ArgArgMetLysProArgSerThrAlaAlaSerLeuSerMetGluLeuIleProIle   40
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Qy   41 GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeuLeuHis   60
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Db   182 GAGTTCGTACTGCCCACCAGCCAGCGCATCAGCAAGACGCCGGCTGCTCAT 241

Qy   61 ValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnAlaValTrpLeuArgAlaLeuGlu   80
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Qy   81 ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuTyr 100
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Db   302 ACCAGTGTGGCTGCGGAGTTCTACCACCGATTGGGCCCGGACCACTTCCTCCTGTCTAC 361

Qy   101 GlnLysLysGlyGlnTrpTrpTyrGluIleTyrAspLysTyrGlyLeuIleLeuThrLeuAsp 120
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Qy   141 HisAlaProSerGluGluThrAspSerAsnValHisLeuAsnAlaAlaLeuIleGlyTyr 160
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Db   482 CACGTACCTTCTGAGGAGACCGATAGTGCACAATGGCACTCACTCCCGATTGGCTAT 541

Qy   161 AspValThrAspValSerAsnValHisLeuAspAspGlyAspGlnValHisMetHisPro 180
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Qy   181 ValThrProArgMetAlaGluValAlaGlyAlaArgAspProLeuTyrAlaMetHisPro 200
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Qy   241 ProGlyThrIleLeuGlnSerProPhePheThrLysSerLysSerLeuMetAsp 260
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Qy   261 IleProGluSerGlnAsnGluArgAspPheThrLysValCysGlyTyrArgAspGluTyr 280
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Qy   281 LeuValGlyGluThrProIleLeuTyrAsnPheGlnTrpValArgGlnCysLeuLysAsnGly 300
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Db   902 CTGGTGGGTGAAACACCCATTGCTGTTTCCAGTTGGGTAGGCAGGTGCCTCAAGAACGGA 961

Qy   301 GluGluIleHisLeuValLeuValAspAspLeuValProProAspProAlaLeuAspGluValArgLys 320
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Db   962 GATGAAATACACCTGGTGCTCGACGACCTTCCAGACCCCCTTGATGAGGTGAGGAAG 1021

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Db   1082 ATCCATGGCAAGGACCACCGAGAGTGTTCACCAGTGTCTTTGTGGGACTGCGACCGAAAG 1141

Qy   361 PheArgValLysIleArgGlyIleArgGlyIleAspIleProValLeuProArgThrAlaAspLeuThr 380

Db   ...
Db   1142 TTCAGGGTCAAGATCAGAGGCATTGATATCCCTGTCCTGCCTCGGACACCGACCTCACT 1201

Qy   381 ValPheValGluAlaAsnIleGlnTyrGlyValGlnIleValLeuCysGlnArgThrSer 400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1202 GTGTTTGTGGAGGCAAACATCCAGACACGGGACAACGTCCTCTGCCAAAGGACCAGC 1261

Qy   401 ProLysProPheGluThrGluGluValLeuTrpLeuValAsnValTrpLeuGluPheIleLeuLysIle 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1262 CCTAAGCCCTTCGAGACAGAGGTACTCTGGAATGTGGCGGAGTTGGCATCAAAAATC 1321

Qy   421 LysAspLeuProLysGlyTyrAlaLeuLeuAsnLeuGlnIleLeuTyrCysGlyLysAlaProAla 440
          |||||||||||||||||||||||||||||||||||||||||||::::|||||||||||
Db   1322 AAAGACTTGCCCAAAGGGCTCTATTGAACCTACAGATCTACTGCTGTGCAAAACCCCATCA 1381

Qy   441 LeuSerGlyLysThrSerAlaGluMetProSerProGluSerLysGlyLysLysAlaGlnLeu 460
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1382 CTGTCCAGCAAGGCTTCTGCAGAGACTCCAGGTCCCGAGTCCAAGGGCAAAGCCCAGCTT 1441

Qy   461 LeuTyrTyrValAsnLeuLeuLeuIleAspAspHisArgPheLeuLeuArgHisGlyGluTyr 480
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Db   1442 CTCTATTACGTGAACTTGCTGTTAATAGACGACCACCGGTTCCTCCTCCGCCACGGGGACTAT 1501

Qy   481 ValLeuIleMetTrpGlnLeuSerGlyGlyLysGlyGlyGlnLeuGlyLeuSerPheAsnAlaAsp 500
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Db   1502 GTGCTCCACATGTGGCAGATATCTGGCAAGGGCAGGAGGGCAGGGCAGCCTTCAATGCTGAC 1561

Qy   501 LysLeuThrSerAlaThrAsnProAspLysHisProLeuProIleAlaLeuProLysSerIleLeuLeuLeu 520
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Qy   521 AspAsnTyrCysHisProIleAlaLeuProLysHisArgProThrProAspProGluGlyGly 540
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Db   1622 GACAATTACTGTCACCCCATAGCTTTGCCTAAGCACCGGCCCACCCCTGACCCTGACCAGAGGGA 1681

Qy   541 AspArgValAlaArgAlaGluMetProAsnGlnLeuArgLysGlnLeuGluAlaIleIleAla 560
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Qy   561 ThrAspProLeuAsnProLeuThrAlaGluAspLysLysGlyLeuLeuTrpHisPheArgTyr 580
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Qy   581 GluSerLeuLysAspProLysProLeuAlaTyrProLysSerLeuPheSerSerValTrpGlyGln 600
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Db   1802 GAAAGCCTGAAGCATCCGAAGCCTCTAGCCTATCCCTAAGTCAGTGAAATGGGGGCAG 1861

Qy   601 GlnGlyIleLeuValAlaAlaLysValThrTyrGlnLeuLeuLeuAlaLysArgGluValTrpAspGlnSer 620
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Db   1862 CAAGAAATTGTTGCAGCAAAGGTAACGTACCAGCTGTTAGCCAGAGGGAGATCTGGGATCCAGAAGT 1921

Qy   621 AlaLeuAspAlaValGlyLeuThrMetGlnLeuLeuLeuAspLeuLeuAspCysAsnPheSerGluAsnVal 640
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Db   1922 GCTTTGGACGTTGCTGTTGGACTTGCAACTTTTCAGACGAGAATGTC 1981

Qy   641 ArgAlaIleAlaValGlnLysLysGluSerLeuGluGlnAspArgAspValHisTyrLeu 660
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Db   1982 CGGGCCATTGCAGTTCAGTTCAGAAGGCTTAGAGGAGAGCTTAGAGGACGATGACGTTTTACATTACCTT 2041

Qy   661 LeuGlnLeuValLeuProLeuAsnAlaValLysPheHisGluProTyrHisAspSerAlaLeuAlaArgPhe 680
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||::::
Db   2042 CTCCAGCTGGTACGGCCTGTGAAAATTTGAACCGTACCACGACAGTGCGCTGGCCAGATTCC 2101

Qy   681 LeuLeuLysArgGlyLeuArgAsnLysArgIleGlyHisHisPheLeuHisPheLeuArg 700
          |||||||||||||||||||||||||||||||||||||||||||||||||||::::
Db   2102 CTGCTGAAGCGTGGCTTGAGGAACAAAAGAATCGGTCACTTTCTTGTCTGTCCTGGA 2161

Qy   701 SerGluIleAlaGlnSerArgHisTyrGlnIleAsnArgPheAlaValIleLeuGluAlaTyr 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||::::
Db   2162 AGTGAGATGCAACAGTCCAGACACTATCAGCAGAGGTTCGCTGATCCTGGAGGCGTAC 2221

Qy   721 LeuArgArgGlyCysGlyThrAlaMetLeuHisAspPheThrGlnAsnValGlnIleValIleAsp 740
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Db   ...

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Qy      1101 SerAla 1102
Db      3362 TCCGCT 3367
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RESULT 13

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LOCUS       A50265                           4137 bp    DNA        linear    PAT 07-MAR-1997
DEFINITION  A50265 Sequence 3 from Patent WO9612024.
ACCESSION   A50265
VERSION     A50265.1  GI:2303321
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4137)
  AUTHORS   Stoyanov,B., Hanck,T. and Wetzker,R.
  TITLE     CLONING, EXPRESSION AND CHARACTERISATION OF A NOVEL FORM OF
            PHOSPHATIDYLINOSITOL-3-KINASE
  JOURNAL   Patent: WO 9612024-A 3 25-APR-1996;
            MAX PLANCK GESELLSCHAFT (DE)
COMMENT     Other publication DE 4445562 960404.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT    1127 a    999 c    1001 g    1010 t
ORIGIN
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Alignment Scores:
Pred. No.:                      0          Length:        4137
Score:                      5499.50        Matches:       1048
Percent Similarity:         96.92%         Conservative:    21
Best Local Similarity:      95.01%         Mismatches:      32
Query Match:                94.98%         Indels:           2
                                           Gaps:             1
DB:
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US-09-974-573-1 (1-1102) x A50265 (1-4137)

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Qy      1 MetGluLeuGluAsnTyrGluGlnProValValLeuArgGluAsnArgArgArgArg   20
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Db    324 ATGGAGCTGGAGAACTATAAACAGCCCGTGGTGCTGAGAGAGAACAACCGCCGAGGCGC  383

Qy     21 ArgArgMetLysProArgSerThrAlaAlaSerLeuSerMetGluLeuIleProIle   40
            ||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db    384 CGGAGGATGAAGCCGCGGAGT---GTGCCCAGCCTGTCCATGGAGCTCATCCCCATC  440

Qy     41 GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeuLeuHis   60
            ||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||
Db    441 GAGTTCGTGCTGCCCACCAGCCAGAGCAAATGCAAGAGCCCGAAACGGCCTGCTGCAC  500

Qy     61 ValAlaGlyHisGlyAsnValGluGlnMetLysAlaGluAspArgAlaGlnLeuGlu   80
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    501 GTGGCCGGCCACGGCAACGTGGAGCAGATGAAAGCCGAAGACCCGAGCGTGGCGGAG  560

Qy     81 ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTyr  100
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    561 ACCAGCGTGGCGGCCGACTTCTACCACCGGCTGGGACCCGATCACTTCCTCCTGCTCTAT  620

Qy    101 GlnLeuLysGlyGlnTrpTyrlleArglleArgSerProGlyAsnGlySer  120
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Db    621 CAGAAGAAGGGGCAGTGGTACCGGATCCGCAGATCTACGACAAGTACCCGAGACTCTGGAC  680

Qy    121 CysLeuArgTyrLysProLysValLeuHisArgSerProGlyAsnValGlnArg  140
            |||||||||||||||||||||||||||||||||||||||||  ||||||||||
Db    681 TGCCTGCGCTACTGGAGGCCCACCAGGTCGGCAGGACCAAGGATGG  740

Qy    141 HisAlaProSerGluGluThrLeuAlaPheGlnArgGlnLeuAsnAlaLeuIleGlyTyr  160
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Db    741 CACCCGCCCTCCGAGGAGTCCAGCCTGCCGGCCTCACGGCCGCTGATTGGCTAT  800
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Db   2222 CTGGCGAGGCTGTGGCACAGCCATCGTGCTGCGGACTTCACACAGCAGGTCCATGTGAGGAG  2281
Qy    741 MetGluLeuGlnLysValThrAlaThrlleAspIlelleAspLysSerLeuSerLeuSerAlaGluLysTyrAspValSer  760
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2282 ATGTTACAGAAAGTCACCATTGATATTAAATCGCTCTCGGCAGAAGTATGACGTCAGT  2341
Qy    761 SerGlnValIleSerGlnlleuLeuLysGlnlleLysLeuGluAsnLeuGluAsnLeuPro  780
            |||||||||||||||||||||||||||||||||||||||   ||||||||||||||||||
Db   2342 TCCCAAGTTATTATTCACAGCTTAAGCAAAAGCTTGAAAGCTTCAGAACTCCAATCTCCCC  2401
Qy    781 GlnSerPheArgValProTyrAspProGlyLeuLysAlaGlyAlaLeuValIleGluGlyLys  800
            |||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2402 GAGAGCTTTAGAGTTCCCATATGATCCTGGACTAAAAGCCGGTACCCTGGTGATCGAGAAA  2461
Qy    801 CysLysValMetAlaSerlleLysLysProLeuTrpLeuGluPheLysCysAlaAspPro  820
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Db   2462 TGCAAAGTGATGGCCTCCAAGAGAAGCCCCTGGCTTGAGTTTAAGTGTGCTGATCCC  2521
Qy    821 ThrAlaLeuSerArgAsnGluThrlleGlyValllelleProGluLysHisGlyAspAspLeuArgGln  840
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2522 ACAGTCCATCCAAGAGAACCATTGGAATCATCTTTAAACATCGTGATGATCTCGCGCCAA  2581
Qy    841 AspMetLeulleLeuGlnlleLeuLeuArglleMetGluSerlleTrpGluThrGluSerLeu  860
            |||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2582 GACATGTTGATCTTGCAGATTCCACGCATCATGGAGTCCATTTGGGAGACTGAATCTCTG  2641
Qy    861 AspLeuCysSerLeuLeuProTyrGlyGlyCysllleSerSerThrGlyAspAsplleGlyMetlleGlu  880
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2642 GACCTGTGCTCCTTGCCTTACGGTGCCTCAACTGGTGACAAAATAGGAATGATCGAG  2701
Qy    881 IleValLLysAspAlaThrThrlleAlaLysSerlleGlnAsnSerThrValGlyAsnThrGly  900
            ||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2702 ATTGTAAAGGATGCCACACGATCGCTCAAATTCAGCAAAGCACAGAGTGGGTAACACGGGG  2761
Qy    901 AlaPheLysAspGluValLeuSerHisGlyGlyLysCysProlleGluGluLys  920
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Db   2762 GCATTCAAAGATGAAGTCCTGAATCACGGTGGCTCAAGGAAAAAATGTCCTATTGAAGAAAAG  2821
Qy    921 PheGlnAsnAlaAlaValGluArgPheValTyrSerCysAlaGlyTyrCysValAlaThrPhe  940
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Db   2822 TTTCAGGCCGCAGTGGAAAGGTTTGTTTACTCTGCGGCTACGTGTGTGCCACCATTT  2881
Qy    941 ValLeuGlyTyrlleGlyArgHisAsnAspAsnProHisGlyAsnLeuSerGluThrGlyAsnLeu  960
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Db   2882 GTTCTTGGGATCGGTGACAGGCACAACGATCGCTCAAATTCAGAGACACAGAAACCTA  2941
Qy    961 PheHislleAspPheGlyHislleLeuGlyAsnTyrLysSerPheLeuGlylleAsnLys  980
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Db   2942 TTTCATATAGACTTCGGACACATTCTTGGGAATTACAAGAGTTTCCTGGGCATCAATAAA  3001
Qy    981 GluArgValProPheValLeuProThrAspPhePheLeuValMetGlyValThrSerGlyLys  1000
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Db   3002 GAGAGAGTGCCCTTCGTCCTACCCACAGACTTCTTTGTTGTGATGGGGATCTTCTGAAA  3061
Qy   1001 LysThrSerLeuHisPheGlnLysPheGlnlleLeuLeuPheSerMetMetThrGlyMetPro  1020
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Db   3062 AAGACAAGTCCACACTTCCAGAAATTCCAGGATCTGTGTTTTAGAGCTTACCTAGCTCTT  3121
Qy   1021 ArgHisHisThrAsnLeulleLeuLeuPheSerMetMetThrGlyMetPro  1040
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Db   3122 CGCCATCACACAAACCTGTTGATCATCTTGTTTCTCCATGATGCTGATGAGAATGCCC  3181
Qy   1041 GlnLeuThrSerGluAspllleGlullleArgThrValGlyLysSer  1060
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Db   3182 CAGCTGACAAGCAAGGAGGGCAGTGGTACGGGATGCCCTCACGGTGGGAAAAAGC  3241
Qy   1061 GluGlulleaspPheLysLysTyrPheLeuAspLysllleGluValCysProlleTrp  1080
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Db   3242 GAGGAGGAGATCGACTTCAAGAAGTACTTCCTTGATAAAATTTCGGCATGCCCCGGGATGG  3301
Qy   1081 ThrValGlnPheAsnTrpPheLeuHisLeuValLeuGlylleLeuLysGlnGluGlyLysHis  1100
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Db   3302 ACTGTGCAGTTTAACTGGTTCCTACACTTGGTCCTGGGCATCATCAAAACAAGAAGAAAAGCAC  3361
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Qy 161 AspValThrAspValSerAsnValHisAspAspGluGluThrArgArgLeu 180
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Db 801 GACGTCACTGACGTCAGCAACGTGCACGATGAGGTTGGAGTTCACGCGCCGCTGGCTTG 860

Qy 181 ValThrProArgMetAlaGluValAlaGlyTyrArgAspProLeuTyrAlaMetHisPro 200
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Db 861 GTGACCCCGCCATGGCCGAGGTGGCCAGGTACCGCGACCCCCTACGCCATGCACCCG 920

Qy 201 TrpValThrSerIleSerProLeuProGluTyrTyrLeuLeuLysIleLysThrAsnAsnCysVal 220
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Qy 221 PheIleValIleHisArgSerThrThrSerGlnThrIleLeuLysValSerAlaAspAspThr 240
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Db 981 TTCATCGTCATTCACCGCAGCACCACCAGCCAGACCATTAAGGTCTCACCCGACGACACC 1040

Qy 241 ProGlyThrIleLeuGlnSerPhePheThrLysMetAlaLeuAlaLysLysSerLeuMetAsp 260
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Db 1041 CCCGGCACCATCCTGCAGAGCTTCTTCACCAAGATGGCCCAAGAGAGAAATCTCGATGAT 1100

Qy 261 IleProGluSerGlnAsnGluArgValAspPheValLeuArgValCysGlyArgAspGluTyr 280
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Db 1101 ATTCCCGAAAGCCAAAGCCAAAGGAGATTTTGTGCTGCGCGTGTGCGGCCGTGATGAGTAC 1160

Qy 281 LeuValGlyThrProIleLeuTyrAsnPheGlnTyrIleArgGlnCysLeuLysAsnGly 300
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Qy    921  PheGlnAlaAlaValGlnArgPheValTyrSerCysAlaGlyTyrCysValAlaThrPhe  940
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Db   3081                                                                    3140
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BASE COUNT   900 a   853 c   837 g   750 t   2 others
ORIGIN

US-09-974-573-1 (1-1102) x AF208345 (1-3342)

Length:      3342
Matches:     1037
Conservative: 31
Mismatches:   34
Indels:      11
Gaps:         1
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RESULT 14
LOCUS       AF208345               3342 bp    mRNA    linear   ROD 19-DEC-2000
DEFINITION  Mus musculus phosphatidylinositol 3-kinase gamma isoform (Pik3cg)
            mRNA, complete cds.
ACCESSION   AF208345
VERSION     AF208345.1  GI:11890407
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 3342)
  AUTHORS   Chakravarti,S. and McColl,S.R.
  TITLE     Cloning of a murine ortholog of PI 3-kinase gamma
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 3342)
  AUTHORS   Chakravarti,S. and McColl,S.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-NOV-1999) Microbiology & Immunology, University of
            Adelaide, Frome Road, Adelaide, SA 5005, Australia
FEATURES             Location/Qualifiers
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Db        421 CACGTACCTTCTGAGGAGACCTTGGCTTTCCAGAAGCAGCTCACCTCCCTGATTGGCTAT 480

Qy        161 AspValThrAspValSerAsnValHisAspAspGluLeuGluPheThrArgArgArgLeu 180
              ||||||||||||:::|||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACGTCACTGACATCAGCAATGTGCACGATGATGAGCTAGAGTTCACTCGCCGCCGTCTG 540

Qy        181 ValThrProArgMetAlaGluValAlaGlyArgAspProLysLeuTyrAlaMetHisPro 200
              ||||||||||||||||||||||||||||||||||||   |||||||||||||||||||||
Db        541 GTTACGCCCCGCATGGCTGAAGTGGCTGGCCGGGATGCCAAACTCTATGCTATGCACCCT 600

Qy        201 TrpValThrSerLysProLeuProGluTyrLeuLeuLysLysIleThrAsnAsnCysVal 220
              ||||||||||||||||||||||||:::||||||   |||||||||   |||||||||:::
Db        601 TGGGTAACGTCCAAACCTCTCCCAGACTACCTGTCAAAAAAAATTGCCAACAACTGCATC 660

Qy        221 PheIleValIleHisArgSerThrThrSerGlnThrIleLysValSerAlaAspAspThr 240
              ||||||||||||||||||   |||||||||||||||||||||||||||||||||||||||
Db        661 TTCATCGTCATCCACCGCGGTACCACCAGCCAAACCATCAAGGTCTCCGCAGATGATACT 720

Qy        241 ProGlyThrIleLeuGlnSerPhePheThrLysMetAlaLysLysLysSerLeuMetAsp 260
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        721 CCTGGTACCATCCTCCAGAGCTTCTTCACCAAGATGGCCAAGAAGAAGTCCCTAATGAAT 780

Qy        261 IleProGluSerGlnAsnGluArgAspPheValLeuArgValCysGlyArgAspGluTyr 280
              |||   |||||||||:::|||:::||||||||||||||||||||||||||||||||||||
Db        781 ATCTCAGAAAGTCAAAGTGAGCAGGATTTTGTATTGCGGGTTTGTGGCCGCGATGAGTAC 840

Qy        281 LeuValGlyGluThrProIleLysAsnPheGlnTrpValArgGlnCysLeuLysAsnGly 300
              ||||||||||||||||||:::|||||||||||||||||||||||||||||||||||||||
Db        841 CTGGTGGGTGAAACACCCCTCAAAAATTTCCAGTGGGTGAGGCAGTGCCTCAAGAACGGA 900

Qy        301 GluGluIleHisLeuValLeuAspThrProProAspProAlaLeuAspGluValArgLys 320
              :::|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GATGAAATACACCTGGTGCTCGACACGCCTCCAGACCCAGCCCTTGATGAGGTGAGGAAG 960

Qy        321 GluGluTrpProLeuValAspAspCysThrGlyValThrGlyTyrHisGluGlnLeuThr 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAAGAATGGCCGCTGGTGGATGACTGCACTGGAGTCACCGGCTACCACGAGCAGCTGACC 1020

Qy        341 IleHisGlyLysAspHisGluSerValPheThrValSerLeuTrpAspCysAspArgLys 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATCCATGGCAAGGACCACGAGAGTGTGTTCACAGTGTCTTTGTGGGACTGCGACCGAAAG 1080

Qy        361 PheArgValLysIleArgGlyIleAspIleProValLeuProArgThrAlaAspLeuThr 380
              |||||||||||||||||||||||||||||||||||||||||||||      |||||||||
Db       1081 TTCAGGGTCAAGATCAGAGGCATTGATATCCCTGTCCTGCCTCGGAACACCGACCTCACT 1140

Qy        381 ValPheValGluAlaAsnIleGlnTyrGlyGlnGlnValLeuCysGlnArgArgThrSer 400
              ||||||||||||||||||||||||:::|||||||||||||||||||||||||||||||||
Db       1141 GTGTTTGTGGAAGCGAACATCCAGCACGGGCAACAAGTCCTCTGCCAAAGGAGAACCAGC 1200

Qy        401 ProLysProPheThrGluGluValLeuTrpAsnValTrpLeuGluPheSerIleLysIle 420
              ||||||||||||   |||||||||||||||||||||||||||||||||   |||||||||
Db       1201 CCTAAGCCCTTCGCAGAAGAGGTACTCTGGAATGTGTGGCTGGAGTTTGGCATCAAAATC 1260

Qy        421 LysAspLeuProLysGlyAlaLeuLeuAsnLeuGlnIleTyrCysGlyLysAlaProAla 440
              |||||||||||||||||||||||||||||||||||||||||||||   |||   |||:::
Db       1261 AAAGACTTGCCCAAAGGGGCTCTATTGAACCTACAGATCTACTGCTGCAAAACCCCATCA 1320

Qy        441 LeuSerGlyLysThrSerAlaGluMetProSerProGluSerLysGlyLysAlaGlnLeu 460
              ||||||   |||   |||||||||   |||      ||||||||||||||||||||||||
Db       1321 CTGTCCAGCAAGGCTTCTGCAGAGACTCCAGGCTCCGAGTCCAAGGGCAAAGCCCAGCTT 1380

Qy        461 LeuTyrTyrValAsnLeuLeuLeuIleAspHisArgPheLeuLeuArgHisGlyGluTyr 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||:::|||
Db       1381 CTCTATTACGTGAACTTGCTGTTAATAGACCACCGTTTCCTCCTCCGCCACGGGGACTAT 1440

Qy        481 ValLeuHisMetTrpGlnLeuSerGlyLysGlyGluAspGlnGlySerPheAsnAlaAsp 500
              ||||||||||||||||||:::|||||||||   |||:::|||||||||||||||||||||
Db       1441 GTGCTCCACATGTGGCAGATATCTGGCAAGGCAGAGGAGCAGGGCAGCTTCAATGCTGAC 1500

Qy        501 LysLeuThrSerAlaThrAsnProAspLysGluAsnSerMetSerIleSerIleLeuLeu 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 AAGCTCACATCCGCAACCAATCCTGACAAGGAGAACTCAATGTCCATTTCCATCCTGCTG 1560

Qy        521 AspAsnTyrCysHisProIleAlaLeuProLysHisArgProThrProAspProGluGly 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GACAATTACTGTCACCCCATAGCTTTGCCTAAGCACCGGCCCACCCCTGACCCAGAGGGA 1620

Qy        541 AspArgValArgAlaGluMetProAsnGlnLeuArgLysGlnLeuGluAlaIleIleAla 560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GACAGGGTTCGGGCTGAAATGCCCAATCAGCTTCGAAAGCAATTGGAGGCGATCATAGCC 1680

Qy        561 ThrAspProLeuAsnProLeuThrAlaGluAspLysGluLeuLeuTrpHisPheArgTyr 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 ACAGATCCACTTAACCCCCTCACAGCAGAGGACAAAGAATTGCTCTGGCATTTTCGATAT 1740

Qy        581 GluSerLeuLysAspProLysAlaTyrProLysLeuPheSerSerValLysTrpGlyGln 600
              ||||||||||||   |||||||||||||||||||||||||||||||||||||||||||||
Db       1741 GAAAGCCTGAAGCATCCGAAGGCTTACCCTAAGCTATTCAGCTCAGTGAAATGGGGGCAG 1800

Qy        601 GlnGluIleValAlaLysThrTyrGlnLeuLeuAlaLysArgGluValTrpAspGlnSer 620
              ||||||||||||||||||||||||||||||||||||:::||||||:::||||||||||||
Db       1801 CAAGAAATTGTTGCCAAAACGTACCAGCTGTTAGCCAGAAGGGAGATCTGGGATCAAAGT 1860

Qy        621 AlaLeuAspValGlyLeuThrMetGlnLeuLeuAspCysAsnPheSerAspGluAsnVal 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 GCTTTGGACGTTGGCTTAACCATGCAGCTCCTGGACTGCAACTTTTCAGACGAGAATGTC 1920

Qy        641 ArgAlaIleAlaValGlnLysLeuGluSerLeuGluAspAspAspValLeuHisTyrLeu 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 CGGGCCATTGCAGTTCAGAAACTGGAGAGCTTAGAGGACGATGACGTTTTACATTACCTT 1980

Qy        661 LeuGlnLeuValGlnAlaValLysPheGluProTyrHisAspSerAlaLeuAlaArgPhe 680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 CTCCAGCTGGTACAGGCTGTGAAATTTGAACCGTACCACGACAGTGCGCTGGCCAGATTC 2040

Qy        681 LeuLeuLysArgGlyLeuArgAsnLysArgIleGlyHisPheLeuPheTrpPheLeuArg 700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 CTGCTGAAGCGTGGCTTGAGGAACAAAAGAATCGGTCACTTCTTGTTCTGGTTCCTGCGA 2100

Qy        701 SerGluIleAlaGlnSerArgHisTyrGlnGlnArgPheAlaValIleLeuGluAlaTyr 720
              ||||||||||||||||||   |||||||||||||||||||||||||||||||||||||||
Db       2101 AGTGAGATCGCACAGTCCANACACTATCAGCAGAGGTTCGCTGTGATCCTGGAGGCGTAC 2160

Qy        721 LeuArgGlyCysGlyThrAlaMetLeuHisAspPheThrGlnGlnValGlnValIleAsp 740
              |||||||||||||||||||||||||||   ||||||||||||||||||   ||||||:::
Db       2161 CTGCGAGGCTGTGGCACAGCCATGTTGCAGGACTTCACACAGCAGGTCCATGTGATTGAG 2220

Qy        741 MetLeuGlnLysValThrIleAspIleLysSerLeuSerAlaGluLysTyrAspValSer 760
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Db       2221 ATGTTACAGAAAGTCACCATTGATATTAAATCGCTCTCGGCAGAGAAGTATGACGTCAGT 2280

Qy        761 SerGlnValIleSerGlnLeuLysGlnLysLeuGluAsnLeuGlnAsnLeuAsnLeuPro 780
              ||||||||||||||||||||||||||||||||||||:::|||||||||   |||||||||
Db       2281 TCCCAAGTTATTTCACAGCTTAAGCAAAAGCTTGAAAGCCTTCAGAACTCCAATCTCCCC 2340

Qy        781 GlnSerPheArgValProTyrAspProGlyLeuLysAlaGlyAlaLeuValIleGluLys 800
              :::|||||||||||||||||||||||||||||||||||||||   |||||||||||||||
Db       2341 GAGAGCTTTAGAGTTCCCTATGATCCTGGACTAAAAGCCGGTACCCTGGTGATCGAGAAA 2400

Qy        801 CysLysValMetAlaSerLysLysLysProLeuTrpLeuGluPheLysCysAlaAspPro 820
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 TGCAAAGTGATGGCCTCCAAGAAGAAGCCCCTGTGGCTTGAGTTTAAGTGTGCTGATCCC 2460

Qy        821 ThrAlaLeuSerAsnGluThrIleGlyIleIlePheLysHisGlyAspAspLeuArgGln 840
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 ACAGTCCTATCCAACGAAACCATTGGAATCATCTTTAAACATGGTGATGATCTGCGCCAA 2520

Qy        841 AspMetLeuIleLeuGlnIleLeuArgIleMetGluSerIleTrpGluThrGluSerLeu 860
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Db       2521 GACATGTTGATCTTGCAGATTCTACGCATCATGGAGTCCATTTGGGAGACTGAATCTCTG 2580

Qy        861 AspLeuCysLeuLeuProTyrGlyCysIleSerThrGlyAspLysIleGlyMetIleGlu 880
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 GACCTGTGCCTTCTGCCTTACGGNTGCATCTCAACTGGTGACAAAATAGGAATGATCGAG 2640
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Alignment Scores:
Pred. No.:                              0        Length:          4134
Score:                            5440.00        Matches:         1046
Percent Similarity:                96.65%        Conservative:      20
Best Local Similarity:             94.83%        Mismatches:        35
Query Match:                       93.96%        Indels:             4
DB:                                             Gaps:               1

US-09-974-573-1 (1-1102) x A50263 (1-4134)
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Qy      1 MetGluLeuGlnAsnTyrGluGlnProValValLeuGlnProValLeuAsnArgGluArgArgArg   20
            ||||||||||||||||||||||||||||||||||||||| :||:||:|||||||||||||||||
Db    324 ATGGAGCTGGAGAACTATAAACAGCCCGTGGTGCTGCAGCCAGTGCTGAACAGGGAGAGGAGGCGC  383

Qy     21 ArgArgMetLysProArgSerThrAlaAlaSerLeuSerMetGluLeuIleProIle   40
            ||||||||||||||||||||||||||     ||||||||||||||||||||||||||
Db    384 CGGAGGATGAAGCCGCGGCAGT--GCTGCCAGCCTGTCCATGGAGCTCATCCCCATC  440

Qy     41 GluPheGlnAlaAlaValGluArgPheValTyrSerCysAlaGlyTyrCysValAlaLeuLeuHis   60
            ||||||||||||||||||||||||||||||||||||||||||:::||||||||||||||||||
Db    441 GAGTTCCAGTGCTCCTGCACCAGGCAGCCGAAATGCAAGAGCCCCGAAAACGGGCCTGCTGCAC  500

Qy     61 ValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnHisValTrpLeuArgAlaLeuGlu   80
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Db    501 GTGGCCGGCCACGGCAACGTGGAGCAGATGAAGGCCCAGGTGTGGCTGCGGGCGTTGGAG  560

Qy     81 ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTyr  100
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Db    561 ACCAGCT--GGCGGCGGACTTCTACCACCGGCTGGGACCCGATCACTTCCTGCTGCTCTAT  618

Qy    101 GlnLysGlyGlnTrpIleTyrGluIleTyrAspLysTyrGlnValValGlnThrLeuAsp  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    619 CAGAAGA-GGGCAGTGGTACGAGATCTACGACAAGTACCAGGTGGTGCAGACTCTGGAC  677

Qy    121 CysLeuArgTyrTrpLysTrpLysSerArgSerProGlyGlnIleHisValValGlnArg  140
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Db    678 TGCCTGCGCTACTGGAAGTGGAAGAGCCGCAGCCCCGGGCAGATCCACGTGGTGCAGCGG  737

Qy    141 HisAlaProSerGluGluThrLeuAlaPheGlnLeuAsnAlaLeuIleGlyTyr  160
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Db    738 CACGCCCGCTCCGAGGAGACCTTGGCGTTTCAGCTCAACGCGCTCATCGGCTAT  797

Qy    161 AspValThrAspValSerAsnValHisAspAspGluLeuGluPheThrArgArgLeu  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    798 GACGTCACTGACGTCAGCAACGTGCACGACGATGAGCTGGAGTTCACGCGCCGTGGCTTG  857

Qy    181 ValThrProArgMetAlaGluAlaAlaGlyArgAspProLeuTyrAlaMetHisPro  200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    858 GTGACCCCGCGCATGGCGGAGGCTGGCCAGCCGGACCCCAAGCTCTACGCCATGCACCCG  917

Qy    201 TrpValThrSerLysProLeuProGluTyrLeuLeuLysIleThrAsnAsnCysVal  220
            ||||||||||||||||||||||||||||||||:::|||||||||||||||||||||
Db    918 TGGGTGACGTCCAAGCCCCTCCCGGAGTACCTGCTGAAGAAGATTGCCAACAACTGCATC  977

Qy    221 PheIleValIleHisArgSerThrThrSerGlnThrIleLysValSerAlaAspAspThr  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    978 TTCATCGTCATTCACCGCAGCACCACCAGCCAGACCATTAAGGTCTCACCCGACGACACC  1037

Qy    241 ProGlyThrIleLeuGlnSerPhePheLysMetAlaLysLysSerLeuMetAsp  260
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Db   1038 CCCGGGCGCCATCCTGCAGAGCTTCTTCACCAGATGGCCAAGAAGAAATCCTGATGGAT  1097

Qy    261 IleProGluSerGlnAsnGluArgAspPheValLeuArgValCysGlyValTyrGluTyr  280
            ||||||||||||||||||||||||||||||||:::||||||||||||||||||||||||
Db   1098 ATTCCCGAGAGCCAAAGCGAACAGGATTTTGTGCTGCGGGTCTGCGGCGTGTACGAGTAC  1157

Qy    281 LeuValGlyGluThrProIleLysAsnPheGlnInTrpValArgGlnCysLeuLysAsnGly  300
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Db   1158 CTGGTGGGCGAAACGCCCATCAAAAACTTCCAGTGGGTGAGGCAGTGCCTCAAGAACGGA  1217

Qy    301 GluGluIleHisLeuValLeuAspThrProProAlaLeuAspGluGluAlaArgLys  320
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Db   1218 GAGGAGATCCAC
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Qy    881 IleValLysAspAlaThrThrIleAlaLysIleIleGlnGlnSerThrValGlyAsnThrGly  900
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Db   2641 ATTGTAAAGGATGCCACAACGATCGCTAAAATTCAGCAAAGCACAGTGGGTAACACGGGG  2700

Qy    901 AlaPheGluSerHisSerLeuArgLeuSerHisTrpLeuLysGluLysCysProIleGluGluLys  920
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Db   2701 GCATTCAAAGATGAGAGTCCTGAATCACTTGGCTCAAGGAAAAAGTCCATTGAAGAGAAAG  2760

Qy    921 PheGlnAlaAlaValGluArgPheValTyrSerCysAlaGlyTyrCysValAlaThrPhe  940
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Db   2761 TTTCAGGCCGCAGTGGAAAGGTTTGTTTACTCCTGCGCAGGCTACTGTGTGGCCACATT  2820

Qy    941 ValLeuGlyIleGlyAspAspArgHisAsnAspAsnIleSerGluThrGlyAsnLeu  960
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Db   2821 GTTCTTGGGATCGGTGACAGGCACAGACATTATGATCTCAGACAGACAGAAACCTA  2880

Qy    961 PheHisIleAspPheGlyHisPheLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLys  980
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 TTTCATATAGACTTCGGACACATTCTTGGGAATTACAAGAGTTTCCTGGGCATCAATAAA  2940

Qy    981 GluArgValProPheValLeuThrProAspPheValMetGlyThrSerGlyLys  1000
            |||||||||||||||||||||||||||:::||||||||||||||||||||||
Db   2941 GAGAGAGTGCCCTTCGTCCTAACCCCAGACTTTGTGATGGGATCTTCTGGAAAA  3000

Qy   1001 LysThrSerLeuHisLysPheGlnGln  1010
            |||||||||||||||||||||
Db   3001 AAGACAAGTCCACTTCACAAATTCCAGGAGAAATTTCCAGGATTGCTGTGTGTCTACTTACAGTACTAT  3060

Qy   1011 ---AspValCysLysValAlaTyrLeuAlaLeuArgHisHisAsnLeuLeuIleIle  1029
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Db   3061 GGGGGATGTCTGTGTGTAGAGCTTACCTAGCTCTTCGCCATCACAACAAACCTGTTGATCATC  3120

Qy   1030 LeuPheSerMetMetLeuMetThrGlyMetProGlnLeuThrSerLysGluAspIleGlu  1049
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 TTGTTCTCCATGATGCTGATGACAGGAATGCCCCAGCTGACAAGCAAGGAAGACATTGAA  3180

Qy   1050 TyrIleArgAspAlaLeuThrValGlyLysSerGluGluAspAlaLysLysTyrPheLeu  1069
            |||||||||||||||||||||||||||||||||||||||:||||||||||||||||||
Db   3181 TATATCCGGGATGCCCTCACCGTCGGGAAAAGCGAAGAGGACGCCAAGAAATATTTCCTT  3240

Qy   1070 AspGlnIleGluValCysArgAspLysGlyTrpThrThrValGlnPheAsnTrpPheLeuHis  1089
            ||||||||||||||||||||||||||||||||||||||:::||||||||||||||||||
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Qy   1090 LeuValLeuGlyIleLeuLysGlnGlyGlnGluLysSerHisSerAla  1102
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RESULT 15
A50263
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DEFINITION  Sequence 1 from Patent WO9612024.
ACCESSION   A50263
VERSION     A50263.1    GI:2303320
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 4134)
  AUTHORS   Stoyanov,B., Hanck,T. and Wetzker,R.
  TITLE     CLONING, EXPRESSION AND CHARACTERISATION OF A NOVEL FORM OF
            PHOSPHATIDYLINOSITOL-3-KINASE
  JOURNAL   Patent: WO 9612024-A 1 25-APR-1996;
            MAX PLANCK GESELLSCHAFT (DE)
COMMENT     Other publication DE 4445562 960404.
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT     1127 a   998 c    999 g   1010 t
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Qy   681 LeuLeuLysArgGlyValLeuArgAsnIleArgIleGlyHisPheLeuTrpPheLeuArg   700
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Db   2358 CTGCTGAAGCGCTGGTTGAAGAACAAAAGAAATTGGTCACTTTTGTTTGTTTGGTCTTGAGA 2417

Qy   321 GluGluTrpProLeuValAspAspCysThrGlyValThrGlyTyrHisGlnLeuThr   340
Db   1278 GAAGAGTGGCCGCTGGTGGACGACTGCACGGGAGTCACCGGCTACCATCAGCTTACC   1337

Qy   701 SerGlnIleAlaGlnSerArgHisTyrGlnArgGlnProAlaValIleLeuGlnAlaTyr   720
            ||||||||||| |||||||||||||| |||||||||||
Db   2418 AGTGAGATAGCCCAGTCCAGACACTATCAGCAGCAGCCTGCTGTGATCTTGGAAGCCTAT 2477

Qy   341 IleHisGlyLysAspHisGluSerValPheThrValSerLeuTrpAspCysArgArgLys   360
            |||||||| ||||||||||||||||||||||||||| ||||||||||||| |||||||
Db   1338 ATCCACGGCAAGGACCACGAGAGTGTGTTCACCGTGTCCCTGTGGGACTGCCGACCCAAG   1397

Qy   721 LeuArgGlyCysGlyThrAlaMetLeuHisAspPheThrArgGlnValGlnValIleAsp   740
            ||||||| ||||||| || ||||| ||||||| ||||||||||| ||||||| :::
Db   2478 CTGAGGGGCTGTGGCACAGCCATGCTGCACGACTTTACCCAACAAGTCCAAGTAATCGAG 2537

Qy   361 PheArgValLysIleArgGlyIleLeuProValLeuProArgThrAlaAspLeuThr   380
Db   1398 TTCAGGGTCAAGATCAGAGGCATTGATATCCCGGTCCTCGGACACCGACCTCACA   1457

Qy   741 MetLeuGlnLysValThrIleAspPheLeuSerLeuSerAlaGluLysHisTyrAspValSer   760
            |||||| ||||||||||| ||:::|
Db   2538 ATGTTACAAAAAGTCACCCTTGATATTAAATCGCTTCTGCTGAAAGTATGACGTCAGT   2597

Qy   381 ValPheValGluAlaGlnIleGlnTyrGlyIleGlyGlnValLeuCysGlnArgThrSer   400
Db   1458 GTTTTTGTAGAGGCACAAATCCAGCATGGCAACAAGTCCTTTGCCAAGGAGAACCAGC   1517

Qy   761 SerGlnValIleSerGlnLeuLeuLysGlnLysGlnLeuGlnLeuAsnLeuGlnAsnLeuAsnLeuPro   780
            || ||||| || || |||| | |||
Db   2598 TCCCAAGTTATTTCACAACTTAAACAAAAGCTTGAAAACCTGCAGAATTCCAACTCCCC   2657

Qy   401 ProLysProPheThrGluLeuValLeuTrpAsnValTrpLeuGluPheSerIleLeuIle   420
            |||||||||||||||||||||| ||||||||| |||||||| |||||||||||||||
Db   1518 CCCAAACCCTTCACAGAGCTGGTGCTGTGGAATGTGTGGCTTGAGTTCAGTATCAAAATC 1577

Qy   781 GlnSerPheArgValProTyrAspAspProGlyLeuLysValAlaGlyAlaLeuValIleGluLys   800
            ::::|||| |||||||| ||||||||||||
Db   2658 GAAAGCTTTAGAGTTCCATATGATCCTGGACTTAAAGTCGCTGGCAATTGAAAAA   2717

Qy   421 LysAspLeuProLysGlyAlaLeuLeuAsnLeuGlnIleTyrCysGlyLysLysAlaProAla   440
            ||||||||||||||||||||||| ||||||||| |||||||||||||||||||||||||
Db   1578 AAAGACTTGCCCAAAGGGGCTCTACTGAACCTCCAGATCTACTGCGGTAAAGCTCCAGCA   1637

Qy   801 CysLysValMetAlaSerLysLysProLeuTrpLeuGluTrpLeuGlyLysAlaAspPro   820
            |||| |||||||||| ||||||||||||||||| ||||| ||||| |||||||||
Db   2718 TGTAAAGTAATGGCCTCCAAGAAAAAACCACTATGGCTTGAGTTTAAATGTCCGGATCCT   2777

Qy   441 LeuSerGlyLysThrSerAlaGluMetProSerProLysSerGlyLysAlaGlnIleLeu   460
            || || ||||||||||| ||||||||||||| ||||||||||||| |:::|
Db   1638 CTGTCCAGGAAGACCTCTGCAGAGTCCCAGTCTCAGAGCGGCAAAGTTCGGCTT   1697

Qy   461 LeuTyrTyrValAsnLeuLeuLeuHisAspHisArgPheLeuArgHisGlyGluTyr   480
            |||||||||| ||||||||| |||||||||||| |||||||||||||||| |||||
Db   1698 CTCTATTATGTGAACCTGCTGCTGATAGACCACCGTTTCCTCCGCCGTGGAGAATAC   1757

Qy   821 ThrAlaLeuSerAsnGluThrIleGlyIleIleGluAsnIleTyrAspAspLeuLysArgGln   840
            || |||||| || |||||||||| ||| ||||||||| ||||||||| ||||| ||||
Db   2778 ACAGCCCTATCAAATGAAACAATTGGAATTATCTTTAAACATGGTGATGATCTGAAGCGGCCAA   2837

Qy   481 ValLeuHisMetTrpGlnLeuSerGlyGlyValGlyGluSerGlySerPheAsnAlaAsAsp   500
            |||||| ||||| ||||| ||||||||||||||| ||||||||||| ||||||||
Db   1758 GTCCTTCACATGTGGCAGATATCTGGAGGGAGAAGAAGCTTCAATGCTGAC   1817

Qy   841 AspMetMetLeuGlnIleLeuArgIleMetGluSerIleLeuTrpGluTrpGluSerLeu   860
            ||||| |||||||| |||| || ||||| ||||| ||||| |||||| |||||||
Db   2838 GACATGTTATTTACAGATCCACAATCATGGGAGTCTATTGGACTTATTGGGAGACTTTTG   2897

Qy   501 LysLeuThrSerAlaThrAsnProAspLysGluAsnSerMetSerIleSerLeuLeuLeu   520
            || ||||||||||||| | ||||| ||||||| |||||||||||||||||||||||
Db   1818 AAACTCCACGTCTGCAACTCTGACAAACCCAGACAAGGAACTCAATGTCCCATCTCCATTCTCTG 1877

Qy   861 AspLeuCysGlyLeuLeuProTyrGlyCysIleSerThrGlyLysLysIleGlyGlyMetIleGlu   880
            |||| ||||||| |||||||| |||||||||||||| |||| |||||||| |||||
Db   2898 GATCTATGCTGTCCTGCCATATGGTTGCATTTCAACTGGTGACAAAATAGGAATGATCGAG   2957

Qy   521 AspAsnTyrCysHisProIleAlaLeuProLysHisArgProThrProAspProGluGly   540
            || ||||| || ||||||||||||||||||| |:::|
Db   1878 GACAATTACTGCCACCCGATAGCCCTGCCTAAGCATCGACCCCCGACCCCGGAGGG 1937

Qy   901 AlaPheLysAspGluValLeuSerHisTrpLeuLysSerCysProIleGluGluLys   920
            || |||||||||||| ||||||||| :::|
Db   3018 GCATTTAAAGATGAAGTCCTGAATCACTGGCTCAAAGAAAAATCCCTACTGAAGAAAAG   3077

Qy   541 AspArgValArgAlaGluMetProAsnGlnLeuArgLysLysGlnLeuGluAlaIleIleAla   560
            ||||||||||| |||||||| |||||||||||||||| |||||||||| |||||||
Db   1938 GACCGGGTTCGAGCAGAAATGCCAAACCAGCTTCGCAAGAAGCAATTGGAGGCGATCATAGCC   1997

Qy   921 PheGlnAlaAlaValAlaArgPheValSerCysValAlaGlyTyrCysValAlaThrPhe   940
            ||| ||||| || || ||||| |||| ||| || |||||| ||||||||||||||||
Db   3078 TTTCAGGCAGCAGTGGCAGGATTTGTTATTCCTGCGACTTGTTGGCAACCTTT   3137

Qy   561 ThrAspProLeuAsnProLeuThrArgMetGlnLeuLeuLeuLeuTrpLeuHisPheArgTyr   580
            ||||||||||| ||||| | ||||| |||||||||||||| |||||||||| |||||
Db   1998 ACTGATCCACTTAACCCTCTCACAAGGATGCAGTTGCTCCTGCTTTGGCTCCATTTTAGATAC   2057

Qy   941 ValLeuGlyIleGlyAspArgHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeu   960
            |||||| ||||||||| || ||||| |||||||||||||| |||||||| |||||||
Db   3138 GTTCTTGGAATAGGCGACAGGCACAATGACAATATTATGATCAGCGAGACAGGGAACCTA   3197

Qy   581 GlySerLeuLysAspProLysGlyTyrAlaTyrProLysSerValLysTrpProGlyGln   600
            ||||| |||||||||| ||||||||||||||||||| ||||| || ||||| || |||
Db   2058 GAAAGCCTTAAGGACCCCAAAGGCTATGCCTATCCTAAGTCGGTAAAGTGGGGACAG   2117

Qy   961 PheHisIleAspPheGlyHisPheLeuAspHisLeuAsnTyrLysSerPheGlyLeuGlyIleLeuAsnLys   980
            ||| |||||||||| |||| || || ||||||||| |||||| |||||||| |||||
Db   3198 TTTCATATTGACTTCGGGCACATTCTTGGAATTACAAAAGTTCCTGGGCATTAATAAA   3257

Qy   601 GlnIleLeuValAlaLysThrTyrGlnLeuLeuAlaArgGluValAlaTrpAspGlnSer   620
            |||| ||||||||||||||||| |||| |:::|
Db   2118 CAAGAAATTGTGGCCAAAACATACCAATTGTTGCCCAGAGGAAGTCTGGGATCAAAGT   2177

Qy   981 GluArgValProPheValMetLeuThrProAspPheLeuGlnProThrSerGlyGlyLys   1000
            |||||||| || |||| || ||||| || |||||||||| ||||||| || |||||||
Db   3258 GAGAGAGTGCCATTTGTGATGCTAACCCCCGACTTCCTCCTTTGTGATCCGGATTTCTGGAAAG   3317

Qy   621 AlaLeuAspProLeuAsnProLeuThrArgMetGlyLeuThrMetLeuSerAspGluAsnVal   640
Db   2178 GCTTTGGATCCTTTGAACCCTCTCACACGCATGGGGTTAACAATGCTTTCTGATGAAAATGTA   2237

Qy   1001 LysThrSerLeuHisPheGlnLysLeuGlyLysArgHisAsnAspAspAsnIleLeuAsnLeu   1020
             |||||| |||||||| || |||||||||| ||||||||||| ||||| |||||| ||||
Db   3318 AAGACAAGCCCCACTTCCAGAAATTTCCAGGACATCTGTGTTAAGGCTTATTACCTCGGAAAG   3377

Qy   641 ArgAlaIleAlaValGlnLysLeuGlnSerLeuGluLeuGluAspAspAsnValProValLeuGlnHisTyrLeu   660
             ||||| || ||||| ||||| || || || ||||||||||| |||| |:::|
Db   2238 AGAGCAGTTGCAGTTCAGAAATTGCAGAGCCTGGAGCTGGAGGATGACAATGTGCCTGTGTTCCAGCATTACCTT   2297

Qy   1021 ArgHisHisThrAsnLeuLeuIleLeuLeuPheSerMetLeuMetThrGlyMetPro   1040
Db   3378 CGTCATCACACAAACCTACTGATCATCCTGTTTTCCATGATGCTAATGACAGGAATGCCC   3437

Qy   661 LeuGlnLeuValGlnLysLysLysPheGluTyrHisAspSerAlaLeuAlaArgPhe   680
Db   2298 CTACAAATTGGTCCAGGCTGTGAAATTTGAACATGATAGCGCCCTTGCCAGATTT   2357

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Qy    1041  GlnLeuThrSerLysGluAspIleGluTyrIleArgAspAlaLeuThrValGlyLysSer 1060
            ||||||||||||||||||||||||||||||||||||||||||||||||||||  :::
Db    3438  CAGTTAACAAGCAAAGAAGACATTGAATATATCCGGGATGCCCTCACAGTGGGGAAAAAT 3497

Qy    1061  GluGluAspAlaLysTyrPheLeuAspGlnIleGluValCys-ArgAspLysGlyGlyTr 1080
            |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db    3498  GAGGAGGATGCTAAAAAGTATTTTCTTGATCAGATCGAAGTTTGGCAGAGACAAAGGATG 3557

Qy    1080  pThrValGlnPheAsnTrpPheLeuHisLeuValLeuGlyTyrIleLysGlnGlyGluLysHi 1100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3558  GACTGTGCAGTTTAATTGGTTTCTACATCTTGTTCTTGGCATCAAACAAGGAGAGAAACA 3617

Qy    1100  sSerAla 1102
            |||||||
Db    3618  TTCAGCC 3624
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Search completed: February 15, 2004, 05:14:43
Job time : 9973 secs

OM protein - nucleic search, using frame_plus_p2n model

Copyright   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

Run on: February 15, 2004, 02:08:02 ; Search time 663 Seconds
                                         (without alignments)
                                         4486.849 Million cell updates/sec

Title: US-09-974-573-1
Perfect score: 5790
Sequence: 1 MELENYEQPVVLREDNRRRR.........QFNWFLHLVLGIKQGEKHSA 1102

Scoring table: BLOSUM62
     Xgapop 10.0 , Xgapext 0.5
     Ygapop 10.0 , Ygapext 0.5
     Fgapop   6.0 , Fgapext 7.0
     Delop   6.0 , Delext   7.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
  -MODEL=frame+_p2n.model -DEV=xlh
  -Q=/cgn2_1/USPTO_spool/US09974573/runat_11022004_180012_18083/app_query.fasta_1.1287
  -DB=N_Geneseq_19Jun03 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
  -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
  -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
  -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
  -USER=US09974573 @CGN_1_1.434 @runat_11022004_180012_18083 -NCPU=6 -ICPU=3
  -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
  -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
  -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   N_Geneseq_19Jun03:*
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  24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
  25: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Query Length	DB	ID	Description
1	5726	98.9	3808	19	AAV04634	Porcine phosphoino
2	5726	98.9	3808	20	AAV74100	Porcine G-protein
3	5726	98.9	3808	21	AAZ86813	Pig p120 regulator
4	5534	95.6	5162	20	AAV74104	Human G-protein re
5	5534	95.6	5162	21	AAZ86814	Human p120 regulat
6	5523.5	95.4	5397	24	ABL59522	Human phosphatidyl
7	5523.5	95.4	5397	24	AAS14367	cDNA encoding huma
8	5499.5	95.0	4137	17	AAT58546	Human phosphatidyl
9	5440	94.0	4134	17	AAT58545	Human phosphatidyl
10	1467.5	25.3	3498	15	AAQ57012	Ptdins 3-kinase 11
11	1466.5	25.3	3424	24	ABL59523	Human phosphatidyl
12	1466.5	25.3	3424	24	AAS14365	cDNA encoding huma
13	1465.5	25.3	3207	14	AAQ51155	p110 cDNA. Homo s
14	1460.5	25.2	3412	21	AAQ51156	Human p110 cDNA.
15	1354.5	23.4	3213	21	AAC65600	Human PI3 kinase p
16	1354.5	23.4	3213	24	ABV78026	Hypoxia-regulated
17	1354.5	23.4	3213	24	AAS14366	cDNA encoding huma
18	1352.5	23.4	5220	19	AAV31330	Human phosphatidyl
19	1352.5	23.4	5220	20	AAX15932	cDNA sequence enco
20	1352.5	23.4	5220	21	AAZ32882	Human PI 3-kinase-
21	1350.5	23.3	3868	21	AAA13154	Human phosphatidyl
22	1350.5	23.3	3868	24	ABK84750	Human cDNA differe
23	1350.5	23.3	3868	24	AAS14363	cDNA encoding huma
24	1349.5	23.3	3387	19	AAV16533	cDNA encoding mamm
25	1290	22.3	3525	24	ABK84381	Human cDNA differe
26	1283	22.2	3773	23	ABL07215	Drosophila melanog
27	1076.5	18.6	5285	18	AAT80199	Phosphatidyl inosi
28	1074	18.5	5061	19	AAV42920	cDNA encoding a hu
29	1074	18.5	5061	25	ABT17093	Androgen-independe
30	1073.5	18.5	7114	23	ABL07214	Drosophila melanog
31	1034	17.9	3504	19	AAV18654	Caenorhabditis ele
32	1034	17.9	3504	24	AAA62300	Caenorhabditis ele
33	922	15.9	5990	24	ABK62570	Rat sequence diffe
34	873.5	15.1	6871	23	ABL10307	Drosophila melanog
35	873.5	15.1	7191	23	ABL20119	Drosophila melanog
36	866.5	15.0	6831	18	AAT80200	Phosphatidyl inosi
37	856.5	14.8	4491	23	AAS71517	DNA encoding novel
38	856.5	14.8	4878	23	ABN59725	Novel human coding
39	785	13.6	4498	23	AAS68360	DNA encoding novel
40	784	13.5	4747	22	ABA08693	Human PI3-kinase h
41	784	13.5	4747	22	AAH99523	Human protein enco
42	773.5	13.4	17344	23	ABL20118	Drosophila melanog
43	773.5	13.4	17358	23	ABL10306	Drosophila melanog
44	767.5	13.3	1074	23	AAS73988	DNA encoding novel
45	709.5	12.3	3063	22	AAI58587	Human polynucleoti

ALIGNMENTS

RESULT 1
AAV04634
ID   AAV04634 standard; cDNA; 3808 BP.
XX
AC   AAV04634;
XX
DT   17-AUG-1998 (first entry)
XX
DE   Porcine phosphoinositide 3OH-kinase p120 subunit cDNA.
XX
KW   G-beta-gamma regulated phosphatidylinositol-3' kinase; pig;
KW   phosphoinositide 3OH-kinase; PI3K; signal transduction;
KW   phosphatidylinositol (3,4,5)-triphosphate; G-protein; receptor;
KW   transgenic animal; knockout animal; inflammation; arthritis;
KW   septic shock; adult respiratory distress syndrome; pneumonia;
KW   asthma; allergy; reperfusion injury; atherosclerosis; cancer;
KW   Alzheimer's disease; cancer; antisense; ribozyme; diagnosis;

```
KW   therapy; drug screening; ss.
XX
OS   Sus scrofa.
XX
FH   Key             Location/Qualifiers
FT   CDS             89..3397
FT                   /*tag= a
XX
PN   WO9749818-A2.
XX
PD   31-DEC-1997.
XX
PF   26-JUN-1997;  97WO-US11219.
XX
PR   27-JUN-1996;  96US-0672211.
XX
PA   (ONYX-) ONYX PHARM.
XX
PI   Braselmann S, Hawkins PT, Stephens L;
XX
DR   WPI; 1998-077181/07.
DR   P-PSDB; AAW23948.
XX
PT   DNA encoding G-beta-gamma regulated phosphatidyl-inositol-3' kinase,
PT   p101 and p120 subunits - useful for diagnosis, drug screening,
PT   clinical trial monitoring and treatment of inflammatory disorders
XX
PS   Claim 54; Fig 3A-C; 151pp; English.
XX
CC   This cDNA sequence codes for the p120 catalytic subunit (see
CC   AAT23948) of pig G-protein regulated phosphatidylinositol-3' kinase,
CC   a heterodimeric enzyme which produces the intracellular messenger
CC   phosphatidylinositol (3,4,5)-triphosphate in response to activation
CC   of trimeric G protein-linked receptors.  This novel protein, which
CC   also contains a regulatory subunit, p101 (see AAV04633), is found in
CC   cells of haematopoietic origin and is involved in immune system
CC   responses which cause inflammation.  p120 cDNA was obtained from a
CC   pig neutrophil cDNA library using a degenerate oligonucleotide
CC   probe (see AAT99713) based on an isolated p120 tryptic peptide.  The
CC   p120 cDNA clone in pCMV3mycp120 is deposited as ATCC 97637.  The
CC   invention encompasses pig and human p101 and p120 proteins (see
CC   host cell expression systems, p101 and p120 proteins (see
CC   AAW23946-49), fusion proteins, polypeptides and peptides, antibodies
CC   to these proteins, and transgenic animals and knockout animals.
CC   Compounds which are useful for treating inflammatory response
CC   disorders can be identified by screening assays using a G protein
CC   activated PI3K, or a cultured host cell that expresses the p101
CC   gene.  Antagonists of G protein stimulated PI3K (acting through the
CC   p101 subunit, especially by disrupting the interaction between the
CC   p101 and p120 subunits) can be used to treat arthritis, septic
CC   shock, adult respiratory distress syndrome (ARDS), pneumonia,
CC   asthma, allergies, reperfusion injury, atherosclerosis, cancer and
CC   Alzheimer's disease.  The nucleic acids and their products can also
CC   be used for diagnosis, drug screening and clinical trial monitoring
CC   of inflammatory diseases.
XX
SQ   Sequence 3808 BP; 1010 A; 965 C; 953 G; 880 T; 0 other;
```

Alignment Scores:
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Pred. No.:              0                Length:         3808
Score:                  5726.00          Matches:        1090
Percent Similarity:     99.46%           Conservative:   6
Best Local Similarity:  98.91%           Mismatches:     6
Query Match:            98.89%           Indels:         0
DB:                     19               Gaps:           0
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US-09-974-573-1 (1-1102) x AAV04634 (1-3808)

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Db   149 ...CGGAGGATGAGAAGCCGGCACGGCACGGCAGCCAGCCTGCCTCCATGGAGCTCATCCCCATC 208

Qy    41 GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeuLeuHis 60
Db   209 GAGTTTGTTTTGGCCACCAGCCAACACCAAGACCCCGAAACGGCACTGCTGCAC 268

Qy    61 ValAlaGlyHisGlyAsnValGluMetLysAlaGlnLeuMetLysAlaLeuArgAlaLeuGlu 80
Db   269 GTGGCCGGCCACGGCAATGTGGAGAAGATGAAGGCCCAGTTGTGTTGCGCGGCCGCTGGAG 328

Qy    81 ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTyr 100
Db   329 ACGAGCGTTTCTTGGGACTTCTACCACCGGTTCGGCCCCGACCACTTCCTCCTGCTGTCTTC 388

Qy   101 GlnLysLysGlyGlnTrpTyrGluIleTyrAspLysTyrValGlnIleThrLeuAsp 120
Db   389 CAGAAGAAGGGGAGTGGTTACGAGATCTATGACAAGTACGTGCAGATCACCCTGGAC 448

Qy   121 CysLeuArgTyrTrpLysValLeuHisArgSerProGlyIleIleHisValValGlnArg 140
Db   449 TGCCTGCGCTACTGGAAGGTGTTGCACCGGAGCCCCGGCAGATCCACGTGGTCCAGCCG 508

Qy   141 HisAlaProSerGluGluThrLeuAlaPheGlnArgGlnLeuAsnAlaLeuIleGlyTyr 160
Db   509 CACGCGCCCTCGGAGGAGACATTGGCCTTCCAGCGCCAGCTTCAACGCCCTCATCGGCTAC 568

Qy   161 AspValThrAspValSerAsnValHisAspGluGluThrProThrArgArgLeu 180
Db   569 GACGTCACCGACGTCAGCAACGTGCATGACGATGAGCTCACGCGGCGGCCCTG 628

Qy   181 ValThrProArgMetAlaGluValAlaGlyArgAspProLysLeuTyrAlaMetHisPro 200
Db   629 GTCACCCCGCGCATGGCCGAGGTGGCCGGGCGCGACCCCAAGCTTACGGCCATGCACCCC 688

Qy   201 TrpValThrSerLysProLeuProGluTyrLeuLeuLysLysIleThrAsnAsnCysVal 220
Db   689 TGGGTGACATCCAAGCCCCTCCCTGAGTACCTTCTGAAGAAGATCACTAACAACTGCGTC 748

Qy   221 PheValIleHisArgSerThrArgSerGlnThrIleLysValSerAlaAlaAspThr 240
Db   749 TTCATCGTCATTCACCGCAGCACCAGGAGCCAGACCATCAAGGTTCGGCCGATGACACC 808

Qy   241 ProGlyThrIleLeuGlnSerPhePheThrLysMetAlaLeuLysLysSerLeuMetAsp 260
Db   809 CCAGGCACCATCTCCAGAGCTTCTTTACCAAGATGGCCAAGAAGAAATCTCTGATGGAT 868

Qy   261 IleProGluSerGlnAsnGluAspPheValCysGlyArgAspGluTyr 280
Db   869 ATCCCTGAAAGCCAGAACGAGGACTTTGTGTGCGGTCGCGGGGATGAGTAC 928

Qy   281 LeuValGlyGluThrProIleLysAsnPheGlnTrpValArgGlnCysLeuAsnGly 300
Db   929 CTGGTGGGTGAGACGCCCATCAAAAATTTCCAGTGGGTGAGGCAGTGCCTCAAGAATGGG 988

Qy   301 GluGluIleHisLeuValLeuAspThrProProAspProAlaLeuAspLeuValArgLys 320
Db   989 GAGGAGATTCACCTTGTGCTGGACACTCCTCCAGACCCTGCCCTGGACGAGGTGAGGAAG 1048

Qy   321 GluGluTrpProLeuValAspAspCysThrGlyValThrGlyTyrHisGlyGlnLeuThr 340
Db  1049 GAAGAGTGGCCGCTGGTGGATGACTGCACGGGAGTCACTGGCTACCACGGCCAGCTGACC 1108

Qy   341 IleHisGlyLysAspHisGluSerLeuPheThrValSerLeuTrpAspCysAspArgLys 360
Db  1109 ATCCACGGCAAGGACCATGAAAGTGTGTTCACCGTGTCCCTGTGGGACTGTGACCGCAAG 1168

Qy   361 PheArgValIleArgIleAspIleProArgValLeuProArgThrAlaAspLeuThr 380
Db  1169 TTCAGGGTCAAAATCAGAGGCATTGATATCCCTCGTGTCCTGCCCCGGACCGCTGACCTACG 1228

Qy   381 ValPheValGluAlaAsnIleGlnTyrGlyGlnValLeuCysGlnValArgArgThrSer 400
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US-09-974-573-1 (1-1102) x AAV04634 (1-3808)

Qy     1 MetGluLeuGluAsnTyrGluGlnProValValLeuArgGluAspAsnArgArgArgArg 20
Db    89 ATGGAGCTGGAGAACTATGAACAGCCCGTGGTGCTGAGAGAGGACAACCGCCGCAGGCGT 148
Qy    21 ArgArgMetLysProArgSerThrAlaAlaSerLeuSerMetGluLeuLeuProIle 40
```

Qy 761 SerGlnValIleSerGlnLysLeuGlnLysLeuGluAsnLeuGlnAsnLeuPro 780
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2369 TCCCAAGTTATTTCCCAACTTAAGCAAAGGTTGAAAAACTACAGAATTTGAATCTCCCC 2428

Qy 781 GlnSerPheArgValProTyrAspProTyrLeuLysAlaGlyAlaLeuValIleGluLys 800
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2429 CAAAGCTTTAGAGTTCCCATGATCCTGGACTGGAAAGCCCGGGCACTGGTCGATCGAAAAA 2488

Qy 801 CysLysValMetAlaSerLysLysProLeuTrpLeuGluPheLysLysCysAlaAspPro 820
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2489 TGTAAGGTGATGGCCTCCAAGAAGAGCCCCGTGGCTGAGTTTAAATGTGCCGATCCT 2548

Qy 821 ThrAlaLeuSerArgAsnGluThrIleGlyIleIleAlaLysHisGlyAspAspLeuArgGln 840
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2549 ACGGCTCTATCAAATGAAACAATTGGAATTATCTTTAAACACGGTGACGATCTGCGCCAA 2608

Qy 841 AspMetLeuIleLeuGlnIleLeuArgIleMetGluSerIleTrpGluThrGluSerLeu 860
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2609 GACATGCTTATTTTACAGATTCTACGAATCATGGAGTCCATTTGGGAGACCGAATCTTTG 2668

Qy 861 AspLeuCysLeuLeuProTyrGlyCysIleSerThrGlyAspLysIleGlyMetIleGlu 880
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2669 GATCTGTGCCTCCTGCCCATATGGCTGCATTCAACTGGTGACAAAATAGGAATGATCGAG 2728

Qy 881 IleValLysAspAlaThrThrIleAlaLysIleGlnSerThrValGlnSerThrGly 900
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2729 ATCGTGAAGGACGCCACGACAATTGCCAAAATTCAGAGCACAGTGGGCAACACGGGT 2788

Qy 901 AlaPheLysAspGluValValLeuSerHisTrpLeuLysGluLysCysProIleLeuGluGluLys 920
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2789 GCCTTTAAAGATGAAGTCGTGCTGAGTCACTGGCTCAAAGAAAAATGCCCTATTGAAGAAAAG 2848

Qy 921 PheGlnAlaAlaValGluArgPheValTyrSerCysAlaGlyTyrCysValAlaThrPhe 940
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2849 TTTCAGGCAGCTGTGGAGAGATTTGTTTATTCCTGTGCCGGCTACGTGTGCCAACCTTT 2908

Qy 941 ValLeuGlyTyrIleGlyValAspArgHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeu 960
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2909 GTTCTCGGAATAGGCGACAGACACAATGACAATATTATGATCTCAGAAACAGGAAATCTA 2968

Qy 961 PheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLys 980
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2969 TTTCATATTGATTTCGGACACATTCTTGGGAATTACAAAAGTTTCCTGGGCATTAATAAA 3028

Qy 981 GluArgValProPheValLeuThrProAspPheLeuPheValMetGlyThrSerGlyLys 1000
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3029 GAGAGGGTGCCATTTGTGCTAACCCCAGACTTCCTGTTTGTGATGGGGACTTCTGGAAAG 3088

Qy 1001 LysThrSerLeuHisPheGlnLysPheGlnAspValCysAsnAsnValHisTyrLeu 1020
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3089 AAGACAAGTCTACACTTCCAGAAATTTCAGGATGTCTGCGTCAAGGCTTACCTAGCCCTT 3148

Qy 1021 ArgHisThrAsnLeuLeuIleLeuLeuPheSerMetMetLeuMetThrGlyMetPro 1040
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3149 CGTCATCACACCAACCTACTGATCATCCTCTTCTCCATGATGCTGATGACAGGAATGCCC 3208

Qy 1041 GlnLeuThrSerLysGluAspIleLeuTyrIleLysGluThrValGlyLysSer 1060
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3209 CAGTTAACCAGCAAAGAAGAGACATTGTATATCAAAGAGACAGTGGGCAAAAGT 3268

Qy 1061 GluGluAspAlaLysLysTyrPheLeuAspCysGlnAspLysTrp 1080
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3269 GAGGAGGACGCTAAAAAGTATTTTCTGGATTGCCAAGACAAAGGATGG 3328

Qy 1081 ThrValGlnPheAsnTrpPheLeuHisLeuValLeuGlyIleLysGlyGluLysHis 1100
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3329 ACCGTGCAGTTTAACTGGTTCCTTACATCTTGTTCTTGGCATCAAACAGGGGAGAAGCAT 3388

Qy 1101 SerAla 1102
        |||
Db 3389 CCCGCA 3394

RESULT 2
AAV74100
ID   AAV74100 standard; DNA; 3808 BP.
XX
AC   AAV74100;
XX
DT   09-MAR-1999 (first entry)
XX
DE   Porcine G-protein regulated PI3K p120 adapter subunit DNA.
XX
KW   Phosphoinositide 3-hydroxykinase; PI3K; trimeric G protein; porcine;
KW   adapter subunit; regulatory subunit; p101; p120; catalytic subunit;
KW   detection; diagnosis; activation disorder; haematopoietic system;
KW   treatment; immune disorder; inflammation; arthritis; septic shock;
KW   adult respiratory distress syndrome; pneumonia; asthma; allergy;
KW   reperfusion injury; atherosclerosis; Alzheimer's disease; cancer; ss.
XX
OS   Sus scrofa.
XX
PN   US5856132-A.
XX
PD   05-JAN-1999.
XX
PF   15-AUG-1997;   97US-0916917.
XX
PR   15-AUG-1997;   97US-0916917.
PR   27-JUN-1996;   96US-0672211.
XX
PA   (ONYX-) ONYX PHARM.
XX
PI   Braselmann S, Hawkins PT, Stephens L;
XX
DR   WPI; 1999-105107/09.
DR   P-PSDB; AAW90083.
XX
PT   Nucleic acid encoding regulatory (p101) and catalytic (p120)
PT   subunits of a heterodimeric phosphatidylinositol-3' kinase - useful
PT   in treatment and diagnosis of immune system disorders, e.g.
PT   arthritis, cancer and Alzheimer's disease
XX
PS   Example IX; Fig 3A-C; 75pp; English.
XX
CC   This sequence encodes a novel catalytic subunit, p120, from porcine
CC   phosphoinositide 3-hydroxykinase (PI3K) which is regulated by beta-gamma
CC   subunits of trimeric G-protein. Nucleic acid coding for p101 or p120, or
CC   their fragments, are used as probes and primers for identifying p101 or
CC   p120 gene mutations, allelic variations or regulatory defects,
CC   particularly for the diagnosis of activation disorders (or
CC   susceptibility) in cells of the haematopoietic system. The related
CC   proteins, antibodies, agonists and antagonists can be used similarly. The
CC   p101 and p120 proteins, peptides or fusion proteins are used to treat or
CC   screen for potential agents for treating immune disorders, particularly
CC   inflammation, e.g. arthritis, septic shock, adult respiratory distress
CC   syndrome, pneumonia, asthma, allergies, reperfusion injury,
CC   atherosclerosis, Alzheimer's disease and cancer.
XX
SQ   Sequence 3808 BP; 1010 A; 965 C; 953 G; 880 T; 0 other;

Alignment Scores:
Pred. No.:   0   Length: 3808
Score: 5726.00   Matches: 1090
Percent Similarity: 99.46%   Conservative: 6
Best Local Similarity: 98.91%   Mismatches: 6
Query Match: 98.89%   Indels: 0
DB: 20   Gaps: 0

US-09-974-573-1 (1-1102) x AAV74100 (1-3808)

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Db   149 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         CGGAGGATGAAGCGGCCGGCAGCAGCGGCAGCCAGCCTGTCCTCCATGGAGCTCATCCCCATC  208

Qy    41 GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeuLeuHis   60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   209 GAGTTTGTTTTGGCCACCAGCCAACACCAGGACCCCGAAACCGGACTGCTGCAC   268

Qy    61 ValAlaLeuGlyHisGlyAsnValGluGlnMetLysAlaGlnValTrpLeuArgAlaLeuGlu   80
         |||||||||||||||||||||||||||||||||:|::|||||||||||||||||||||
Db   269 GTGGCCCGGCCGCCAATGTGGAGAAGATGAAGGCCCAGGTGTGGTTGCGGCGCTGGAG   328

Qy    81 ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuTyr   100
         |||||||||||||||||||||||||||||||::::::::||||||||||||||||||||
Db   329 ACGAGCGTTTCTTGGACTTCTACCACCGGTTCGGCCCGGACCACTTCCTCCTGGTCTTC   388

Qy   101 GlnLysLysGlyGlnTrpTyrGluIleTyrGluLeuTyrArgGlnValValGlnThrLeuAsp   120
         |||||||||||||||||||||||||||||||:|||:||||||||||||||||||||||||||
Db   389 CAGAAGAAGGGGGAGTGGTACGAGATCTATGACGAGCTGTGTCGACAAGTACCAGGTGGTCGACACCCTGGAC   448

Qy   121 CysLeuArgTyrTrpLysValLeuHisArgSerProGlyGlnIleHisValGlnIleArg   140
         |||||||||||||||||||||||:|||:|||||||||||||||||||||||||||||||||
Db   449 TGCCTGCGCTACTGGAAGGTGTTGCACCGCAGCCCGGGCAGATCCACGTGGTCCAGCGG   508

Qy   141 HisAlaProSerGluGluThrLeuAlaPheGlnArgGlnLeuAsnAlaAlaLeuIleGlyTyr   160
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   509 CACGGCCCCTCGGAGGAGACATTGGCCTTCCAGCGCCAGCTGAACGCCCTCATCGGCTAC   568

Qy   161 AspValThrAspValSerAsnValHisAspGluGluMetAspSerAlaAspAspThr   180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   569 GACGTCACCGACGTCAGCAACGTGCATGACGAGGAGATGGACAGCGCCGGCGCCGCCTG   628

Qy   181 ValThrProArgMetAlaGluGlyValAlaGlyTyrArgAspProLysLeuTyrArgAlaMetHisPro   200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   629 GTCACCCCGCGCATGGCCGAGGGCGTGGCCGGCTACCGCGACCCCAAGCTTTACGCCATGCACCCC   688

Qy   201 TrpThrThrSerLysProLeuProTyrLeuLeuLysIleThrAsnCysVal   220
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   689 TGGGTGACATCCAAGCCCCTCCCTGAGTACCTTCTGAAGAGATCACTAACAACTGCGTC   748

Qy   221 PheIleValIleHisArgSerThrThrSerGlnThrIleLeuValSerAlaAsAspThr   240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   749 TTCATCGTCATTCACCGCAGCACCACCAGCCAGACCATCAAGGTCTCGGCCGATGACACC   808

Qy   241 ProGlyThrIleLeuIleSerPhePheThrLysMetAlaLysLysLysSerLeuMetAsp   260
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   809 CCAGGGACCACCATCCTCCAGAGTTCTTACCAAGATGGCCAAGAAGAAATCTCTGATGGAT   868

Qy   261 IleProGluSerGlnAsnGluArgAspPheValLeuArgValCysGlyValArgAspGluTyr   280
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   869 ATCCCTGAAAGCCAGAACGAACGGGACTTTGTGCTGCGCGTGTGCGGCGTCCGGGATGAGTAC   928

Qy   281 LeuValGlyGluThrProIleLysPheAsnPheGlnTrpValArgGlnCysLeuLysAsnGly   300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   929 CTGGTGGGTGAGACGCCCATCAAAATTTCCAGTGGGTGAGGCAGTGCCTCAAGAATGGG   988

Qy   301 GluGluIleHisLeuValLeuAspThrProProAspProAlaLeuArgGluValValArgLys   320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   989 GAGGAGATTCACCTTGTCCTGGACACTCCTCCAGACCCTGACGGAGGTGAGGAGAAG   1048

Qy   321 GluGluTrpProLeuValAspAspCysThrGlyValThrHisGlyLeuGluGlnLeuThr   340
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1049 GAAGAGTGGCCCCTGGTGGATGACTGCACGGGGAGTCACTGGCTACCACGAGCAGCTGACC   1108

Qy   341 IleHisGlyLysAspHisGluSerValPheThrValSerLeuTrpAspCysAspAspArgLys   360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1109 ATCCACGGCAAGGACCATGAAAGTGTGTTCACCGTGTCCCTGTGGGACTGTGACCGCAAG   1168

Qy   361 PheArgValLysIleArgGlyTyrIleAspIleProValLeuProArgThrAlaAspLeuThr   380
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1169 TTCAGGGTCAAAATCAGAGGCTATATCGACATTCCTGTCCTGCCCCGAACCGCTGACTTCACG   1228

Qy   381 ValPheValGluAlaAsnIleGlnTyrGlyGlnHisValLeuCysGlnArgThrSer   400
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     1 MetGluLeuGluAsnTyrGluGlnProValLeuArgGluAspAsnArgArgArgArg   20
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db    89 ATGGAGCTGGAGAACTATGAACAGCCCGTGCTGTCGTGCTGAGAGGAGACAACCGCCGCCAGGCGT   148

Qy    21 ArgArgMetLysProArgSerThrAlaAlaSerLeuSerSerMetGluLeuIleProIle   40
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db 1229 GTGTTGTGGAGGCAAACATCCAGTATGGGCAGCAAGTCCTTTGCCAAAGGAGAACCAGC 1288

Qy   761 SerGlnValIleSerGlnLeuLysGlnLysGluAsnLeuGlnAsnLeuAsnLeuPro 780
Db 2369 TCCCAAGTTATTTCCCAACTTAAGCAAAAGCTTGAAAACTTCAGAGATTTGAATCTCCCC 2428

Qy   401 ProLysProPheThrGluLeuTrpAsnValPheLeuGluPheSerIleLysIle 420
Db 1289 CCCAAACCCTTCACGGAGGAGGTGCTCTGGAACGTGTGGCTTGAGTTCAGTATTAAAATC 1348

Qy   781 GlnSerPheArgValProTyrAspTyrLeuLysAlaGlyAlaLeuValIleGluLys 800
Db 2429 CAAAGCTTTAGAGTTCCCATGACTACCTGAAAGCCGGGGCACTCGTGATCGAAAAA 2488

Qy   421 LysAspLeuProLysGlyAlaLeuLeuLeuAsnLeuGlnIleLeuTyrCysGlyLysAlaProAla 440
Db 1349 AAAGACTTACCCAAAGGGGCTCTGCTGAACCTCCAGATTCTACTGCGCAAAGTCCAGCA 1408

Qy   441 LeuSerGlyLysThrSerAlaGluMetProSerProGluSerLysGlyLysAlaGlnLeu 460
Db 1409 CTGTCTGGCAAGACCTCTGCAGAGATGCCCAGTCCCAGTGCCAAAGGCAAAGCTCAGCTT 1468

Qy   461 LeuTyrTyrValAsnLeuLeuLeuLeuIleAspHisArgPheLeuLeuArgHisGlyLeuTyr 480
Db 1469 CTGTACTATGTCAACCTATTGCTGATAGACCACCGCTTCCTCCTGCGCCATGGCAGTAT 1528

Qy   481 ValLeuHisMetTrpGlnLeuSerGlyLysGlyGluAspGlnGlySerPheAsnAlaAsp 500
Db 1529 GTGCCCCACATGTGGCAGTTATCCGGGAAGGGGGAAGACCAAGGGAGCTTCAATGCCGAC 1588

Qy   501 LysLeuThrSerAlaThrAsnProAspLysProLysHisArgProThrProProGluGly 520
Db 1589 AAGCTCACGTCGGCAACCAACCCGGACAAGCCGAAGCACTCAATGTCCATCTCCATTCTG 1648

Qy   521 AspAsnTyrCysHisProIleAlaLeuProLysHisArgProThrProProGluGly 540
Db 1649 GACAATTACTGCCACCCCATAGCCTTGCCTAAGCATCGGCCTACCCCTGACCCCAGAAGG 1708

Qy   541 AspArgValArgAlaGluMetProAsnGlnLeuArgGlyGlnLeuLeuGluAlaIleIleAla 560
Db 1709 GACCCGGTTCGGGCAGAAATGCCCAATCAGCTTCGGAAGCAACTGGAGGCAATCATAGCC 1768

Qy   561 ThrAspProLeuAsnProLeuThrAlaGluThrLeuLysLysGluLeuTrpHisPheArgTyr 580
Db 1769 ACGGATCCGCTTAACCCACTCACAGCTGAAGACAAGAAACTGCTCTGGCATTTCAGATAT 1828

Qy   581 GluSerLeuLysAspProLysAlaTyrProLysLeuPheSerSerValLysTrpGlyGln 600
Db 1829 GAAAGCCTGAAGGATCCCAAAGGCTATCCCAAGCTCTTTAGCTCGGTGAAATGGGGACAG 1888

Qy   601 GlnIleLeuValAlaLysGlyValThrLeuThrMetGlnLeuTyrArgGluValTrpAspGlnSer 620
Db 1889 CAAGAAATTGTGGGCCAAAACATACCAATTATTAGCCAAAAGGGAGGTCTGGAATCAGAGT 1948

Qy   621 AlaLeuAspAspValGlyValThrMetGlnLeuAspCysAsnPheSerArgGluAsnVal 640
Db 1949 GCTTTAGATGGTGGGGTTAACCATGCAGTCCTGGACTGCAACTTCTCGGATGAAAACGTG 2008

Qy   641 ArgAlaIleAlaValGlnLysArgHisTyrGlnArgPheLeuAlaValIleLeuGluHisTyr 660
Db 2009 AGAGCCATTGCAGTCCAGTCTGAGAACTGGAGAGCTTGAGGATGATGAAGTTTGCAGAAGCCTAC 2068

Qy   661 LeuGlnLeuValGlnAlaValLysPheGluProTyrHisAspSerAlaLeuAlaArgPhe 680
Db 2069 CTCCAGCTGGTCCAGGCTGTGAAATTTGAACCATACACATGACGACATTT 2128

Qy   681 LeuLeuLysArgGlyLeuArgAsnLysArgIleGlyHisPheLeuPheLeuArg 700
Db 2129 CTGCTGAAGCCTGGTTGGTTTAAGAAACAAGAGAATTGCTCACTTCTGTTTCTGTTCTGAGA 2188

Qy   701 SerGluIleAlaGlnSerArgHisTyrArgGlnArgPheLeuAlaValIleLeuGluHisAlaTyr 720
Db 2189 AGTGAGAATTGCCCAGTCTAGGCACTATCAGCAGAGGTTTGCAGTGATCCTGGAAGCCTAC 2248

Qy   721 LeuArgGlyCysGlyThrAlaMetLeuHisAspPheThrGlnAsnValGlnValIleAsp 740
Db 2249 CTGAGGGGCTGTGGCACAGCCATGCTGCACGACTTCACCCAGAATGTCCAAGTAATTGAC 2308

Qy   741 MetLeuGlnLysValThrIleLysAspIleLeuLysSerLeuSerAlaGluLysTyrAspValSer 760
Db 2309 ATGTTACAAAAAGTCACCATTAAATCGGTCTTCTGCCATCAAATGACGTCAGT 2368

Qy   761 SerGlnValIleSerGlnLeuLysGlnLysGluAsnLeuGlnAsnLeuAsnLeuPro 780
Db 2369 TCCCAAGTTATTTCCCAACTTAAGCAAAAGCTTGAAAACTTCAGAGATTTGAATCTCCCC 2428

Qy   781 GlnSerPheArgValProTyrAspTyrLeuLysAlaGlyAlaLeuValIleGluLys 800
Db 2429 CAAAGCTTTAGAGTTCCCATGACTACCTGAAAGCCGGGGCACTCGTGATCGAAAAA 2488

Qy   801 CysLysLysValMetAlaSerLysLysLysProGluPheLysCysAspAlaAspPro 820
Db 2489 TGTAAAGTGATGGCCTCAAGAAGAAGCCCCTGTGGCTTGAGTTTAAATGTCCGGATCCT 2548

Qy   821 ThrAlaLeuSerArgAsnGluThrLeuGlyTyrIleLeuGlyHisGlyAspTyrLeuArgGln 840
Db 2549 ACGGCTCTATCAAATGAAACAAATTGGATTATCTTTAAACACGGTGACGATCTGGCGCCAA 2608

Qy   841 AspMetLeuIleLeuGlnIleLeuGluArgIleMetGluSerIleTrpProThrGluSerIleLeu 860
Db 2609 GACATGCTTATTTTACAGATTCTACGAATCATGGAGTCCATTTGGGACCGAACCGAATCTTTG 2668

Qy   861 AspLeuCysLeuLeuProTyrGlyLyCysIleSerSerThrGlyLysIleGlyMetIleGlu 880
Db 2669 GATCTGTGCCTCCTGCCATATGGCTGCATTTCAACTGTGACAAAATAGGAATGATCGAG 2728

Qy   881 IleValLysAspAlaThrThrIleAlaLysIleGlnInSerThrGlyLyAsnThrGly 900
Db 2729 ATCGTGAAGGACGCCACACACAATCGCCAAAATTCAGCAAGCACAGTGGGCAACACGGGT 2788

Qy   901 AlaPheLysAspGluValLeuSerHisTrpLeuLysCysProIleGluGluLys 920
Db 2789 GCCTTTAAAGATGAAGTCCTGAGTCACTGGCTCAAAGAAAAATGCCCTATTGAAGAAAAG 2848

Qy   921 PheGlnAlaAlaValGluArgPheValTyrSerCysAlaGlyTyrCysValAlaAlaThrPhe 940
Db 2849 TTTCAGGCAGCTGTGGAGAGATTTGTTTATTCCTGTGCCGGCTACTGTGTGGCAACCTTT 2908

Qy   941 ValLeuGlyIleIleGlyAspArgHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeu 960
Db 2909 GTTCTCGGAATAGGCGACAGACCACAATGACAATTATGATCTCAGAAACAGGAAATCTA 2968

Qy   961 PheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLys 980
Db 2969 TTTCATATTGATTTCGGACACATTCTGGGAAATTACAAAAGTTTCCTGGGCATTAATAAA 3028

Qy   981 GluArgValProPheValLeuThrProAspPheLeuPheValMetGlyThrSerGlyLys 1000
Db 3029 GAGAGGGTGCCATTTGTGCTAACCCCAGACTTCCTGTTTGTGATGGGGACTTCTGGAAAG 3088

Qy 1001 LysThrSerLeuHisPheGlnLysPheGlnAspValCysValLysAlaTyrLeuAlaLeu 1020
Db 3089 AAGACAAGTCTACACTTCCAGAAATTTCAGGATGTCTGCGTCAAGGCTTACCTAGCCCTT 3148

Qy 1021 ArgHisHisThrAsnLeuLeuIleIleLeuPheSerMetMetLeuMetThrGlyMetPro 1040
Db 3149 CGTCATCACACACAAACCTACTACTGATCATCCTCTTCTCCATGATGCTGATGACAGGAATGCCC 3208

Qy 1041 GlnLeuThrSerLysGluAspProIleGluArgIleLeuAspAlaLeuThrLeuGlyLysSer 1060
Db 3209 CAGTTAACCAGCAAGGAAGACATTGAATACATTCGGGATGCCCTCACAGTGGGCAAAAGT 3268

Qy 1061 GluGluIleAlaGlnSerAlaLysLysPheLeuLeuValCysArgAspLysGlyTrp 1080
Db 3269 GAGGAGAGGATGCTAAAAGTAGTATTTCTGGATCAGATTGAAGTTTGCAGAGACAAAGAATGG 3328

Qy 1081 ThrValGlnPheAsnTrpPheLeuHisLeuValLeuGlyIleLysLysGlyGluLysHis 1100
Db 3329 ACCGTGCAGTTTAACTGGTTCTTACATCTTGTCTTGGCATCAAACAGGGGAGAAGCAT 3388

Qy 1101 SerAla 1102
Db 3389 CCCGCA 3394

RESULT 3
AAZ86813
ID   AAZ86813 standard; DNA; 3808 BP.
XX
AC   AAZ86813;
XX
DT   20-APR-2000 (first entry)
XX
DE   Pig p120 regulatory subunit coding sequence.
XX
KW   p101 protein; p120 protein; regulatory subunit; immune system disorder;
KW   trimeric G-protein regulated PI3K; phosphoinositide 3OH-kinase; asthma;
KW   inflammatory response disorder; arthritis; septic shock; allergy;
KW   adult respiratory distress; cancer; reperfusion injury; atherosclerosis;
KW   Alzheimer's disease; haematopoietic lineage cell activation disorder;
KW   therapy; pig; ss.
XX
OS   Sus sp.
XX
PN   US6017763-A.
XX
PD   25-JAN-2000.
XX
PF   04-JAN-1999;   99US-0225170.
XX
PR   15-AUG-1997;   97US-0916917.
PR   27-JUN-1996;   96US-0672211.
XX
PA   (ONYX-) ONYX PHARM INC.
PA   (BABR-) BABRAHAM INST.
XX
PI   Braselmann S, Stephens L, Hawkins PT;
XX
DR   WPI; 2000-136682/12.
DR   P-PSDB; AAY76802.
XX
PT   Isolated p101 regulatory polypeptide, a subunit of the trimeric
PT   G-protein regulated PI3K, is useful for screening compounds which can
PT   be used to treat inflammatory response disorders -
XX
PS   Example; Fig 3; 75pp; English.
XX
CC   This sequence encodes the pig p120 regulatory protein.
CC   The invention relates to the human p101 regulatory protein,
CC   which is a subunit of the trimeric G-protein regulated phosphoinositide
CC   3OH-kinase (PI3K). The p101 regulatory protein can be used in screening
CC   assays to detect compounds which can be used to treat inflammatory
CC   response disorders. The compounds identified may be antagonists or
CC   agonists of G protein-regulated PI3K gene expression and/or p101 or p120
CC   gene product activity. These compounds may then be used to control immune
CC   system disorders, in particular arthritis, septic shock, adult
CC   respiratory distress, asthma, allergies, reperfusion injury,
CC   atherosclerosis, Alzheimer's disease and cancer. p101 proteins and
CC   peptides can be used in the detection of mutant or inappropriately
CC   expressed p101 regulatory subunits for the diagnosis of immune disorders
CC   and haematopoietic lineage cell activation disorders which will also
CC   assist in devising a proper treatment or therapeutic regime. Using
CC   genetically engineered host cells to screen for compounds also allows
CC   compounds which affect the signal transduced by the activated p101
CC   regulatory subunit to be identified.
XX
SQ   Sequence 3808 BP; 1010 A; 965 C; 953 G; 880 T; 0 other;

Alignment Scores:
Pred. No.:   0   Length: 3808
Score: 5726.00   Matches: 1090
Percent Similarity: 99.46%   Conservative: 6
Best Local Similarity: 98.91%   Mismatches: 6
Query Match: 98.89%   Indels: 0
DB: Gaps: 21

US-09-974-573-1 (1-1102) x AAZ86813 (1-3808)

Qy   1 MetGluLeuGluAsnTyrGluGlnProValValLeuArgGluAspAsnArgArgArgArg   20
Db   89 ATGGAGCTGGAGAACTATGACAGCCGTGCTGTGCTGAGAGGAGACAACCGCCGCAGGCGT 148

Qy   21 ArgArgMetLysProArgSerThrAlaAlaSerLeuSerMetGluLeuProIle   40
Db   149 CGGAGGATGAAGCCGCGGCACGGCCAGCCTGTCCTCCATGGAGCTTCATCCCCATC 208

Qy   41 GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeuLeuHis   60
Db   209 GAGTTTGTTTTGCCACACGCCAGCCGCAACACCAAGACCCCGAAACGGCACTGCTGCAC 268

Qy   61 ValAlaAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnValTrpLeuArgLeuGlu   80
Db   269 GTGGCCGCCGGCAATGTGGAGAAGATGAAGGCCCAGGTGTGTTGCGCGCGTGGAG 328

Qy   81 ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTyr 100
Db   329 ACGAGCGTTTCTTGGGACTTCTACCACCGGTTCGGCCCGACCACTTCCTCCTGGTCTTC 388

Qy   101 GlnLysGlyGlyGlnTrpTrpTyrGlnIleTyrAspLysTyrGlnValValGlnThrLeuAsp 120
Db   389 CAGAAGAAGGGGGAGTTGGTACGAGATCTATGACAAGTACCAGGTGGTGCAGACCCTGGAC 448

Qy   121 CysLeuArgTyrTrpLysValLeuHisArgSerProGlyGlnIleHisValValGlnArg 140
Db   449 TGCCTGCGCTACTGGAAGGTGTTGCACCGCAGCCCCGGGCAGATCCACGTGGTCCAGCGG 508

Qy   141 HisAlaProSerGluGluThrLeuAlaPheGlnArgGlnLeuAsnAlaLeuIleGlyTyr 160
Db   509 CACGCGCCCTCCGAGGAGACATTGGCCTTCCAGCGCCAGCTCAACGCCCTCATCGGCTAC 568

Qy   161 AspValThrAspValSerAsnValHisAspAspValLeuGluPheThrArgArgLeu 180
Db   569 GACGTCACCGACGTCAGCAACGTGCATGACGATGAGGTGGAGTTCACGCGGCGCCGCCTG 628

Qy   181 ValThrProArgMetAlaGluValAlaGlyArgAspProLysLeuTyrAlaMetHisPro 200
Db   629 GTCACCCCGCGGATGGCCGAGGTGGCCGGGCGGGACCCCAAGCTTTACGCCATGCACCCC 688

Qy   201 TrpValThrSerLysProGluProLeuLeuTyrLeuLeuLysIleLysThrAsnAsnCysVal 220
Db   689 TGGGTGACATCCAAGCCCCTCCCTGAGTACCTTCTGAAGAAGATCACTAACAACTGCGTC 748

Qy   221 PheIleValIleHisArgSerThrSerGlnThrIleLysValSerAlaAspThr 240
Db   749 TTCATCGTCATTCACCGCAGCACCAGCCAGACCATCAAGGTCTCGGCCGATGACACC 808

Qy   241 ProGlyThrIleLeuGlnSerPhePheThrLysLysLysSerLeuMetAlaAsp 260
Db   809 CCAGGCACCATCCTCCAGGCTCTTTACCAAGATGGCCAAGAAGAAATCTCTGATGGAT 868

Qy   261 IleProGluSerGlnAsnGlnArgAspPheValLeuArgValCysLysGlyArgAspGluTyr 280
Db   869 ATCCCTGAAAGCCAGAACCAGGGACTTTGTGCTGCGGGTCTGCGGCCCGGATGAGTAC 928

Qy   281 LeuValGlyGluThrProIleLeuLysAsnPheGlnTrpValArgGlnCysLeuGlyAsnGly 300
Db   929 CTGGTGGGTGAGACGCCCATCAAAATTTCCAGTGGTGAGGAGGCAGTGCCTCAAGAATGGG 988

Qy   301 GluGlyIleHisLeuValLeuAspThrProProAspProAlaLeuAspAspValAlaArgLys 320
Db   989 GAGGAGATTCACCTTGTGCTGGACACTCCTCCAGACCCTGCACAGGTGAGGAAG 1048

Qy   321 GluGluTrpProLeuValAspAspCysThrGlyValThrGlyTyrHisGluGlnLeuThr 340
Db   1049 GAAGAGTGGCCGCTGGTGGATGACTGCACGGGAGTCACTGGCTACCACGAGCAGTGACC 1108

Qy   341 IleHisGlyLysAspHisGluSerValPheThrValSerLeuValTrpAspCysAspArgLys 360
Db   1109 ATCCACGGCAAGGACCATGAAAGTGTTCACCGTGTCCCTGGGACTGTGACCGCCAAG 1168

Qy   361 PheArgValLysIleArgGlyIleAspIleProValLeuProArgThrAlaAspLeuThr 380

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Db                                                                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2249  CTGAGGGCTGTGCACAGCCATGCTGCGACTCACCCAGCTCCAAGTAATTGAC  2308
Qy    741  MetLeuGlnLysValThrIleAspIleAspIleLysSerLeuSerAlaGluLysTyrAspValSer  760
Db    2309  ATGTTACAAAAAGTCACCATTGACATTAAATCGCTTCTCTGCTGAAAAGTATGACGTCAGT  2368

Qy    761  SerGlnValIleSerGlnLeuLysGlnLysLeuLeuGlnAsnLeuGlnAsnLeuAsnLeuPro  780
Db    2369  TCCCAAGTTATTTCCCAACTTAAGCAAAAGTTGAAAACCTACAGAATTTGAATCTCCCC  2428

Qy    781  GlnSerPheArgValProTyrAspProGlyLeuLysAlaGlyAlaLeuValIleGluLys  800
Db    2429  CAAAGCTTTAGAGTTCCTTATGATCCTGGACTTAAAGCCGGGGCACTCGGTGATCGAAAAA  2488

Qy    801  CysLysValMetAlaSerLysLysLysProLeuTrpLeuGlnPheLysCysAlaAspPro  820
Db    2489  TGTAAAGTGATGGCCTCCAAGAAGAAGCCCCTGTGGCTTCAGTTTAAATGTGCCGATCCT  2548

Qy    821  ThrAlaLeuSerAsnGluThrIleGlyIleIlePheLysHisGlyAspAspLeuArgGln  840
Db    2549  ACGGCCTCATCAAATGAACAAATTGGAATTATCTTTAAACACGGTGACGATCTGCGCCAA  2608

Qy    841  AspMetLeuIleLeuGlnIleLeuArgIleMetGluSerIleTrpThrGluSerLeu  860
Db    2609  GACATGCTTATTTTACAGATTCTCAGAATCATGGAGTCCATTTGGGAGACCAGAATCTTG  2668

Qy    861  AspLeuCysLeuLeuProTyrGlyCysIleSerThrGlyAspLysIleIleGlyMetIleGlu  880
Db    2669  GATCTGTGCCTCCTGCCATATGGCTGCATTTCAACTGGTGACAAAATAGGGATGATCGAG  2728

Qy    881  IleValLysAspAlaThrThrIleAlaLysIleGluGlnSerThrValGlyAsnThrGly  900
Db    2729  ATCGTGAAGGACGCCACGACAATCGCCAAAATTGAGCAAAGCACAGTGGGCAACACGGGT  2788

Qy    901  AlaPheLysAspGluValLeuSerHisTrpLeuLysCysProIleGluGluLys  920
Db    2789  GCCTTTAAAGATGAAGTCCTGAGTCACTGGCTCAAAGAAAAATGCCCTATTGAAGAAAAG  2848

Qy    921  PheGlnAlaAlaValGlyTyrCysSerAlaGlyTyrCysValAlaThrPhe  940
Db    2849  TTTCAGGCAGCTGTGGGATATTGTTCTGCTGGCTACTGTGTCGCCACCTTT  2908

Qy    941  ValLeuGlyIleGlyAspArgHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeu  960
Db    2909  GTTCTCGGAATAGGCGACAGACACAATGACAATATTATGATCTCAGAAACAGGAAATCTA  2968

Qy    961  PheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLys  980
Db    2969  TTTCATATTGATTTCGGACACATTCTTGGGAATTACAAAAGTTTCCTGGGCATTAATAAA  3028

Qy    981  GluArgValProPheValLeuThrProAspPheLeuPheValMetGlyThrSerGlyLys  1000
Db    3029  GAGAGGGTGCCATTTGTGCTAACCCCAGACTTTCTGTTTGTGATGGGGACTTCTGGAAAG  3088

Qy    1001  LysThrSerLeuHisGlnLysPheGlnLeuCysCysAspValThrSerAlaLysLeu  1020
Db    3089  AAGACAAGTCTACACTTCCAGAAATTTCAGGATGTCTGCGCTAAGGCTTACCTAGCCCTT  3148

Qy    1021  ArgHisHisThrAsnLeuLeuIleIleLeuPheSerMetMetLeuMetThrGlyMetPro  1040
Db    3149  CGTCATCACACAAACCTACTGATCATCCTCTTCTCCATGATGCTGATGACAGGAATGCCC  3208

Qy    1041  GlnLeuThrSerLysGluGlyLysGluThrArgAspAlaLeuThrValGlyLysSer  1060
Db    3209  CAGTTAACCAGCAAAGAAGGAAAAGAAACACGTGATGCTCTCACAGTGGGCAAAAGT  3268

Qy    1061  GluGluAspAlaLysLysTyrPheLeuAspLysArgAspLysCysArgAspLysGlyTrp  1080
Db    3269  GAGGAGGATGCTAAAAAGTATTTTCTGGATAAGAGGGATAAGTGCAGAGACAAAGGATGG  3328

Qy    1081  ThrValGlnPheAsnTrpPheLeuHisLeuValLeuGlyIleLysGlyLysHis  1100
Db    3329  ACCGTGCAGTTTAACTGGTTCTTACATCTTGTTCTTGGCAATCAAAGGGAGAAGCAT  3388
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Db    1169  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TTCAGGGTCAAAATCAGAGGCCATTGATATCCCTGTTCCTGCCCCGGACCCTGACCTCACG  1228
Qy    381  ValPheValGlnAlaAsnIleGlnTyrGlyValGlyGlnLeuCysGlnArgArgThrSer  400
Db    1229  GTGTTTGTGAGCAGAAACATCCAGTATGGGCAGCAGTCCTTTGCCAAAGGAGAACCAGC  1288

Qy    401  ProLysProPheThrGluValLeuTrpProAsnValTrpLeuGluPheSerIleLeuLys  420
Db    1289  CCCAAACCCTTCACGGAGGAGGTGCTCTGGCCTGAGAACGTGGCTTGAGTTCAGTATTAAAATC  1348

Qy    421  LysAspLeuProLysGlyAlaLeuLeuAsnLeuAsnLeuIleTyrCysGlyLysAlaProAla  440
Db    1349  AAAGACTTACCCAAAGGGCTCTGCTCGACCTCAGATCTGCGGCAAAGCTCCAGCA  1408

Qy    441  LeuSerGlyLysThrSerAlaGluMetProSerProGluSerProLysGlyLysAlaGlnIleLeu  460
Db    1409  CTGTCTGGCAAGAACCTCTGCAGAGATGGCCTCCCAGTCCCAGTCCAAAGGCAAAGTCAGCTT  1468

Qy    461  LeuTyrTyrValAsnLeuGluIleLeuAspHisAlaArgPheLeuGluArgHisGlyGluTyr  480
Db    1469  CTGTACTATGTCAACATGGAGATTCTCGATAGACCACCGCTTCCTCCTGCGCGGCCAGTAT  1528

Qy    481  ValLeuHisMetTrpGlnLeuSerGlyLysLysGlyGlnAspGlnAspSerPheAsnAlaAsp  500
Db    1529  GTGCTCCACATGTGGCAGTTATCCGGGAAGAAAGGACCAAGGGAGTTCAATGCCGAGTAT  1588

Qy    501  LysLeuThrSerAlaThrAsnProAspLysGlyAsnSerMetSerIleLeuSerIleLeuLeu  520
Db    1589  AAGCTCACGTCGGGAACCAACCCCGACAAGGGAACTCAATGTCCATCCATTCTTCTG  1648

Qy    521  AspAsnTyrCysHisHisProIleAlaLeuProLysHisArgProThrProAspProGluGly  540
Db    1649  GACAATTACTGCCACCCCATAGCCTTGCCTAAGCATCGGCCTACCCCCTGACCCAGAAGGG  1708

Qy    541  AspArgValArgAlaGluMetProAsnProLeuThrAlaGluLysLysGluLeuGlnLeuGluAlaIleAla  560
Db    1709  GACCGGGTTCGGGCAGAAATGCCCAATCCACTCACAGCTGAGAAGAAACTGCCTCGAGGCCAATCATAGCC  1768

Qy    561  ThrAspProLeuAsnProLeuTyrAlaGluLeuTrpHisArgTyr  580
Db    1769  ACGGATCCGCTTAACCCACTCACAGCTCTGAGAACAAAGACTGCTCTGGCATTTCAGATAT  1828

Qy    581  GluSerLeuValAspProLysAlaTyrProLeuPheSerSerValLysTrpGlyGln  600
Db    1829  GAAAGCCTGAAGGATCCCAAAGCTATCCCAAGCGTCTTTAGCCTCGGTGAAATGGGGACAG  1888

Qy    601  GlnGluIleValAlaLysThrThrTyrGlnIleValAlaLysArgGluValArgTrpAspGlnSer  620
Db    1889  CAAGAAATTGTGGCCAAAACAACATACCAATTATTAGCCAAAAGGAGGAGGTCGGGATCAGAGT  1948

Qy    621  AlaAlaAspValGlyLeuThrMetGlnLeuLeuLeuAspCysAsnPheSerAspCysGluAsnVal  640
Db    1949  GCTTTGGATGTGGGGTTAACCATGCAGCTCCTGCTCGACTGTAACTTCTCCGATGAAAACGTG  2008

Qy    641  ArgAlaIleAlaAlaValGlnIleLysLysLeuLeuSerLeuGluGluAspAspAspAspSerValLeuHisTyrLeu  660
Db    2009  AGAGCCATTGCAGTCCAGATCAAGAAACTGCTCAGTCTGGAGGAAGATGATGACGTGCTCATTACCTG  2068

Qy    661  LeuGlnLeuValGlnAlaValLysHisLeuAspValLysHisIleLysAlaArgPhe  680
Db    2069  CTCCAGCTGGTCCAGGCTGTGAAATTTGAACCATACCATGACAGTGCCCTAGCCAGATTT  2128

Qy    681  LeuLeuGluLysArgGlyLeuValArgAsnLysArgIleGlyHisLeuGlyPheLeuPheLeuArgArg  700
Db    2129  CTGCTCGAAAGCGTGGTTTAAGAGAACAAGAGAGAATTGGTCACCTTCTTTTGTTTCTTGGAGA  2188

Qy    701  SerGluIleGluAlaGlnSerArgHisTyrArgGlnArgPheGlnAlaValIleLeuGluGluAlaTyr  720
Db    2189  AGTGAGATTGAAGCTCAGTCCAGGCACTATCGACAGAGGTTTGCAGTTGCGTGATCCTGAAGCCTAC  2248

Qy    721  LeuArgGlyCysGlyThrArgLeuHisAlaMetLeuHisAspPheHisLeuGlnAsnValGlnIleIleAsp  740
Db    2249  ...
```

```
Qy      1101 SerAla 1102
             |||
Db      3389 CCCGCA 3394

RESULT 4
AAV74104
ID   AAV74104 standard; DNA; 5162 BP.
XX
AC   AAV74104;
XX
DT   09-MAR-1999  (first entry)
XX
DE   Human G-protein regulated PI3K p120 adapter subunit DNA.
XX
KW   Phosphoinositide 3-hydroxykinase; PI3K; trimeric G protein; human;
KW   adapter subunit; regulatory subunit; p101; p120; catalytic subunit;
KW   detection; diagnosis; activation disorder; inflammation; arthritis;
KW   treatment; immune disorder; inflammation; arthritis; septic shock;
KW   adult respiratory distress syndrome; pneumonia; asthma; allergy;
KW   reperfusion injury; atherosclerosis; Alzheimer's disease; cancer; ss.
XX
OS   Homo sapiens.
XX
PN   US5856132-A.
XX
PD   05-JAN-1999.
XX
PF   15-AUG-1997;   97US-0916917.
XX
PR   15-AUG-1997;   97US-0916917.
PR   27-JUN-1996;   96US-0672211.
XX
PA   (ONYX-) ONYX PHARM.
XX
PI   Braselmann S, Hawkins PT, Stephens L;
XX
DR   WPI; 1999-105107/09.
DR   P-PSDB; AAW90089.
XX
PT   Nucleic acid encoding regulatory (p101) and catalytic (p120)
PT   subunits of a heterodimeric phosphatidylinositol-3' kinase - useful
PT   in treatment and diagnosis of immune system disorders, e.g.
PT   arthritis, cancer and Alzheimer's disease
XX
PS   Example X; Fig 12A-C; 75pp; English.
XX
CC   This sequence encodes a novel catalytic subunit, p120, from human
CC   phosphoinositide 3-hydroxykinase (PI3K) which is regulated by beta-gamma
CC   subunits of trimeric G-protein. Nucleic acid coding for p101 or p120, or
CC   their fragments, are used as probes and primers for identifying p101 or
CC   p120 gene mutations, allelic variations or regulatory defects,
CC   particularly for the diagnosis of activation disorders (or
CC   susceptibility) in cells of the haematopoietic system. The related
CC   proteins, antibodies, agonists and antagonists can be used similarly. The
CC   p101 and p120 proteins, peptides or fusion proteins are used to treat or
CC   screen for potential agents for treating immune disorders, particularly
CC   inflammation, e.g. arthritis, septic shock, adult respiratory distress
CC   syndrome, pneumonia, asthma, allergies, reperfusion injury,
CC   atherosclerosis, Alzheimer's disease and cancer.
XX
SQ   Sequence 5162 BP; 1471 A; 1173 C; 1149 G; 1367 T; 2 other;

Alignment Scores:
Pred. No.:                          0           Length:        5162
Score:                        5534.00           Matches:       1049
Percent Similarity:            97.10%           Conservative:    21
Best Local Similarity:         95.19%           Mismatches:      32
Query Match:                   95.58%           Indels:           0
DB:                                20           Gaps:             0

US-09-974-573-1 (1-1102) x AAV74104 (1-5162)
```

```
Qy      1 MetGluLeuGluAsnTyrGluGlnProValValLeuArgGluAspAsnArgArgArgArg       20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     84 ATGGAGCTGGAGAACTATAAACAGCCCGTGTGCTGAGAGAGACAACTGCCGAAGGGCGC      143

Qy     21 ArgArgMetLysProArgSerThrAlaAlaSerLeuSerMetGluLeuIleProIle       40
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    144 CGGAGGATGAAGCCGCAGTGACCGCAGCCTGTCTCCATGGAGCTCATCCCCATC      203

Qy     41 GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeuLeuHis       60
          ||||||||||||||||::::||||||||||||||||||||||||||||||||||||||||
Db    204 GAGTTCGTGCTGCCCACCAGCCAGCGCAAATGCAAGACCCCGAAACGGGCGTGCTGCAC      263

Qy     61 ValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnAlaValTrpLeuArgAlaLeuGlu       80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    264 GTGGCCGGCCACGGCAACGTGGAGCAGATGAAGGCCCAGGCTGTGCGTGCTGGAG      323

Qy     81 ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTyr      100
          ||||::::||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    324 ACCAGCGTGGCGGCACTTCTACCACCGGCTGGGACCGCATCACTTCCCTGCTCTAT      383

Qy    101 GlnLysGlyGlnTrpTyrGluIleTyrAspLysTyrGlnValValGlnThrLeuAsp      120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    384 CAGAAGAAGGGGCAGTGGTACGAGATCTACGACAAGTACCAGGTGGTGCAGACTCTGGAC      443

Qy    121 CysLeuArgTyrTrpLysValHisArgSerProGlyGlnIleHisValValGlnArg      140
          |||||||||||||||||||||||||||||||::::|||||||||||||||||
Db    444 TGCCTGCGCTACTGGAAGGCCCACCGCACCGGAGCCCAGGCCAGATCCACCTGGTGCAGCCG      503

Qy    141 HisAlaProSerGluThrLeuAlaPheGlnAsnArgGlnLeuAsnAlaLeuIleGlyTyr      160
          ||||||||||||||||||||||||||::::|||
Db    504 CACCCGCCCTCCGAGAGTCCCAAGGCTTCCAGCGGCTGGCAGCTCACGGCGCTGATTGGCTAT      563

Qy    161 AspValThrAspValSerAsnValHisAspAspAspGlnAspGlnAspAspAspAspThr      180
          |||||||||||||||||||||||||||||||||||||||||||||
Db    564 GACGTCACTGACGTCAGCAACGTGCACGACGATAGCTGAGTTCACGGCCGTGGCTTG      623

Qy    181 ValThrProArgMetAlaGluValAlaGlyArgAspProLysLeuTyrAlaMetHisPro      200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    624 GTGACCCCGCGCTACTGGACGCGGAGGTGGCCAGCCGGCGACCCCCAAGCTTACGCCATGCACCCG      683

Qy    201 TrpValThrSerLysProLeuGluTyrLeuLeuLysLysIleLysThrAsnAsnCysVal      220
          ||||||||||||||||||||||||||||||||||||||::::
Db    684 TGGGTGACGTCCAAGCCCCTCCGAGTACCTGTGAAGAAGATTGCCACAACTGCATC      743

Qy    221 PheIleValIleHisArgSerThrThrSerGlnThrIleLysValSerAlaAspAspThr      240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    744 TTCATCGTCATTCACCGCAGCACCACCAGCCAGACCATTAAGGTCTCACCCGACGACACC      803

Qy    241 ProGlyThrIleLeuGlnSerPhePheThrLysMetAlaLysLysLysSerLeuMetAsp      260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    804 CCCGGGCGCCATCTGCAGAGTTCTTCACCAAGATGGCCAAGAAGAAATCTCTGATGGAT      863

Qy    261 IleProGluSerGlnAsnGluArgAspPheValLeuArgValCysGlyValArgAspGluTyr      280
          |||||||||||||::::||||||||||||||||||||||||||||||||||||||||||||
Db    864 ATTCCCGAAAGCCAAAGGCCAAGACAGAGATTTTGTGCTGCGCGTCTGTGGCCGGATGAGTAC      923

Qy    281 LeuValGlyGluThrProIleLysAsnPheIleTrpValArgGlnCysLeuLysAsnGly      300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    924 CTGGTGGGCGAAACGCCCATCAAAAACTTCCAGTGGGTGAGGCAGTGCCTCAAGAACGGA      983

Qy    301 GluGluIleHisLeuValLeuAspThrProAspProAlaLeuAspProLeuValAlaArgLys      320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    984 GAAGAGATTCACGTGGTACTGGACACGCCCTCCAGACCCGGCCTCCAGACGAGGTGACGAAG      1043

Qy    321 GluGluTrpProLeuValAspAspCysThrGlyTyrHisGlyGluLeuThr      340
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1044 GAAGAGTGGCCCTGGTGGACGACTGCACGGGAGTCCACGGGGAGTTGACCAGCTTACC      1103

Qy    341 IleHisGlyLysHisGluSerValPheThrValSerLeuTrpAspCysAspArgLys      360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1104 ATCCACCGGCAAGGACGAGAGTGTGTTCACCGTGTCCCTGTGGGACTGCGACCGCCAAG      1163

Qy    361 PheArgValIleArgGlyIleAspPheIleProValLeuProValValProArgAspThrAlaAspLeuThr      380
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```
Qy  1101 SerAla 1102
         ||||||
Db  3384 TCAGCC 3389
```

RESULT 5
AA286814
ID   AA286814 standard; DNA; 5162 BP.
XX
AC   AA286814;
XX
DT   20-APR-2000 (first entry)
XX
DE   Human p120 regulatory subunit coding sequence.
XX
KW   p101 protein; p120 protein; regulatory subunit; immune system disorder;
KW   trimeric G-protein regulated PI3K; phosphoinositide 3OH-kinase; asthma;
KW   inflammatory response disorder; arthritis; septic shock; allergy;
KW   adult respiratory distress; cancer; reperfusion injury; atherosclerosis;
KW   Alzheimer's disease; haematopoietic lineage cell activation disorder;
KW   therapy; human; ss.
XX
OS   Homo sapiens.
XX
PN   US6017763-A.
XX
PD   25-JAN-2000.
XX
PF   04-JAN-1999; 99US-0225170.
XX
PR   15-AUG-1997; 97US-0916917.
PR   27-JUN-1996; 96US-0672211.
XX
PA   (ONYX-) ONYX PHARM INC.
PA   (BABR-) BABRAHAM INST.
XX
PI   Braselmann S, Stephens L, Hawkins PT;
XX
DR   WPI; 2000-136682/12.
DR   P-PSDB; AAY76803.
XX
PT   Isolated p101 regulatory polypeptide, a subunit of the trimeric
PT   G-protein regulated PI3K, is useful for screening compounds which can
PT   be used to treat inflammatory response disorders -
XX
PS   Disclosure; Fig 12; 75pp; English.
XX
CC   This sequence encodes the human p120 regulatory protein.
CC   The invention relates to the human p101 regulatory protein,
CC   which is a subunit of the trimeric G-protein regulated phosphoinositide
CC   3OH-kinase (PI3K). The p101 regulatory protein can be used in screening
CC   assays to detect compounds which can be used to treat inflammatory
CC   response disorders. The compounds identified may be antagonists or
CC   agonists of G protein-regulated PI3K gene expression and/or p101 or p120
CC   gene product activity. These compounds may then be used to control immune
CC   system disorders, in particular arthritis, septic shock, adult
CC   respiratory distress, asthma, allergies, reperfusion injury,
CC   atherosclerosis, Alzheimer's disease and cancer. p101 proteins and
CC   peptides can be used in the detection of mutant or inappropriately
CC   expressed p101 regulatory subunits for the diagnosis of immune disorders
CC   and haematopoietic lineage cell activation disorders which will also
CC   assist in devising a proper treatment or therapeutic regime. Using
CC   genetically engineered host cells to screen for compounds also allows
CC   compounds which affect the signal transduced by the activated p101
CC   regulatory subunit to be identified.
XX
SQ   Sequence 5162 BP; 1471 A; 1173 C; 1149 G; 1367 T; 2 other;

Alignment Scores:
Pred. No.:   0
Score: 5534.00
Percent Similarity: 97.10%
Best Local Similarity: 95.19%

Query Match: 95.58%   Indels: 0
DB: 21   Gaps: 0

Length: 5162
Matches: 1049
Conservative: 21
Mismatches: 32

US-09-974-573-1 (1-1102) x AA286814 (1-5162)

```
Qy     1 MetGluLeuGluAsnTyrGluGlnProValValLeuArgGluAspAsnArgArgArgArg 20
           | ||||||||||||||||||||| |||
Db    84 ATCGAGCTGGAGAACTATAAACAGCCCGTGGTGCTGAGAGAGGACAACTGCCGAAGGCGC 143

Qy    21 ArgArgMetLysProArgSerThrAlaAlaSerLeuSerMetGluLeuIleProIle 40
         ||||||||||||||||||||||||||||||||||||||||||
Db   144 CGGAGGATGAAGCCGCAGTGCGCCAGCCTGTCCTCCATGGAGCTCATCCCCATC 203

Qy    41 GluPheValLeuProThrSerGlnArgAsnThrLysAsnThrProGluThrAlaLeuLeuHis 60
         ||||||||||||| ::::||||
Db   204 GAGTTCGTGCTGCCCACCAGCCAGCGCGAAATGCAAGACCCCGAAACGGGCGCTGCTGCAC 263

Qy    61 ValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnValTrpLeuArgAlaLeuGlu 80
         ||||||||||||||||||||||||||||||
Db   264 GTGGCCGGCCACGGCAACGTGGAGCAGATGAAGGCCCAGGTGCGTGGGCGCGCGTGGAG 323

Qy    81 ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTyr 100
         |||||||:::||||||||||
Db   324 ACCAGCGTGGCCGGCGGACTTCTACCACCCGGCTGGGACCGCATCACTTCCTCCTGCTCTAT 383

Qy   101 GlnLysLysGlyGlnTrpTyrGluIleTyrArgGluLysTyrGlnValValGlnThrLeuAsp 120
         ||||||||||||||||||||||
Db   384 CAGAAGAAGGGGCAGTGGTACGAGATCTACAGAGAAAGTACCAGGTGGTGCAGACTCTGGAC 443

Qy   121 CysLeuArgGlyTyrTrpLysValLeuHisArgSerProGlyGlnIleHisValValGlnArg 140
         ||||||||||||||||||:::|||
Db   444 TGCCTGCGCTACTGGAAGGTGCACCGGAGCCCCGGCCAGATCCACGTGGTGCAGCGG 503

Qy   141 HisAlaProSerGluGluThrLeuAlaPheGlnArgGlnLeuAsnAlaLeuGlyLeuIleGlyTyr 160
         |||||||||||||||||||:::||
Db   504 CACCCGGCCTCCGAGGAGTCCCAGGCTTCCAGCGGACCTTCCAGCGGCGCTGATTGGCTAT 563

Qy   161 AspValThrAspValSerAsnValHisAspAspSerGluLeuGluPheThrArgArgArgLeu 180
         |||||||||||||||||||||
Db   564 GACGTCACTGACGTCAGCAACGTGCACGACGATGAGTTCACGCGCCGTGGCTTG 623

Qy   181 ValThrProArgMetAlaGluAlaGlyValAlaGlyTyrArgAspProLysLeuTyrArgAlaMetHisPro 200
         |||||||||||||||||||||||
Db   624 GTGACCCCGCGCATGGCCGAGGTGGCCGGCTACCGCGACCCCAAGCTCTACCGCGCCATGCACCCG 683

Qy   201 TrpValThrSerLysProGluProGluTyrLeuLeuLysLysIleLeuThrArgAsnAsnCysVal 220
         ||||||||||||||||||:::
Db   684 TGGGTGACGTCCAAGCCCGAGCCCGAGTACCTGCTGAAGAAGATTGCCAACACTCGCATC 743

Qy   221 PheIleValIleHisArgSerThrThrSerGlnThrThrLysValSerAlaAspAspThr 240
         ||||||||||||||||||||||:::
Db   744 TTCATCGTCATTCACCGCAGCACCACCAGCCAGACCATTAAGGTCTCACCCGACGACACC 803

Qy   241 ProGlyThrIleLeuGlnSerPhePheThrArgLysMetAlaLysLysSerLeuMetAsp 260
         |||||||||||||||||||||
Db   804 CCCGGCCGCCATCCTGCAGAGCTTCTTCACCAAGATGGCCAAGAAGAAATCTCTGATGGAT 863

Qy   261 IleProGluSerGlnAsnGluArgAspPheValLeuArgValCysGlyValArgAspGluTyr 280
         ||||||||||||||:::|||
Db   864 ATTCCCGAAAGCCAAAGCGAACAGGATTTTGTCTGCCGCGTCGTGCGGGATGAGTAC 923

Qy   281 LeuValGlyGluThrProIleLeuLysAsnPheGlnTrpValArgGlnCysLeuLysAsnGly 300
         ||||||||||||||||||||:::
Db   924 CTGGTGGGCGAAACGCCCATCATAAAAAACTTCCAGTGGGTGAGCGCACTGCCTCAAGAACGGA 983

Qy   301 GluGluIleHisLeuValLeuAspThrProProAlaLeuAspGlnProAlaLeuAspArgLys 320
         ||||||||||:::||
Db   984 GAAGAGATTCACGTGGTACTGGACACGCCTCCAGCACCCGGCCCTCAGACGGAGGTGAGGAAG 1043

Qy   321 GluGluTrpProLeuValAlaAspAspCysTyrThrGlyValThrGlyTyrHisGluGlnLeuThr 340
         ||||||||||||||||||||||
Db  1044 GAAGAGTGGCCCCTGGTGGCCGACGACTGCTACACGGGAGTCACGGGCTACCATGAGCAGCTTACC 1103
```

Qy 341 IleHisGlyLysAspHisGluSerValPheThrValSerLeuTrpAspCysAspArgLys 360
         ATCCACGGGCAAGGACCACAGAGTGTTCACCGTGTCCCTGTGGGACTGCGACCGCAAG 1163
Db 1104

Qy 361 PheArgValLysIleArgGlyIleIleAspIleProValLeuProValThrAlaAspLeuThr 380
         TTCAGGGTCAAGATCAGAGATCGCATTGATATCCCGGTCCTGCCTCGGAACACCGACCTCACA 1223
Db 1164

Qy 381 ValPheValGluAlaAsnIleGlnTyrGlyGlnValLeuCysGlnArgArgThrSer 400
         GTTTTTGTAGAGGCAAACATCCAGCATGGGCAACAAGTCCTTTGCCAAAGGAGGAACCAGC 1283
Db 1224

Qy 401 ProLysPheThrGluValTrpAspValTrpLeuTrpLeuPheAsnValPheLeuGluSerIleLysIle 420
         CCCAAACCCTTCACGAGGAGGTGCTGTGAATGTGTGCCTTGGCTTGGTTGAGTTCAGTATCAAAATC 1343
Db 1284

Qy 421 LysAspLeuProLysGlyAlaLeuLeuAsnLeuIleTyrCysGlyLysLysAlaProAla 440
         AAAGACTTGCCCAAAGGGGCTCTACTGAACCTCCAGATCTACTGCGGTAAAGCTCCAGCA 1403
Db 1344

Qy 441 LeuSerGlyLysThrSerAlaGluMetProSerProGluSerLysGlyLysAlaGlnLeu 460
         CTGTCCAGCAAGGGCCTCTGCAGAGTCCCCCAGTTCTGAGTCCAAGGGCAAAGTTCGGCTT 1463
Db 1404

Qy 461 LeuTyrTyrValAsnLeuLeuLeuIleAspHisArgPheLeuLeuArgHisGlyGluTyr 480
         CTCTATTATGTGAACCTGCTGCTGATAGACCACCGTTCCTGCTCCGGCCGTGAGAATAC 1523
Db 1464

Qy 481 ValLeuHisMetTrpGlnIleLeuSerGlyLysGlyGlyAspGlnGlySerPheAsnAlaAsp 500
         GTCCTCCACATGTGGCAGATATCTGGAAGGAGAAGAACCAAGGAAGCTTCAATGCTCAC 1583
Db 1524

Qy 501 LysLeuThrSerAlaThrAsnProAspLysGlyGluAsnSerMetSerIleSerLeuLeu 520
         AAACTCACGTCTGCAACTAACCCAGACAAGGAGAACTCAATGTCCATCTCCATTCTCTG 1643
Db 1584

Qy 521 AspAsnTyrCysHisProIleAlaLeuProLysHisArgProThrProAspProGluGly 540
         GACAATTACTGCCACCCGATAGCCCTGCCTAAGCATCGACCCCCTCCAAGCCCGGAGGG 1703
Db 1644

Qy 541 AspArgValAlaArgGluAlaGluMetProAsnGlnLysLysGlnLeuGluLeuAlaIleIleAla 560
         GACCGGGTTGCAGAGAAATGCCCAACCAGCTTCGCAAGGCAAATTGGAGGCGATCATAGCC 1763
Db 1704

Qy 561 ThrAspProLeuAsnProLeuThrAlaGluAspAspLysAspLysGluLeuTrpHisPheArgTyr 580
         ACTGATCCACTTAACCCTCTCACAGCAGAGGACAGACAAAGAATTGGCTCGGCATTTTAGATAC 1823
Db 1764

Qy 581 GluSerLeuLysAspProLysTyrProLysLeuPheSerGlnSerValLysTrpGlyGln 600
         GAAAGCCTTAAGGACCCCAAAAGCATACCCAAGCTATTTAGTTCAGTGAAATGGGGACAG 1883
Db 1824

Qy 601 GlnGluIleValAlaAlaLysThrTyrGlnLysLeuLysAlaArgGlnValLeuTyrLeu 620
         CAAGAAATTGTGGCCAAAACATACCAATTGTTGCCAAGAGGAAGTCCTGGGCATTATAA 1943
Db 1884

Qy 621 AlaLeuAspValGlnLysLysGlnGluSerLeuGluGluLysAspCysAsnPheSerGluAspAspGlnValAsnVal 640
         GCTTTGGATGTTGGGTTAACAATGGCAGAGCTTCGGAGAGCTTGATGATGTTCTGCAATTACCTT 2003
Db 1944

Qy 641 ArgAlaIleAlaLysGlnGlnThrTyrGlnMetLeuGlnGluGlnLysLysAspGlnValLeuHisTyrLeu 660
         AGAGCCATTGCAGTTGCAGTTGGGTTTAACAATGGAGAGCTTGGAAGTGGAGAGAGT...TGGAAG 2063
Db 2004

Qy 661 LeuGlnLeuValGlnAlaValLysPheGluPheHisAspSerAlaLeuAlaArgPhe 680
         CTACAATTGGTCCAAGGCTGTGAAATTGAACCATCATACAACATCATAGAGTGCAAGATTT 2123
Db 2064

Qy 681 LeuLeuLysLysArgGlyLeuArgAsnArgIleGlyHisPheLeuTrpPheLeuArg 700
         CTGCTGAAGCGTGGTTTAAGAAACAAAGAAATTGGTCACTTTTTGTTTTGGTTCTTGAGA 2183
Db 2124

Qy 701 SerGluIleAlaGlnSerArgHisTyrArgGlnIleArgPheAlaAlaValLeuGluAlaTyr 720
Db

Qy 721 LeuArgGlyCysGlyThrAlaMetLeuHisAspPheThrGlnGlnValGlnValIleAspHisAsp 740
         CTGAGGGGCTGTGGCACAGCCATGTTGCACGACTTTACCCAACAGGTAACAAGTAATCGAG 2303
Db 2244

Qy 741 MetLeuGlnLysValThrArgIleAspIleLysSerLeuSerArgSerAlaGluLysTyrValSer 760
         ATGTTACAAAAGTCACCCTGATATATAAATCGCTCTCGTGCTGAAAAGTATGACGTCAGT 2363
Db 2304

Qy 761 SerGlnValIleSerGlnLeuLysGlnLysLeuGluAsnLeuGluAsnLeuGlyAsnLeuPro 780
         TCCCAAGTTATTTCACAACTTAAACAAAAACTGGAAAACCTGCAGAATTCTCAACTCCCC 2423
Db 2364

Qy 781 GlnSerPheArgValProTyrAspProGlyLeuLysAlaGlyAlaLeuValIleLeuGluLys 800
         GAAAGCTTTAGAGTTCCATACGATCCTGGACTGAAAGCAGGAGCGCTGGCAATTGAAAAA 2483
Db 2424

Qy 801 CysLysLysValMetAlaSerLysLysSerProLeuTrpLeuGluPheLysGluLysSerAlaAspProPro 820
         TGAAAGTAATGGCCTCCAAGAAAAACCACCATGGCTTGAGTTTAAATGTCCGGATCCTCCT 2543
Db 2484

Qy 821 ThrAlaLeuSerAsnGluThrArgIleGlyIleGluIleGluGlyAspAspLeuArgArgGln 840
         ACAGCCCTATCAAATGAAACAATTGGAATTATCTTTAAAACATGGTGATGATCTGCGGCAA 2603
Db 2544

Qy 841 AspMetLeuIleLeuGlnIleLeuGluArgIleMetGluSerIleTrpGluThrGluSerLeu 860
         GACATGCTTATTTTACAGATTCTACGAGTCTATTGGGAGACTGAATCTTTG 2663
Db 2604

Qy 861 AspLeuCysLeuLeuProTyrGlyCysIleSerSerThrGlyAspLysLysIleGluMetIleGlu 880
         GATCTATGCCTCCTGCCATATGGTTGCATTTCAACTGGTGACAAAATGATCGAG 2723
Db 2664

Qy 881 IleValLysAspAlaThrThrLeuIleIleGlnIleSerThrValGlyLysAsnThrGly 900
         ATTGTGAAAGACGCCACGACAATTGCCAAATTCAGCAACACGTGGGCAACACGGGA 2783
Db 2724

Qy 901 AlaPheLysAspGluValLeuSerHisTrpLeuLysCysProIleGluGluLys 920
         GCATTTAAAGATGAAGTTCTGAATCACTGGCTCAAAGAAAATCCCCTACTGAAGAAAAG 2843
Db 2784

Qy 921 PheGlnAlaAlaValGluArgPheValSerCysValTyrCysValAlaGlyThrPhe 940
         TTTCAGGCAGCAGTGGAGAGATTTGTTTATTCCTGTGCAGGCTACTGTGTGGCAACCTTT 2903
Db 2844

Qy 941 ValLeuGlyIleGlyTyrAspArgHisAlaAsnIleMetIleSerGluThrGlyAsnLeu 960
         GTTCTTGGAATAGGCGACGACAGACAATATATGATCAGTGAAACTGGAAACCTA 2963
Db 2904

Qy 961 PheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLys 980
         TTTCATATTGACTTCGGGCACATTCTGGGAAATTACAAAAGTTTCCTGGGCATTAATAAA 3023
Db 2964

Qy 981 GluArgValProPheValProPheGlnLysProPheValMetGlyTyrSerGlyLys 1000
         GAGAGAGTGCCATTTGTGCCATTCCAGAAATTTCCAACCCCTGACTTCCTCTTTGTGATGGGAACTTCTGGAAAG 3083
Db 3024

Qy 1001 LysThrSerLeuHisPheGlnLysPheGlnAspLysCysValLysValAlaLysAlaLeu 1020
          AAGACAAGCCCACTTGTGCTAACCCCTGACTTCCTCTTTGTGATGGGAGGAATGCCC...TTCTAGCCCTT 3143
Db 3084

Qy 1021 ArgHisHisThrAsnLeuLeuIleIleLeuPheSerMetMetLeuMetThrGlyMetPro 1040
          CGTCATCACACAAACCTACTGATCATCCTGTTCTCCATGATGCTGATGACAGGAATGCCC 3203
Db 3144

Qy 1041 GlnLeuThrSerLysGluAspIleGluTyrIleArgAspAlaLeuThrValGlyTyrLysSer 1060
          CAGTTAACAAGCAAGGAAGAGAGACATTGAATATATCCGGGATGCCCTCACAGTGGGAAAAAT 3263
Db 3204

Qy 1061 GluGluAspAlaLysValSerTyrPheLeuAspGlnIleGluValCysArgAspLysGlyTrp 1080
Db

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Db    3264  GAGGAGGATGCTAAAAAGTATTTCTTGATCAGATCGAAGTTGCAGAGACAAAGGATGG  3323

Qy    1081  ThrValGlnPheAsnTrpPheLeuHisLeuValLeuGlyIleLeuGlyIleLysHis  1100
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3324  ACTGTGCAGTTTAATTGGTTTCTACATCTTGTTCTTGGCATCAAACAGGAGAAACAT  3383

Qy    1101  SerAla  1102
                 ||||||
Db    3384  TCAGCC  3389

RESULT 6
ABL59522
ID    ABL59522 standard; cDNA; 5397 BP.
XX
AC    ABL59522;
XX
DT    16-JUL-2002  (first entry)
XX
DE    Human phosphatidylinositol-3-kinase gamma cDNA SEQ ID NO:22.
XX
KW    Human; phosphatidylinositol-3-kinase gamma; enzyme;
KW    tumour; lipid associated gene; lipid metabolism; lipid synthesis;
KW    chromosome 7q22.1-31.33; gene; ss.
XX
OS    Homo sapiens.
XX
PN    WO200227028-A1.
XX
PD    04-APR-2002.
XX
PF    27-SEP-2001; 2001WO-US30366.
PR    28-SEP-2000; 2000US-0676052.
XX
PA    (ATAI-) ATAIRGIN TECHNOLOGIES INC.
XX
PI    Skinner MK, Patton JL, Chaudhary J;
XX
DR    WPI; 2002-402054/43.
XX
PT    Identifying tumour characteristics in a tissue sample taken from a
PT    patient, involves determining the copy number or expression level of
PT    genes associated with lipid metabolism, synthesis or action -
XX
PS    Example 1; Page 80-81; 113pp; English.
XX
CC    The present invention describes a method for identifying tumour
CC    characteristics, comprising measuring a copy number or expression level
CC    of at least two genes associated with lipid metabolism, synthesis, or
CC    action in cells from a patient tissue sample, and comparing the results
CC    with a copy number or expression level of the genes in a normal cell.
CC    Also described is an array of nucleic acid polymers immobilised on a
CC    solid support, comprising a solid support, at least two different nucleic
CC    acid polymers which are each specific for a different gene associated
CC    with lipid metabolism, synthesis or action, where each nucleic acid
CC    polymer is located at a predetermined position on the solid support, and
CC    the array comprises nucleic acid polymers which are specific for less
CC    than 100 genes other than the selected genes. The method is useful for
CC    determining tumour characteristics in a tissue sample taken from a
CC    patient. The present sequence represents a human lipid-associated gene
CC    related cDNA sequence, which is used in the exemplification of the
CC    present invention.
XX
SQ    Sequence 5397 BP; 1534 A; 1224 C; 1207 G; 1432 T; 0 other;

Alignment Scores:
Pred. No.:                    0            Length:            5397
Score:                        5523.50      Matches:           1049
Percent Similarity:           97.10%       Conservative:        21
Best Local Similarity:        95.19%       Mismatches:          31
Query Match:                  95.40%       Indels:               1
DB:                           24           Gaps:                 1
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US-09-974-573-1 (1-1102) x ABL59522 (1-5397)

Qy       1  MetGluLeuGlnAsnTyrGluGlnProValValLeuArgGluAspAsnArgArgArgArg   20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     324  ATGGAGCTGGAGAACTATAAACAGCCCGTGGTGCTGCGAGAGGACAACCTGCGAAGGCGC  383

Qy      21  ArgArgMetLysProArgSerThrAlaAlaSerLeuSerMetGluLeuIleProIle     40
              |||||||||||||||||||||||||||   ||||||||||||||||||||||||||
Db     384  CGGAGGATGAAGCCGCGGCAGT--GCTGCCAGCCTGTCCTCCATGGAGCTCATCCCCATC  440

Qy      41  GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeuLeuHis   60
              ||||||||||||||||||||||||||||||||||||||||||||||::::::|||||||
Db     441  GAGTTCGTGCTGCCCACCAGCCAGAGAAATGCAAGACCCCGAAACGGCCTGCTGCAC     500

Qy      61  ValAlaGlyHisGlyAsnValGluGluMetLysAlaGlnValTrpLeuArgAlaLeuGlu   80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     501  GTGGCCGGCCACGGCAACGTGGAGGAGATGAAGGCCCAGGTGTGGCTGCGAGCGCTGGAG  560

Qy      81  ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTyr  100
              ||||||||||:::::|||||||||||||||||||||||||||||||||||||||||||||
Db     561  ACCAGCGTGGGCGGGGACTTCTACCACCGGCTGGGACCCGATCACTTCCTCCTGCTCTAT  620

Qy     101  GlnLysLysGlyGlnTrpTyrGlyIleTyrAspLysTyrGlnValValGlnThrLeuAsp  120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     621  CAGAAGAAGGGCCAGTGGTACGGAATCTACGACAAGTACCAGGTGGTGCAGACTCTGGAC  680

Qy     121  CysLeuArgTyrTrpLysValHisSerArgSerProGlyGlnIleHisValValGlnAsn  140
              |||||||||||||||||||||||||||||||||||||||||||||||||::::|||||||
Db     681  TGCCTGCGCTACTGGAAGGTCCACAGCCGCAGATCCACCTGGTGCAGCGG  740

Qy     141  HisAlaProSerGluGluThrLeuAlaPheGlnArgGlnLeuAsnAlaLeuIleGlyTyr  160
              |||:::|||||||||||||||||||::::||||||||||||||||||||||||||||||
Db     741  CACCCCGCCCTCCGAGGATCCCAAGCTTCCAGCGCCAGCTTCACGGCGCTGATTGGCTAT  800

Qy     161  AspValThrAspValSerAsnValHisAspAspGluLeuGluPheThrArgArgLeu     180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     801  GACGTCACTGACGTCAGCAACGTGCACGACGATGAGCTGGAGTTCACGCGCCGTGCTTG  860

Qy     181  ValThrProArgMetAlaGlyValAlaGlyValArgAspProLysLeuTyrAlaMetHisPro  200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     861  GTGACCCCGCGCATGGCAGGCGTGGCCGGCGTGCCGGACCCCAAGCTCTACGCCATGCACCCG  920

Qy     201  TrpValThrSerLysProLeuProGluLeuProThrTyrLeuLeuTyrLeuGluThrArgAsnCysVal  220
              |||||||||||||||||||||||::::||||||||||||||||||||||||||::::|
Db     921  TGGGTGACGTCCAAGCCCCTCCCGGAGTACCTGTGGAAGAGATTGCCAACAACTCATC  980

Qy     221  PheIleValIleHisArgSerThrThrSerGlnThrThrIleLysValSerAlaAspAspThr  240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     981  TTCATCGTCATTCACCGCAGCACCACCAGCCAGACCACCATTAAGGTCTCACCCGACGACACC  1040

Qy     241  ProGlyThrIleLeuGlnSerPhePheLysMetAlaLysLysSerLeuMetAsp    260
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1041  CCCGGGCGCCATCCTGCAGAGCTTCTTCACCAAGATGGCCAAGAAGAAATCTCTGATGGAT  1100

Qy     261  IleProGluSerGlnAsnGluArgAspPheValLeuArgValCysGlyArgAspGluTyr  280
              |||||||||||||||||||||||||||::::|||||||||||||||||||||||||||
Db    1101  ATTCCCGAAAGCCAAAGCCAACAGGATTTGTGCTGCGCGTCTGTGGCCGGGATGAGTAC  1160

Qy     281  LeuValGlyGluThrProIleLysGluAsnPheGlnTrpValArgGlnCysLeuLysAsnGly  300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1161  CTGGTGGGGGAAACGCCCATCAAAGAAACTTCCAGTGGGTGAGGCACTGCCTCAAGAACGGA  1220

Qy     301  GluGluIleHisLeuValLeuAspThrProProAlaLeuAspGluValArgLys     320
              |||||||::::|||||||||||||||||||||||||||||||||||||||||||
Db    1221  GAAGAGATTCACGTGGTACTGGACACGCCTCCAGACCCGGCCCTAGACGAGGTGAGAGAAG  1280

Qy     321  GluGluTrpProLeuValAlaAspAspCysThrGlyValThrGlyValThrHisGluGlnLeuThr  340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1281  GAAGAGTGGCCGCTGGTGGCAGACTGCACGGGAGTCACCGGCTACCATGAGCAGTTACC  1340

Qy     341  IleHisGlyLysAspHisGluSerValPheThrValSerLeuTrpAspCysAspArgLys  360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1341  ATCCACGGCAAGGACCACGAGAGTGTGTTCACCGTGTCCCTGTGGGACTGCGACCGCAAG  1400
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Qy   361 PheArgValLysIleArgGlyIleTyrIleAspIleProValLeuProArgThrAlaAspLeuThr 380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1401 TTCAGGGTCAAGATCAGAGGCATTCATATTGATATCCCCGTCCTGCCTCGCACCGCCGACCTCACA 1460

Qy   381 ValPheValGluAlaAsnIleGlnTyrGlyIleGlnIleValLeuCysGlnAsnArgThrSer 400
         |||||||||| |:::||||||||||:|||||||||||| ::|||
Db  1461 GTTTTTGTAGAGGCAAACATCCAGCAGTGGCAACAAGTCCTTTGCCAAGGAGAACCAGC 1520

Qy   401 ProLysProPheThrGlyGluValLeuTrpAsnValLeuTrpPheLeuGluSerIleLysIle 420
         |||||||||||||||||||||||||||||||||||||||||||||||
Db  1521 CCCAAGCCTTTCACAGGAGAAGTGCTGTGGAATGTGCTTGAGTTCAGTATCAAAAATC 1580

Qy   421 LysAspLeuProLysGlyAlaLeuLeuLeuAsnLeuGlnIleTyrCysGlyLysLysAlaProAla 440
         |||||||||||||||||||||||||||||||||||||||||||||||
Db  1581 AAAGACTTGCCCAAGGGGGCTCTACTGAACCTCCAGATCTACTGCGGTAAAGTCCAGCA 1640

Qy   441 LeuSerGlyLysLysThrSerAlaGluMetProSerProLysSerGlyGlyLysLysAlaGlnLeu 460
         |||||||||||||||||||||||||||||||||||||||||  ::|
Db  1641 CTGTCCAGGCAAGGCCTTCTGCAGAGTCCCCCAGTTCTGAGTCCAAGGGCAAAGTTCGGCTT 1700

Qy   461 LeuTyrTyrValAsnLeuLeuLeuIleAspHisArgPheLeuLeuArgHisGlyValGluTyr 480
         |||||||||||||||||||||||||||||||||||||||||||
Db  1701 CTCTATTATGTGAACCTGCTGCTTATAGACCACCGTTTCCTCCTGCGGCCGTGAGAATAC 1760

Qy   481 ValLeuHisMetTrpGlnLeuSerGlyLysGlyValAspGlnGlySerPheAsnAlaAlaAsp 500
         ||||||||||||||||||||:::||||||||||||||||||||
Db  1761 GTCCTCCACATGTGGCAGATATCTGGAGGGAAGAGACCAAGGAAGCTTCAATGCTGAC 1820

Qy   501 LysGluThrSerAlaThrAsnProAspLysProLysGluSerMetSerIleLeuSerLeuLeu 520
         |||||||||||||||||||||||||||||||||||||||||
Db  1821 AAACTCACGTCTGCCACGAACTAACCCAGAACAAGGAGAACTTCAATGTCCATCTCCATTCTCTG 1880

Qy   521 AspAsnTyrCysHisProIleAlaLeuProArgProHisProThrArgProAspGlyLeuGly 540
         |||||||||||||||||||||||||||||||||||||||||
Db  1881 GACAATTACTGCCACCCCGATAGCCCTGCTAAGCCCCCACCCCCTGACCCGGAGGG 1940

Qy   541 AspArgValAlaArgAlaGluMetProIleLeuGlnLeuLysGlnLeuLeuLeuAlaAlaIleIleAla 560
         |||||||||||||||||||||||||||||||||||||||||
Db  1941 GACCGGGTTGCGAGCGAGATGCCAAATGCCAACCAGCTTCGCAAGCAATTGGAGGCGGATCATAGCC 2000

Qy   561 ThrAspProProLeuAsnProLeuAsnThrAlaGluAspArgAlaAlaLeuAspLeuPheArgTyr 580
         |||||||||||||||||||||||||||||||||||||||||
Db  2001 ACTGATCCATCCTTAACCCTCACACGACCAGGAGGACCAAAGAATTGCTCTGGCATTTAGATAC 2060

Qy   581 GluSerLeuLysAspProLysAlaThrTyrProLysLeuPheSerSerValLysTrpGlyGln 600
         |||||||||||||||||||||||||||||||||||||||||
Db  2061 GAAAGCCCTTAAGCACCCAAAAGCAACTTATCCTAAGCTATTTAGTTCAGTGAAATGGGGACAG 2120

Qy   601 GlnGluIleValAlaAlaLysThrTyrGlnLeuLeuLeuLeuAlaLysArgGluValValTrpAspGlnSer 620
         |||||||||||||||||||||||||||||||||||||||||
Db  2121 CAAGAAATTGTGGCCAAAACATACCAAACTACTGTTTGGCCAAGAGGGAAGTCTGGGATCAAAGT 2180

Qy   621 AlaLeuAspArgValAlaAsnPheSerAspGluAsnVal 640
         |||||||||||||||||||||||||||||||||||
Db  2181 GCTTTGGATCGTGTTGCTAACGAGTCCAACTTCTCAGATGAAAATGTA 2240

Qy   641 ArgAlaIleAlaAlaValAlaGlnValGlnLysLeuSerLeuGluAspAspValLeuHisTyrLeu 660
         |||||||||||||||||||||||||||||||||||||||||
Db  2241 AGAGCCATTGCAGTTGCACAAGTCCAGAAACTGTCTGAGGACGATGTGCTTCACTACCTT 2300

Qy   661 LeuGlnLeuValLeuGlnAlaLysLysThrTyrProTyrHisAspSerAlaAlaArgPhe 680
         |||||||||||||||||||||||||||||||||||||||||
Db  2301 CTACAATTGGTCCAGGCTGTGAAATTGACCATACCATGACTCCAGATTT 2360

Qy   681 LeuLeuLysArgGlyLeuValArgGlyAsnLysArgIleGlyLysHisPheTrpPheLeuAsnArg 700
         |||||||||||||||||||||||||||||||||||||||||
Db  2361 CTGCTGAAGCGTGGTTTAAGAAACAAAGAATGGTCACTTTTTTGTTTTGGTTCTTGAGA 2420

Qy   701 SerGluIleGluAlaGlnSerArgHisTyrGlnArgIleTyrGlnAsnArgPheAlaValIleLeuLeuAlaTyr 720
         |||||||||||||||||||||||||||||||||||||||||
Db  2421 AGTTGAGATAGCCCAGTCCAGAACTATCCAGAGAGTTCGCTGTGAATTCGTGATTCTGGAAGCCTAT 2480


Qy   721 LeuArgGlyCysGlyThrAlaMetLeuHisAspPheThrGlnGlnValGlnValIleValAsp 740
         ||||||||||||||||||||||||||||||||||||||||||:::
Db  2481 CTGAGGGGCTGTGGCACAGCCATGTTGCACGACTTTACCCAACAGGTCCAAGTAATCGAG 2540

Qy   741 MetLeuGlnLysValThrIleAspIleLysSerLeuSerAlaGluLysTyrAspValSer 760
         |||||||||||||||||||:::|||||||||||||||||||||
Db  2541 ATGTTACAAAAAGTCACCCTTGATATTAAATCGCTCTCGCTGAAAAGTATGACGTCAGT 2600

Qy   761 SerGlnValIleSerGlnLeuLysGlnLysLeuGluAsnLeuGlnAsnLeuAsnLeuPro 780
         |||||||||||||||||||||||||||||||||||||||||
Db  2601 TCCCAAGTTATTTCACAACTTAAACAAAAGCTTGAAAACCTGCAGAATTCTCAACTCCCC 2660

Qy   781 GlnSerPheArgValProGlyTyrAspProGlyLeuLysLysGlyAlaLeuValIleGluLysLys 800
         :::|||||||||||||||||||||||||||||||||||||||
Db  2661 GAAAGCTTTAGAGTTCCATATGATCCTGGACTTAAAAAGGGCTGGCAATTGAAAAA 2720

Qy   801 CysLysValMetAlaSerLysLysProLeuTrpLeuGluLysLysCysGlyAlaAspPro 820
         |||||||||||||||||||||||||||||||||||||||||
Db  2721 TGTAAAGTAATGGCCTCAAGAAAACACCATGCTTGAGTTTAAATGTCGGCGATCCT 2780

Qy   821 ThrAlaLeuSerAsnGluThrLeuGlyLysIleIlePheLysHisGlyAspAspLeuArgGln 840
         ||||||||||||||||||||||||||||||||||||||
Db  2781 ACAGCCCTATCAAATGAAACAATTGAATTATCTTTAAACATGGTGATGATCTCGCCAA 2840

Qy   841 AspMetLeuIleLeuGlnIleLeuArgIleMetGluSerIleThrGluThrGluSerLeu 860
         |||||||||||||||||||||||||||||||||||||||||
Db  2841 GACATGTTATTTACAGATTCTACGAATCATGAGTATTGGAGACTGAATCTTTG 2900

Qy   861 AspLeuCysLeuLeuProTyrGlyCysIleSerThrGlyIleLeuAspLysLysMetIleGlu 880
         |||||||||||||||||||||||||||||||||||||||||
Db  2901 GATCTATGCCCTCTGCCATATGGTTGCATTTCAACTGGTGACAAAATAGGAATGATCGAG 2960

Qy   881 IleValLysAspAlaThrThrIleAlaLysIleGlnGlnSerThrGlyValGlyAsnThrGly 900
         |||||||||||||||||||||||||||||||||||||||||
Db  2961 ATTGTGAAAGACGCCACGACAATTGCCAAAATTCAGCAAAGCACAGGAGTGGGCAACACGGGA 3020

Qy   901 AlaPheLysAspGluValLeuSerHisTrpLeuLysGluLysSerCysProIleGluGluLys 920
         ||||||||||:::|||||||||||||||||||||||||
Db  3021 GCATTTAAAGATGAAGTCCTGAATCACTGGCTAAAGGAGAAAATCCCCTACTGAAGAAAAG 3080

Qy   921 PheGluAlaAlaValAlaValGluArgHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeu 940
         |||||||||||||||||||||||||||||||||||||||||
Db  3081 TTTCAGGCAGCAGTGGCAGTGGAGAGATTGTTTATTCCTGGCACCGTGTGTGGCAACCTTT 3140

Qy   941 ValLeuGlyIleGlyAspArgHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeu 960
         |||||||||||||||||||:::|||||||||||||||||||
Db  3141 GTTCTCGGAATAGGCGACAGGCACAATAATATTATGATCAGCGAGACAGGAAACCTA 3200

Qy   961 PheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheGlyLysIleAsnLys 980
         |||||||||||||||||||||||||||||||||||||||||
Db  3201 TTTCATATTGACTTCGGGCACATTCTTGGGAATTACAAAAGTTTCTGGGCATTAATAAA 3260

Qy   981 GluArgValProPheValLeuThrProAspPheValMetGlyThrSerGlyLys 1000
         |||||||||||||||||||||||||||||||||||
Db  3261 GAGAGAGTGCCATTTGTGCTAACCCCTGACTTCGTGATGGGAACTTCTGGAAAG 3320

Qy  1001 LysThrSerLeuHisPheGlnLysPheGlnAspValCysValLysAlaTyrLeuAlaLeu 1020
         |||||||||||||||||||||:::||||||||||||||
Db  3321 AAGACAAGCCCACACTTCCAGAAATTTCAGGACGTCTGTGTTAAGGCTTATATTAGCCCTT 3380

Qy  1021 ArgHisHisThrAsnLeuLeuIleIleLeuPheSerMetMetLeuMetThrGlyMetPro 1040
         |||||||||||||||||||||||||||||||||||||||||
Db  3381 CGTCATCACACAAAACCTACTGATCATCCGTGTTCCATGATGCTGATGACAGGAATGCCC 3440

Qy  1041 GlnLeuThrSerLysGluAspIleIleArgAspAlaLeuThrValGlyLysLysSer 1060
         |||||||||||||||||||:::||||||||||||
Db  3441 CAGTTAACAAGCAAAGAAGACATTGAATATATCCGGGATGCCCTCACAGTGGGGAAAAAT 3500

Qy  1061 GluGluAspAlaLysLysTyrPheLeuAspGlnIleGluValCysArgAspLysGlyTrp 1080
         |||||||||||||||||||||||||||||||||||||||||
Db  3501 GAGGAGGATGCCAAAAAGTATTTTCTGGATCAGATCGAAGTTTGCAGAGACAAAGGATGG 3560

Qy  1081 ThrValGlnPheAsnTrpPheLeuHisLeuValLeuGlyIleLeuLysGlnGluHis 1100
```

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Db   3561  ACTGGTGCAGTTAATTGGTTCTACATCTGTCTTGGCATCAAACAAGGAGAGAAACAT  3620
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1101  SerAla  1102
            ||||||
Db   3621  TCAGCC  3626
```

```
Score:                5523.50          Matches:        1049
Percent Similarity:   97.10%           Conservative:     21
Best Local Similarity: 95.19%          Mismatches:       31
Query Match:          95.40%           Indels:            1
DB:                                    Gaps:              1

US-09-974-573-1 (1-1102) x AAS14367 (1-5397)

Qy    1  MetGluLeuGluAsnTyrGluGlnProValLeuGlnProValLeuAspAsnArgArgArgArg  20
Db  324  ATGGAGCTGGAGAACTATAAACAGCCCGTGGTGCTGCAGACGAGAGGAGACAACTGCGAAGGCGC  383

Qy   21  ArgArgMetLysProArgSerThrAlaAlaSerLeuSerSerMetGluLeuIleProIle  40
Db  384  CGGAGGATGAAGCCGCGCAGT---GCTGCCAGCCTGTCCTCCATGGAGCTCATCCCCATC  440

Qy   41  GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeuLeuHis  60
Db  441  GAGTTCGTGCTGCCCACAGCCAGCGCAAATGCAAGACGCCAAACGGGCCTGCTGCAC  500

Qy   61  ValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnValTrpLeuArgAlaLeuGlu  80
Db  501  GTGGCCGGCCACGGCAACGTGGAGCAGATGAAGGCCCAGGTGTGGCTGCGAGCGCTGGAG  560

Qy   81  ThrSerValSerAlaAspPheTyrHisArgLeuGlyTyrProAspHisPheLeuLeuLeuTyr  100
Db  561  ACCAGCGTGGGCGGGACTTCTACCACCGGCTGGGACCGGCATCACTTCCTCCTGCTCTAT  620

Qy  101  GlnLysGlyGlnGlnTrpTyrAspLysTyrGlnLeuTyrAspIleValValGlnThrLeuAsp  120
Db  621  CAGAAGAAGGGGCAGTGGTACGACAAGTACCAGCTGGTGCAGACCCTGGAC  680

Qy  121  CysLeuArgTyrTrpLysValLeuHisArgSerProGlyGlnIleHisValValGlnArg  140
Db  681  TGCCTGCGCTACTGGAAGGCCACGAGCACCGGAGATCCACCTGGTGCAGCGG  740

Qy  141  HisAlaProSerGluGluThrLeuAlaPheGlnArgGlnLeuAsnAlaLeuIleGlyTyr  160
Db  741  CACCCGCCCTCCGAGGAGTCCCAAGCTTCCAGCGACCTCACCGGCCTCGATTGGCTAT  800

Qy  161  AspValThrAspValSerAsnValHisAspAspGluLeuPheThrArgArgLeu  180
Db  801  GACGTCACTGACGTGCAGCAACGTGCACGACGATGAGCTGGAGTTCACGCGCCGTGGCTTG  860

Qy  181  ValThrProArgMetAlaGlyValAlaGlyValArgProLeuTyrAlaMetHisPro  200
Db  861  GTGACCCCGCGCATGGCAGGCGTGGCCGGAGTGCAGCCGCTCTACGCCATGCACCCG  920

Qy  201  TrpValThrSerLysProLeuProGluTyrLeuLeuLysLysIleThrAsnAsnCysVal  220
Db  921  TGGGTGACGTCCAAGCCCTTCCCGGAGTACCTGTGGAAGAAGATTGCCAACAACTGCATC  980

Qy  221  PheIleValIleHisArgSerThrThrSerGlnThrIleLysValSerAlaAspAspThr  240
Db  981  TTCATCGTCATTCACCGCAGCACCACCAGCCAGACCATTAAGGTCTCACCCGACCACACC  1040

Qy  241  ProGlyThrLeuGlnSerPhePheThrLysMetAlaLysLysLysSerLeuMetAsp  260
Db 1041  CCCGGCACCCTGCAGAGCTTCTTCACCAAGATGGCCAAGAAGAAATCTCTGATGGAT  1100

Qy  261  IleProGluGlnGlnAsnGluValArgAspPheValLeuArgValCysGlyTyrAspGluTyr  280
Db 1101  ATTCCCGAAAGCCAAAGCGAACAGGATTTTGTGCTGCGCGTGTGCGGGATGGAGTAC  1160

Qy  281  LeuValGlyThrProIleLysAsnPheGlnTrpValArgGlnCysLeuLysAsnGly  300
Db 1161  CTGGTGGGCGAAACGCCCATCAAAACTTCCAGTGGTGGAGGCACTGCCTCAAGAACGGA  1220

Qy  301  GluGluIleHisLeuValLeuAspThrProProAlaLeuAspProAlaLeuArgLys  320
Db 1221  GAAGAGATTCACGTGGTACTGACACGCCCTCAGACACGGGCCCTAGACGAGGTGGAAG  1280

Qy  321  GluGluTrpProLeuValAlaAspAspCysThrGlyValThrGlyValThrHisGluGlnLeuThr  340
```

RESULT 7
AAS14367
ID   AAS14367 standard; cDNA; 5397 BP.
XX
AC   AAS14367;
XX
DT   12-MAR-2002 (first entry)
XX
DE   cDNA encoding human p110gamma isoform of PI3-kinase.
XX
KW   Human; phosphatidylinositol 3-kinase; PI3K; p110gamma isoform;
KW   LASP-1; cancer; inflammatory disease; ophthalmic disorder; SH3 domain;
KW   autoimmune disease; inflammatory bowel disease; bacterial pneumonia;
KW   Type I diabetes mellitus; cytostatic; immunosuppressive; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   324..3629
FT   /tag= a
FT   /product= "p110gamma isoform of PI3-kinase"
XX
PN   WO20185986-A2.
XX
PD   15-NOV-2001.
XX
PF   10-MAY-2001; 2001WO-US15065.
XX
PR   10-MAY-2000; 2000US-203346P.
XX
PA   (ICOS-) ICOS CORP.
XX
PI   Sadhu C;
XX
DR   WPI; 2002-075252/10.
DR   P-PSDB; AAU09689.
XX
PT   Identifying a modulator of p110delta polypeptide binding to SH3
PT   domain-containing polypeptides e.g. LASP-1, comprising allowing the
PT   binding partners to interact in the presence and absence of a test
PT   compound -
XX
PS   Example 1; Page 71-77; 85pp; English.
XX
CC   The present invention relates to identifying a modulator of the
CC   phosphatidylinositol 3-kinase (PI3K; p110delta) enzyme that binds to
CC   the catalytic subunit via a SH3 domain-containing polypeptide such as
CC   LASP-1. Also described are methods of assaying the specific binding
CC   affinity of the PI3-kinase binding partner. Such modulators are useful
CC   for the treatment of diseases characterised by the undesirable or
CC   excessive activity of PI3Kdelta. For example the modulators can be used
CC   for inhibiting the growth or proliferation of cancer cells
CC   (e.g. malignant neoplasms of lymphoid and reticuloendothelial tissues,
CC   Hodgkin's lymphoma, leukaemias), inflammatory diseases (e.g. rheumatoid
CC   arthritis), ophthalmic disorders (e.g. allergic conjunctivitis),
CC   autoimmune diseases (e.g. systematic lupus erythematosus), inflammatory
CC   bowel diseases (e.g. chronic inflammatory bowel disease), inflammatory
CC   dermatoses (e.g. contact dermatitis; central or peripheral nervous
CC   system inflammatory disorders (e.g. meningitis), bacterial pneumonia,
CC   and Type I diabetes mellitus. The present sequence encodes for human
CC   p110gamma isoform of PI3k.
XX
SQ   Sequence 5397 BP; 1534 A; 1224 C; 1207 G; 1432 T; 0 other;

Alignment Scores:
Pred. No.:   0   Length: 5397

```
Qy   1061 GluGluAspAlaLysTyrPheLeuAspGlnIleGluValCysArgAspLysGlyTrp 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3501 GAGGAGGATGCTAAAAAGTATTTCTTGATCAGATCGAAGTTTGCAGACAAAGGATGG 3560

Qy   1081 ThrValGlnPheAsnTrpPheLeuHisLeuValLeuGlyIleLysGlnGlyLysHis 1100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3561 ACTGTGCAGTTTAATTGGTTTCTTCACATCTTGTCTTGGCATCAAACAAGGAGAAACAT 3620

Qy   1101 SerAla 1102
          ||||||
Db   3621 TCAGCC 3626
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RESULT 8
AAT58546
ID   AAT58546   standard; cDNA; 4137 BP.
XX
AC   AAT58546;
XX
DT   25-MAR-1997 (first entry)
XX
DE   Human phosphatidylinositol 3-kinase PI3K-gamma cDNA.
XX
KW   Phosphatidylinositol 3-kinase; gamma; PI3K; immunogen; immunoassay;
KW   cell proliferation; receptor-mediated signal transmission;
KW   histamine secretion; nerve cell differentiation; glucose transport;
KW   modulation; regulation; Alzheimer's disease; lipolysis; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             423..3575
FT                   /*tag= a
FT                   /product= PI3K-gamma
XX
PN   DB4445562-C1.
XX
PD   04-APR-1996.
XX
PF   20-DEC-1994; 94DE-4445562.
XX
PR   13-OCT-1994; 94DE-4436696.
XX
PA   (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI   Hanck T, Stoyanov B, Wetzker R;
XX
DR   WPI; 1996-172545/18.
DR   P-PSDB; AAW11577.
XX
PT   New phosphatidyl;inositol 3-kinase protein - useful as immunogen and
PT   for determn. of kinase activity
XX
PS   Claim 5; Page -; 10pp; German.
XX
CC   A 402 bp cDNA fragment was amplified from a human bone marrow
CC   library using PCR primers corresponding to amino acid sequences
CC   KNGDDLR and HIDFG. The amplified fragment was used to probe a human
CC   U937 cell cDNA library and several overlapping clones were isolated.
CC   The largest clone coded for a protein of 1049 residues. The protein
CC   is a novel phosphatidylinositol 3-kinase (PI3K) that differs in its
CC   regulatory mechanism from the known PI3K-alpha and -beta enzymes.
CC   The new enzyme has been designated PI3K-gamma. Another clone, coding
CC   for a PI3K-gamma of 1050 residues and having the present
CC   sequence, was then isolated. The enzyme can be used as an immunogen.
CC   The enzyme, antibodies against it or nucleic acid encoding it can be
CC   used for modulating cell proliferation, receptor-mediated signal
CC   transmission, histamine secretion, nerve cell differentiation,
CC   glucose transport and anti-lipolytic activity or for treating
CC   Alzheimer's disease.
CC   N.B. Although the claimed sequences are referred to by SEQ.ID.
CC   Numbers, a sequence listing did not appear in the original printed
CC   patent application.
```

```
XX
SQ   Sequence 4137 BP; 1127 A; 999 C; 1001 G; 1010 T; 0 other;

Alignment Scores:
Pred. No.:                          Length:              4137
Score:                  0           Matches:             1048
Percent Similarity:     96.92%      Conservative:        21
Best Local Similarity:  95.01%      Mismatches:          32
Query Match:            94.98%      Indels:              2
DB:                                 Gaps:                1

US-09-974-573-1 (1-1102) x AAT58546 (1-4137)

Qy     1 MetGluLeuGluAsnTyrGluGlnProValLeuArgGluAspAsnArgArgArgArg 20
           ||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db   324 ATGGAGCTGGAGAACTATAAACAGCCGGTGCTGAGAGAGGACAACTGCCGAAGGCGC 383

Qy    21 ArgArgMetLysProArgSerThrAlaAlaSerLeuSerSerMetGluLeuIleProIle 40
           |||||||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db   384 CGGAGGATGAAGCCCGGCAGT--GCTGCCAGCTGCTTCCTCCATGGAGCTCATCCCCATC 440

Qy    41 GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeuLeuHis 60
           ||||||||||||||||||||||||       |||:::|||||||||||||||||||||
Db   441 GAGTTCGTGCTGCCCACCAGCCAGCGCAAATGCAAGACCCCGGAAACGGCGCTGCTGCAC 500

Qy    61 ValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnValTrpLeuArgAlaLeuGlu 80
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   501 GTGGCCGGCCACGGCAACGTGGAGCAGATGAAGGCCCAGGTGTGGCTGCGAGCGCTGGAG 560

Qy    81 ThrSerValSerAlaAspPheTyrArgLeuGlyProAspHisPheLeuLeuLeuTyr 100
           |||||::::||||||||||||||||||||||||||||||||||||||||||||||
Db   561 ACCAGCGTGGGCGGGCGACTTCTACCACCGGCTGGGACCCGATCACTTCCTCCTGCTCTAT 620

Qy   101 GlnLysGlyGlnTrpTrpTyrGluIleTyrAspTyrValGlnGlnValValGlnThrLeuAsp 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   621 CAGAAGAGGGGGCAGTGGTACGAGATCTACGACTACGTGCAGCAGGTGGTGCAGACTCTGGAC 680

Qy   121 CysLeuArgTyrTrpLysValLeuHisArgSerProGlyGlnIleHisValValGlnArg 140
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   681 TGCCTGCGCTACTGGAAGGCCACGCACCGCAGCCCCGGGCCAGATCCACCTGGTCAGCGG 740

Qy   141 HisAlaProSerGluGluThrLeuAlaPheGlnHisArgGlnAsnAlaLeuLeuIleGlyTyr 160
           |||||||||||||||||||||||||:::||||||||||||||||||||||||||||||||||
Db   741 CACCCGCCCCTCCGAGAGTCCCGAGGAGACCCTGGCCTTCCAGCACCGCCAGAATGCTGCTAT 800

Qy   161 AspValThrArgValHisAspAsnValHisAspAspAlaGlyLeuGlyPheThrArgArgLeu 180
           |||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||||
Db   801 GACGTGACTCGACGTCAGCAACGTGCACGACGATGAGGCGGGCCTCGGGTTCACGCGCCGTCTG 860

Qy   181 ValThrProArgMetAlaGlyValAlaGlyArgGlyAspProLysLeuTyrAlaMetHisPro 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||| :::
Db   861 GTGACCCCGGCATGGCGGGAGTGGCGGGCCAGCCGGACCCGAAGCTCTACGCCATGCACCCG 920

Qy   201 TrpValThrSerLysProLeuProGluProGluLeuLysTyrIleLeuThrLysAsnCysVal 220
           |||||||||||||||||||||||||||||||||||||||||||||||||:::|||
Db   921 TGGGTGACGTCCAAGCCCCTCCCGGAGTACCTGTGGAAGAGATTGCCAACAACTGCATC 980

Qy   221 PheIleValIleHisArgSerThrSerGlnThrIleLysValSerAlaAspAspThr 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   981 TTCATCGTCATTCACCGCAGCACCACCAGCCACCATTAAGGTCTCACCCGACGACACC 1040

Qy   241 ProGlyThrIleLeuGlnSerPhePheThrLysMetAlaLysLysSerLeuMetAsp 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1041 CCCGGGACCATCCTGCAGAGCTTCTTCACCAAGATGGCCAAGAAGAAATCCTGATGGAT 1100

Qy   261 IleProGluSerGlnAsnGluAspAspPheValLeuArgValCysGlyArgAspGluTyr 280
           |||||||||||||||||||||||||||||||||||||:::||||||||||||||||||
Db  1101 ATTCCCGAAAGCCAAAGCGAACAGGATTTTGTGCTGCGCGTCTGCGGGGATGAGTAC 1160

Qy   281 LeuValGlyGluThrProIleLysAsnPheGlnThrProValArgGlnCysLeuLysAsnGly 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1161 CTGGTGGGCGAAACGCCCATCAAAAACTTCCAGTGGTGGCACTGCCTCAAGAACGGA 1220
```

Qy 301 GluGluIleHisLeuValLeuAspThrProProAspProAlaLeuAspGluValArgLys 320
        |||||||||||||||||::::|||||||||||||||||||||||||||||||||||||
Db 1221 GAAGAGATTCACGTGACTGGTAACGCCTCCAGACGCCCTAGACCAGGTGAGGAAG 1280

Qy 321 GluGluTrpProLeuValAspAspCysThrGlyValThrGlyTyrHisGluGlnLeuThr 340
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1281 GAAGAGTGGCCGCTGGTTGACGACGGAGTCACCGGGTACCACGAGCAGCTTACC 1340

Qy 341 IleHisGlyLysAspHisGluSerValPheThrValSerLeuTrpAspCysAspArgLys 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1341 ATCCACGGCAAGGACCACGAGAGTGTGTTCACCGTGTCCCTGTGGGACTGCGACCGCAAG 1400

Qy 361 PheArgValLysIleArgGlyIleAspIleProValLeuProArgThrAlaAspLeuThr 380
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1401 TTCAGGGTCAAGATCAGAGGCATTGATATCCCTGTCCTCCCGAGAACCGCAGACCTCACA 1460

Qy 381 ValPheValGluAlaAsnIleGlyTyrGlyGlnValLeuCysGlnArgArgThrSer 400
        |||||||||||||||||||||:|:::|||||||||||||||||||||||||||||
Db 1461 GTTTTTGTAGAGGCAAACATCCAGTATGGGCCAACAGTCCTTTGCCAAAGGAGACCAGC 1520

Qy 401 ProLysProPheThrGluVulLeuTrpAsnValTrpLeuPheSerIleLeuLysIle 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1521 CCCAAGCCTTTCACAGAGGTGTTGTGGAATGTGTGGCTTTCAGTATCAAAATC 1580

Qy 421 LysAspLeuProLysGlyAlaLeuAsnLeuGlnIleTyrCysGlyLysLysAlaProAla 440
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1581 AAAGACTTGCCCAAAGGGGCTCTACTGAACCTCCAGATCTACTGCGGTAAAGGTTCCAGCA 1640

Qy 441 LeuSerGlyLysThrSerAlaGluMetProSerProGluSerLysLysGlyGlyAlaGlnLeu 460
        |||||||||||||||||||||||||||||||||::|||
Db 1641 CTGTCCAGCAAGGCCTCCGCAGAGTCCCCAGTCTCGAGTCCAAGGGCAAAGTTCGGCTT 1700

Qy 461 LeuTyrTyrValAsnLeuLeuIleLeuAspHisArgPheLeuLeuArgHisGlyGluTyr 480
        |||||||||||||||||||||||||||||||||||::|||||||||
Db 1701 CTCTATTATGTGAACCTGCTGATAGACCACCGCTTCCTCCTGCGTGGAGAATAC 1760

Qy 481 ValLeuHisMetTrpGlnLeuSerGlyLysGlyValGlySerPheAsnAlaAspAsp 500
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1761 GTCCTCCACATGTGGCAGATCTGGGAAGGGAGAGGACCAAGGAAGCTTCAATGCTGAC 1820

Qy 501 LysAspLeuThrSerAlaThrAsnProAspAspLysGluAsnSerMetSerIleLeuLeuLeu 520
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1821 AAATCAACCCTGACTTCTGCAACTAACCCAGACGACAAGGAGAACTCAATGTCCATTCTCTG 1880

Qy 521 AspAsnTyrCysHisProIleAlaLeuProLysHisArgProThrProAspGluGly 540
        ||||||||||||||||||||||||||||||::|||||||||||||||||||||
Db 1881 GACAATTACTGCCACCCGATAGCCCTGCCTAAGCATCAGCCCACCCCCGACGAGGG 1940

Qy 541 AspArgValAlaArgGluAlaGlyMetProAsnLeuArgLysGlnLeuGluAlaIleAlaAla 560
        |||||||||||||||||||||||||||||||||||||||||||||||
Db 1941 GACCCGGGTTGCAGAGAAGCAAGGAATGCCCAACCTTCGCAAGCAATTGGAGGCGATCATAGCC 2000

Qy 561 ThrAspProLeuAsnProLeuThrAlaAspLysProLysGlnGlnGluLeuLeuTrpHisProPheArgTyr 580
        |||||||||||||||||||||::||||||||||||||||||||||||
Db 2001 ACTGACCCTTAACCCTTAACTGCAGACAGAGGAAAAGAATTGCTCTGGCATTTTAGATAC 2060

Qy 581 GluSerLeuLysAspProLysAlaTyrProLysLeuPheSerSerValLysTrpGlyGln 600
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2061 GAAAGCCCTTAAGCACCCAAAAGCATATCCTAAGCTATTAGTTCAGTGAAAATGGGGACAG 2120

Qy 601 GlnGluIleValAlaLysThrArgLysTyrArgGlyValTrpAspGlnSer 620
        |||||||||||:|||:|||||||||||||||||||||||||||||||||||
Db 2121 CAAGAAATTGTGGCCAAAACACGCAAGTATCGTGGAGTGTGGGATCAAAGT 2180

Qy 621 AlaLeuAspValGlyLeuThrMetGlnLysLeuLeuLeuAspLysCysAsnPheSerAspGluAsnVal 640
        ||||||||||||||||||||||||||||||||||||||||||::||||||||||||||||
Db 2181 GCTTTGGATGTTGGGTTAACAATGCAGAAACTCCTCCTGGACAAATGTAACTTCTCAGATGAAAATGTA 2240

Qy 641 ArgAlaIleAlaValGlnLysGlyLeuGluSerLeuGluAspAspSerValLeuHisTyrLeu 660
        |||||||||||||||||||||||||||||||||::||||||||||||||||||||
Db 2241 AGAGCCATTGCAGTTCAGTTCAGGAACTGGAGGACTGTGAGGACGATGATTCTCTGCATTACCTT 2300

Qy 661 LeuGlnLeuValAlaGlnAlaValLysPheGluLeuIleLeuLeuIleLeuLeuPheSerArgAlaLeuValArgPhe 680

Db 2301 CTACAATGGTCCAGGCGTGAAATTGAACCATACCATGAGATAGGCCCTTGCCAGATT 2360

Qy 681 LeuLeuLysArgGlyLeuArgAsnLysArgIleGlyHisPhePheLeuPheLeuArg 700
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2361 CTGCTGAAGCGTGGTTAAGAACAAAAGAATTGGTCACTTTTGTTTGGTTCTTGAGA 2420

Qy 701 SerGluIleAlaGlnSerArgHisTyrGlnIleArgPheAlaValIleLeuGluAlaTyr 720
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2421 AGTGAGATAGCCCAGTCCAGACACTATCAGCAGAGGGTTCGCTGTGATTCTGGAAGCCTAT 2480

Qy 721 LeuArgGlyCysGlyThrAlaMetLeuHisAspPheThrGlnGlnValIleValIleAsp 740
        ||||||||||||||||||||||||||||||||||||||||||||||||||||::||||
Db 2481 CTGAGGGGCTGTGGCACAGCCATGCTGCACGACTTTACCCAACAAGTCCAAGTAATCGAG 2540

Qy 741 MetLeuGlnLysValThrIleAspIleLysLysSerLeuSerArgAlaGluLysTyrAspValSer 760
        ||||||||||||||||||||:|:::||||||||||||||||||||||||||||||
Db 2541 ATGTTACAAAAAGTCACCATCGATATAAAAAAGTCACTCCCTCGTGCTGAAAAATGACGTCAGT 2600

Qy 761 SerGlnValIleSerGlnLeuGlnLysGluGlnAsnLeuGlnAsnLeuAsnLeuAsnLeuPro 780
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2601 TCCCAAGTTATTTCACAACTTAAACAAAGAGCTGAAAACCTGCAGAATTCTCAACTCCCC 2660

Qy 781 GlnSerPheArgValProTyrAspProGlyLeuLysAlaGlyAlaGluValIleLeuGluLys 800
        :::|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2661 GAAAGCTTTAGAGTTCCATATGATCCTGGACTTAAAGCAGGAGCGCTGGCAATTGAAAAA 2720

Qy 801 CysLysValMetAlaSerLysLysGlyLysSerProLeuGluTrpLeuGluPheLysCysAlaAspPro 820
        |||||||||||||||||||||||||::|||||||||||||||||||||||||||||||
Db 2721 TGTAAAGGCAATGGCCTCCAAGAAAAACCACTATGGCTTGAGTTTAAATGTGCCGATCCT 2780

Qy 821 ThrAlaLeuSerAsnGluThrIleGlyIleLeuIleLeuGluArgIleMetGluSerIleLeuSerLeu 840
        ||||||::|||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2781 ACAGCCCTATCAAATGAAACAATTGGAATTATCTTTAAACATGGTGATGATCTGCGCCAA 2840

Qy 841 AspMetLeuIleLeuGlnIleLeuGluArgIleMetGluSerIleLeuGlyMetIleGlu 860
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2841 GACATGCTTATTCTCCTGCCATATGGTTGCATTTCAACTGGTGACAAAATAGGATGATCGAG 2900

Qy 861 AspLeuCysLeuLeuProTyrGlyCysIleSerThrGlyAspLysValIleGlyMetIleGlu 880
        :::|||||||||||||||||||::|||||||||||||||||::||||||||||||||||
Db 2901 GATCTATGCCTCCTGCCATATGGTTGCATTTCAACTGGTGACAAAATAGGATGATCGAG 2960

Qy 881 IleValLysAspAlaThrThrIleAlaLeuAlaLysGlnIleAsnSerThrValGlyAsnThrGly 900
        ||||||||||||||||||||||::|||||||||||||||||||||||||||||||||||||
Db 2961 ATTGTGAAAGACGCCACGACAGTCCTGGCTTTGGCAAAGCAAATAAATTCAGTGGGCAACACGGGA 3020

Qy 901 AlaPheLysAspGluValArgGluValTyrSerCysSerAlaGlyTyrCysValAlaProGluGluLys 920
        ::|||||||||||||||||||||::||||||||||||||||||||||||||||||||
Db 3021 GCATTTAAAGATGAAGTCCGAGAAGTCTACTCTTGCTCGGCTGGTTATTGTGTTGCTCCTGAAGAAAAG 3080

Qy 921 PheGlnAlaAlaValAlaGluValTyrSerCysValAlaTyrCysValAlaAlaThrPhe 940
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3081 TTTCAGGCAGCAGTGGCAGAGATTGTTATTCCTGTCGCCTACTGTGTGGCAACCTTT 3140

Qy 941 ValLeuValIleGlyValAspArgArgHisAsnAspAsnIleSerGluThrGlyGlyAsnLeu 960
        ||||||||||||||||||::|::|||||||||||||||||||||||||||||||||::||
Db 3141 GTTCTTGGAATAGGCAGGGACAGACAAGACAATATATGATCACCGAGACAGGAGAACCTA 3200

Qy 961 PheHisIleAspPheGlyHisPheLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLys 980
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3201 TTTCATATTGACTTCGGGCACTTCCTGGGAAATTACAAAAGTTTCCTGGGCATTAATAAA 3260

Qy 981 GluArgValProPheValLeuProArgAspPheValMetGlyValThrSerGlyLysLys 1000
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3261 GAGAGAGTGCCATTTGTGCTACCCCGACTTCGTCATGGGTGTGACTTCTGGAAAG 3320

Qy 1001 LysThrSerLeuHisPheGlnLysLeuGluGlnAsnValCysValAlaTyrLeuAlaLeu 1020
        ::::||||||||||||||||||||||||::|||||||||||||||||||||::|||
Db 3321 AAGACAAGCCCACTTGCGAAAATTCAGAAATTCAGCATCTGTGTTGCCTATCTAGCCCTT 3380

Qy 1021 ArgHisHisThrAsnLeuLeuIleLeuLeuPheSerMetMetThrGlyMetPro 1040

```
Db  3381 CGTCATCACACAAACCTACTGATCATCCTGTTCCATGATGCTGATGACAGGAATGCCC 3440

Qy  1041 GlnLeuThrSerLysGluAspIleArgIleArgAspAlaLeuThrValGlyLysSer 1060
         |||||||||||||||||||||||||||||||||||||||||||||||||:::
Db  3441 CAGTTAACAAGCAAGAGACACATTGAATATCCGGGATGCCCTCACAGTGGGAAAAAT 3500

Qy  1061 GluGluAspAlaLysLysTyrPheLeuAspGluValCys-ArgAspLysGlyTyr 1080
         ||||||||||||||||||||||||||||||||||||||  |||||||||||||
Db  3501 GAGGAGGATGCTAAAAAGTATTTTCTTGATCAGATCAAGTTGGCAGAGACAAGGATG 3560

Qy  1080 pThrValGlnPheAsnTrpPheLeuHisLeuValLeuGlyYlleLysGlnGlyGluLysHi 1100
         |||||||||||||||||||||||||||||||||||||||||||||
Db  3561 GACTGTGCAGTTAATTGGTTCTTACACATCTTGTTCTTGGCATCAAACAAGGAGAGAAACA 3620

Qy  1100 sSerAla 1102
         ||||||
Db  3621 TTCAGCC 3627
```

```
Alignment Scores:
Pred. No.:                              0          Length:         4134
Score:                            5440.00          Matches:        1046
Percent Similarity:                96.65%          Conservative:     20
Best Local Similarity:             94.83%          Mismatches:       35
Query Match:                       93.96%          Indels:            4
DB:                                    17          Gaps:              1
```

```
US-09-974-573-1 (1-1102) x AAT58545 (1-4134)

Qy    1 MetGluGluAsnTyrGluGlnProValValLeuArgGluAspAsnArgArgArgArg  20
        |||||||||||||||||            :|:|||
Db  324 ATGGAGGAGAACTATAAACAGCCCGTGGTGCTGAGAGAGGACAACTGCCGAAGGCGC 383

Qy   21 ArgArgMetLysProArgSerThrAlaAlaSerLeuSerMetGluLeuIleProIle  40
        ||||||||||||||||||||   :|||||||||||||
Db  384 CGGAGGATGAAGCCGCGCAGT---GCTGCCAGCCTGTCCATGGAGCTCATCCCCATC 440

Qy   41 GluPheValLeuProThrSerGlnAsnThrLysThrProGluThrAlaLeuLeuHis  60
        |||||||||||||||       |||:|||||||||||||
Db  441 GAGTTCGTGCTGCCCACCAGCCAGAACACGAAGACCCCGAAACGGCTGCTGCTGCAC 500

Qy   61 ValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnHisValTrpLeuArgAlaLeuGlu  80
        ||:||||||||||||||  :||||||||||
Db  501 GTGGCCGGCCACGGCAACGTGGAGCAGATGAAGGCCCAGCATGTGTGGCTGCGCGGCCTGGAG 560

Qy   81 ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspPheLeuLeuLeuTyr 100
        ||||||      ||||||||||||||||||||||||
Db  561 ACCAGT--GGCGCGGACTTCTACCACCGGCTGGGACCCGATCACTTCCTGCTGCTGTAT 618

Qy  101 GlnLysLysGlyGlnTrpTyrGlnGluTyrAspLysLysTyrGlnValValGlnThrLeuAsp 120
        ||||||||||||||||||||||||||||||||||
Db  619 CAGAAGAA-GGGCAGTGGTACGAGATCTACGACAAGTACCAGGTGGTGCAGACTCTGGAC 677

Qy  121 CysLeuArgTyrTrpLysValLeuHisGlySerProGlyGlnIleHisValValGlnArg 140
        |||||||||||||||||||||||||||
Db  678 TGCCTGCGCTACTGGAAGGCCACCACCGGACCCGGCCAGATCCACCTGGTGCAGCCG 737

Qy  141 HisAlaProSerGluGluThrLysAlaPheGlnAsnAlaGlnLeuAsnAlaLeuLeuGlyTyr 160
        |||||||:::          ||||||||
Db  738 CACCCGCCCTCCGAGGAGTCCAAGGCTTCCAGGCCAGTCAGCTGAGTAGC 797

Qy  161 AspValThrAspValSerAsnValHisAspAspGluLeuGluPheThrArgArgArgLeu 180
        |||||||||||||||||||||||||||||
Db  798 GACGTCACTGACGTCAGCAACGTGCACGACGATGAGCTGGAGTTCACGCGCCGTGGCTTG 857

Qy  181 ValThrProArgMetAlaGluValAlaIleAlaGlyArgAspProLeuTyrArgMetHisPro 200
        |||||||||||||||||||||||||||||||||||||
Db  858 GTGACCCCGCGCATGGCGGAGGTGGCCAGCCGGCGACCCCCAAGCTCTACGCCATGCACCCG 917

Qy  201 TrpValThrSerLysProLeuProGluTyrLeuGluLysLysLeuThrAsnAsnCysVal 220
        ||||||||||||||||||||||||:::
Db  918 TGGGTGACGTCCAAGCCCCTCCCGAGTACCTGGAGAAGAAGTTGCCAACAACTGCATC 977

Qy  221 PheIleValIleHisArgSerThrSerGlnThrThrLeuLysValSerAlaSerAlaAspThr 240
        |||||||||||||||||||||||||||
Db  978 TTCATCGTCATTCACCGCAGCACCAGCCAGACCATTAAGGTCTCACCCGACGACACC 1037

Qy  241 ProGlyThrIleLeuGlnSerPhePheThrLysMetAlaLysLysSerLeuMetAsp 260
        |||||||||||||||||||:::
Db 1038 CCCGGCACCATCCTGCAGAGCTTCTTCACCAAGATGGCCAAGAAGAAATCTCTGATGGAT 1097

Qy  261 IleProGluGlnAsnGluArgAspPheValLeuArgValCysGlyArgAspGluTyr 280
        ||||||||||||||::::::
Db 1098 ATTCCCGAAGCCAAAGCCAACAGGGATTTTGTGCTGCGCGTGTGCGGCCGGGATGAGTAC 1157

Qy  281 LeuValGlyGluThrProIleLeuAsnPheGlnTrpValArgGlnCysLeuLysAsnGly 300
```

```
Db   1158 CTGGTGGGCAAACGCCCATCAAAAACTTCCAGTGGGTGGGTGAGGCACTGCCTCAAGAACGGA 1217
          ||||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||
Qy    301 GluGluIleHisLeuValLeuAspThrProProAspProAlaLeuAspGluValArgLys 320
          GAAGAGATTCACGTGGTACTGGACACGCCTCCAGACGCCGGCCCTAGACGAGGTGAGGAAG 1277
Db   1218 |||||||||||||||||||||||:::|||||||||||||||||||||||||||||||||||||
Qy    321 GluGluTrpProLeuValAspAspCysThrGlyValThrGlyValTyrHisGlyGlnLeuThr 340
          GAGGAGTGGCCGCTGGTGGACGACTGCACGGGAGTCACCGGCGTCTACCATGGAGCAGCTGACC 1337
Db   1278 ATCCACGGCCAAGGACCACGAGAGTGTGTTCACCGGTCCCTGTGGGACTGCCGACCGGCAAG 1397
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    341 IleHisGlyGlyLysAspHisGluSerValPheThrValSerLeuTrpAspCysArgArgLys 360
          AGTGAGATAGCCCAGTCCAGACACTATCAGCAGACCACTATCAGCAGCCTAT 2477
```

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Qy  1021  ArgHisThrAsnLeuLeuIleIleLeuPheSerMetMetGlyMetPro  1040
          |||||||||||||||||||||||||||||||||||||||||||||
Db  3378  CGTCATCACACAAACCTACTGATCATCCTTCTCCATGATGCTGATGATGGAATGCCC  3437

Qy  1041  GlnLeuThrSerLysGluAspIleGluTyrIleArgAspAlaLeuThrValGlyLysSer  1060
          |||:|||||||||||||||||||||||||||||||||||||||||:|||
Db  3438  CAGTTAACAGCAAAGAGACATTGAATATATCCGGAGATGCCCTCACAGTGGGGAAAAAT  3497

Qy  1061  GluGluAspAlaLysLysTyrPheLeuAspGlnIleGluGluValCys-ArgAspLysGlyTr  1080
          |||||||||:||||||||||||||||||||||||||||||||  ||||||||||
Db  3498  GAGGAGGATGCTAAAAAGTATTTTCTTGATCAGATCGAAGAAGTTGGCAGAGACAAAGGATG  3557

Qy  1080  pThrValGlnPheAsnTrpPheLeuHisLeuValLeuGlyIleLeuLysGlyIleGlyGluLysHi  1100
          |||||||||||||||||||||||||||||||||||||||||||
Db  3558  GACTGTGCAGTTTAATTGGTTTCACATCTTGTCTTGGCATCAAACAGGGAGAGAAACA  3617

Qy  1100  sSerAla  1102
          ||||||
Db  3618  TTCAGCC  3624
```

```
CC  increased under these conditions. Cells containing constructs such as
CC  this, are useful in assays for detecting compounds involved in cell
CC  growth regulation. It is also used as the basis for detecting
CC  compounds for treating cancers and the formation of blood vessel
CC  plaques.
XX  (Updated on 25-MAR-2003 to correct PN field.)
SQ  Sequence 3498 BP; 1148 A; 627 C; 721 G; 1002 T; 0 other;

Alignment Scores:
Pred. No.:                            3498
Score:                2.44e-129       Length:         3498
Percent Similarity:   1467.50         Matches:        382
                      51.49%          Conservative:   205
Best Local Similarity:  33.51%        Mismatches:     404
Query Match:            25.35%        Indels:         149
DB:                                   Gaps:           39
```

```
US-09-974-573-1 (1-1102) x AAQ57012 (1-3498)

Qy   23  MetLysProArgSerThrAlaAlaSerLeuSerSerMetGluLeuIlePro----------  39
         :::   |||
Db    1  ATGCCTCCAAGACCATCATCAGGTGACCTGTGGGCATCCACTTGGTGCCCCAAGAAATC  60

Qy   40  ---IleGluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeu  58
         :::|||   ||||
Db   61  CTAGTAGAATGTTTACTTACCACAAATGGATGATAGTAGCT--  99

Qy   59  LeuHisValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnValTrpLeuArgAla  78
         |||         :::     |||
Db  100  TTAGAATGCCCCGTGAGGCTACGTTAATAACGATAAAAGCATATTAAAGAAGCA  159

Qy   79  LeuGluThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeu  98
         :::
Db  160  AGAAAATACCCTC------CATCAACTTCTTCAAGATGAATCTTCTTAC  204

Qy   99  LeuTyrGlnLysLysGlyGlnTrpTyrGlnIleTyrGluIleThrValValGlnThr  118
         :::
Db  205  ATTTTCGTAAGTGTACCCAAGAAGCAGAAAAGGAGGAAGAATTTTGATGAAAACAACGA  264

Qy  119  LeuAspCysLeuArgTyrTrpLysValLeuHisArgSerProGlyGlnIleHisValVal  138
         :::   :::
Db  265  CTTTGTGACCCTTCGGCTTTTTCAACCCTTT------TTAAAAGTAATT  306

Qy  139  GlnArgHisAlaProSerGluGluThrLeuAlaPheGlnArgGlnLeuAsnAlaLeuIle  158
         :::
Db  307  GAACCAGTAGGCAACCGTGAAGAAAAGATC---CTCAATCGAGAAATTGGTTTTGCTATC  363

Qy  159  GlyTyrAspValThrAspValSerAsnValHisAspAsnCysValPheThrArg  178
         |||         :::
Db  364  GGCATGCCAGTGTGTGAATTCGATATGGTTAAAGATCCAGAAGTACAGGACTTCCGAAGA  423

Qy  179  ArgLeuValThrProArgMetAlaGluValAlaGlyAlaArgAsp----------  192
         :::
Db  424  AATATTCCAATGTTTGTAAAGAGCTGTGAGATCTTAGGGATCTTAATTCACCTCATAGT  483

Qy  193  ProLysLeuTyrAlaMetHisProTrpValThrSerLysPro---LeuProGluTyrLeu  211
         :::
Db  484  AGAGCAATGTATGTTTATCCCCAAATGAAGAATTCACCAGACTGCAAAGCACATA  543

Qy  212  LeuLysLysIleThrAsnAsnCysValPheValIle---------His  225
         :::   |||
Db  544  TATAAAAAATTGGATAAAGGGCAAATAAATAGTGGTAATAATAGTTTCCAAAT  603

Qy  226  ArgSerThrSerGlnThrIleLysValSerAlaAspThrProGlyThrIleLeu  245
         :::
Db  604  AATGACAAACAGAAGTATACTCTGAAAAATCAACCATGACTGTGTGCCAGAACAAGTAATT  663

Qy  246  GlnSer=PhePheThrLysMetAlaLysLysLysSerLeuMetAspIleProGluSer---  264
         :::
Db  664  GCTGAAGCAATCAGGAAA----AAAACTCGAAGTAGTGTCTATCATCTGAACACTA  717

Qy  265  ------------GlnAsnGluArgAspPheValLeuArgArgValCysGlyArgAspGlu  279
         :::
```

```
RESULT 10
AAQ57012
ID   AAQ57012 standard; cDNA to mRNA; 3498 BP.
XX
AC   AAQ57012;
XX
DT   25-MAR-2003  (updated)
DT   31-AUG-1994  (first entry)
XX
DE   PtdIns 3-kinase 110 kD catalytic subnit cDNA.
XX
KW   110 kD catalytic subunit; phosphatidyl inositol 3-kinase;
KW   transformation; Schizosaccharomyces pombe; nmt promoter; thiamine;
KW   PtdIns 3-kinase; assay; detection; cell growth; regulation; cancer;
KW   blood vessel plaques; ss.
XX
OS   Bos taurus.
XX
FH   Key            Location/Qualifiers
FT   CDS            1..3207
FT                  /*tag= a
FT                  /product= P110
XX
PN   WO9403609-A1.
XX
PD   17-FEB-1994.
XX
PF   05-AUG-1993;  93WO-GB01651.
XX
PR   05-AUG-1992;  92GB-0016654.
XX
PA   (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
XX
PI   Goode NT, Nurse PM, Parker PJJ, Waterfield MD;
XX
DR   WPI; 1994-065697/08.
DR   P-PSDB; AAR46294.
XX
PT   Eukaryotic cells transformed with mammalian phospholipid or
PT   protein kinase DNA - useful in assays for compounds involved in
PT   cell growth regulation and for treating cancers
XX
PS   Disclosure; Fig 1; 71pp; English.
XX
CC   This sequence encodes the 110 kD catalytic subunit of the phosphatidyl
CC   inositol (PtdIns) 3-kinase. This sequence was transformed into
CC   Schizosaccharomyces pombe cells under the regulatory control of the
CC   nmt promoter in an embodiment of the invention. In the presence of
CC   thiamine the promoter is inactive and the cells carrying the PtdIns
CC   catalytic subunit plasmid grow as the parental strain. In the absence
CC   of thiamine the nmt promoter functions and the PtdIns 3-kinase
CC   catalytic subunit in induced. PtdIns activity is substantially
```

```
Qy   606 LysThrTyrGlnLeuLeuAlaLysArgGluValValGly 625
             :::|||
Db  1744 CAGATGTACTGCTTG----------------GTAAAAGATTGGCCTCCAATCAACCCTGAA 1788

Qy   626 LeuThrMetGlnLeuLeuAspCysAsnPheSerAspGluAsnValArgAlaIleAlaVal 645
             |||
Db  1789 CAGGCTATGGAGCTTCTGGACTGCAATACCCAGATCCTATGGTTCGAGGTTTGCTGTT 1848

Qy   646 GlnLysLeuGluSer---LeuGluAspAspValLeuHisTyrLeuLeuGlnLeuVal 664
             :::|||
Db  1849 CCGTGCTTAGAAAAATATTAACAGATGACAAACTTTCTCAGTACCTAATCAGCTAGTA 1908

Qy   665 GlnAlaValLysPheGluProTyrHisAspSerAlaLeuAlaArgPheLeuLeuLysArg 684
Db  1909 CAGGTACTAAAATATGAACAGTATTGGATAACCTGCTTGTGAGATTTTTACTCAAAAA 1968

Qy   685 GlyLeuArgAsnLysArgIleGlyHisPheLeueuTrpPheLeuArgSerGluIleAla- 704
Db  1969 GCGTTAACTAATCAAAGGATCGGTCACTTTTTCTTTTGGCATTTAAAATCTGAGATG--- 2025

Qy   705 GlnSerArgHisTyrGlnLnArgPheAlaValIleLeuGluAlaTyrLeuArgGlyCys 724
             :::|||
Db  2026 CACAATAAAACAGTTAGTACAGAGGGTTTGGCCTGCTTTGGAGTCCTATTGCGTGCATGT 2085

Qy   725 GlyThrAlaMetLeuHisAspPheThrGlnGlnValGlnValIleAspMetLeuGlnLys 744
Db  2086 GGGATGTATCTGAAGCAC---CTTAATAGGCAAGTTGAGGCTCGATCTCATTAAC 2142

Qy   745 ValThrIleAspIleLysSerLeuSerAlaGluLysTyrAspValSerGlnValIle 764
             :::|||
Db  2143 TTGACT---GACATT---CTCAAACAAGAGAGAAGGATGAAACACAAAAGGTA--- 2190

Qy   765 SerGlnLeuLysGlnLysLeuGluAsnLeuGlnAsn---------LeuAsnLeuProGln 781
             :::|||
Db  2191 ---CAGATGAAGTTTTTAGTTGAGCAAATGCGGGACCAGATTTCATGGATGCGTCCCAG 2247

Qy   782 SerPheArgValProTyrAspTyrAspProGlyLeuLysAlaGlyAlaLeuValIleGluLysCys 801
Db  2248 GGCTTTCGTGTCCCTCTAAACCCTGCTCATCAGCTGGGAAATCTCAGGCTTGAAGAGTGT 2307

Qy   802 LysValMetAlaSerLysLysAspHisCysLeuTrpLeuPheLysCysAlaAspProThr 821
             :::|||
Db  2308 CGAATTATGTCTTTCTGCAAAAAGGCCACTGTGGTTGAATTGGGAG----AACCCAGAC 2361

Qy   822 AlaLeuSer---------------AsnGluThrIleGlyIleIlePheLysHisGly 835
             :::|||
Db  2362 ATCATGTCAGAATTACACTTTCAGAACAATGAG------ATCATCTTTAAAAATGGG 2412

Qy   836 AspAspLeuArgGlnAspMetLeuLeuLeuGlnIleLeuArgIleMetGluSerIleTrp 855
Db  2413 GATGATTTACGGCAGATATGCTAACCCTTCAGATTATTCGCATATGGAAAATATCTGG 2472

Qy   856 GluThrGluSerLeuAspLeuCysLeuLeuProTyrGlyCysIleSerThrGlyAspLys 875
             :::|||
Db  2473 CAAAATCAAGGTCCTTGATCTTCGAATGTTACCTTATGGATGTCGTCGTGGTGACTGT 2532

Qy   876 IleGlyMetIleGluIleValLysAspAlaThrIleAlaLysIleGlnSerThr 895
Db  2533 GTGGGACTTATCGAGTGGTGAGAAATTCTCACACTATAAATGCAGATT---CAGTGTAAA 2589

Qy   896 ValGlyAsnThrGlyAla-----PheLysAspGluValLeuSerHisGluLysGlu 913
Db  2590 GGAGGGCCTGAAAGGTGCACTGCAGTTTAACAGCCACAGTCCATCAGTGCTCAAAGAC 2649

Qy   914 LysCysProIleGluGlyPheGlnAlaAlaValGluArgPheValTyrSerCysAla 933
Db  2650 AAGAACAAG---GGGGAAAATATGATGCGGCCATCGATTTGTTTACAGGATCATCATGCT 2706

Qy   934 GlyTyrCysValAlaThrPheValLeuGlyIleGlyAspArgHisAsnAspAsnIleMet 953
             :::|||
Db  2707 GGATATTGTGTTGCCACCTTCATTTTGGGATTGGGAGATCGTCACAATAGTAATATCATG 2766
```

```
Db   718 AAACTCTGTTTAGAATATCAGGCAAGTATATTTAAAAGTGTGGATGTGATGAA 777
             |||
Qy   280 TyrLeuValGlyGluThrProIleLysAsnPheGlnTrpValArgGlnCysLysLeuAsn 299
             :::|||
Db   778 TACTTCCTAGAAAAATATCCTCGAGTCAGTATTAGTAGTATAGAAGCTGTATAATGCT 837

Qy   300 GlyGluGluIleHisLeuValLeuAspThrProProAspProAlaLeuAspGluValArg 319
             |||
Db   838 GGGAGGATGCCCAATTTGATGCTG--------ATGGTAAAGAAAAGCCTC 879

Qy   320 LysGluGluTrpProLeuValAspAspCysGlyThrValThrGlyTyrHisGluGlnLeu 339
             ::: |||
Db   880 TATTCTCAACTGCCAATG-----GACTGTTTTCAAATGCCATCATATTCCAGACGCATC 933

Qy   340 Thr------IleHisGlyLysAspHisLeuSerValPheThrValSerLeu 354
             :::
Db   934 TCCACAGCTACGCCATAATGAATGGAGAA----------ACATCTACAAAATCCCTT 981

Qy   355 TrpAspCysAspArgLysPheArgValLys- 364
             :::
Db   982 TGGGTTAAATAGTGCACTCAGAATAAAAAATTCTTGTGCAACCTATGTGAATGTAAAT 1041

Qy   365 IleArgGlyIleLeuAspIleProValLeuProArgThrArgAlaAspLeuThrPheValGlu 384
             :::|||
Db  1042 ATTCGAGACATTGAC----------------AAGATTTATGTTCGA 1071

Qy   385 AlaAsnIleGlnIleTyrGlyValGlnLnValLeuCysGlnAsnArgThrSerProLysProPhe 404
Db  1072 ACAGGTATCTACCATGGAGGAGAACCCTTATGTGATATGTGAACACTCAAAGAGTACCT 1131

Qy   405 ThrGluValLeuTrpAsnValTrpLeuPheSerIleLeuLysAspLeuPro 424
             |||||
Db  1132 TGTTCCAATCCCAGGTGGAATGGAATGGCTGAATTACGATATATACAATTCCTGATCTTCCT 1191

Qy   425 LysGlyValAlaLeuLeuAsnLeuGlnIleIleTyrCysGlnIleLeuSerGlyLysLys 444
             :::|||
Db  1192 CGTGCAGCTCGACTTCGGCCTTTCCATT---TGT------TCTGTTAAAGGCCGA 1236

Qy   445 ThrSerAlaGluMetProSerProGluSerLysGlyGlyLysLysAlaGlnLeuLeuTyrTyrVal 464
Db  1237 AAAGAGGAACACTGTCCATTGGCCTGGGGA 1275

Qy   465 AsnLeuLeuIleAspHisArgPheLeuArgHisGlyGluTyrValLeuHisIleMet 484
             |||||
Db  1276 AATATAAACTTGTTTGATTACACAGATACTCTAGTATCCTGGAAAAATGCCTTTGAATCTT 1335

Qy   485 TrpGlnLeuSerGlyLysGlyAspAlaAspSerPheAsnAlaAspLysLeuThrSer 504
             |||
Db  1336 TGGGCCAGTACCTCATGGGACTAGAAGAT-----TTGCTGAACCCTATTGGTGTTACT-- 1386

Qy   505 AlaThrAsnProAspLysGluLeuGlnAsnSerMetSerIleSerIleLeuLeuLeuAspAsnTyrCys 524
             ::: |||
Db  1387 GGATCAAATCCAAATAAAGAA----ACTCCATGTTAGAGTTGGAGTTTGACTGGTTCAGC 1443

Qy   525 HisProIleAlaGluProLysHisProArgProThrProGluGlyAspArgVal--- 543
             |||
Db  1444 AGTGTGGTAAAGTTTCCAGATATGTCAGTGATTGAAGAGCATGCCAATGGTCGTGTATCC 1503

Qy   544 ---------------ArgAlaGluMetProAsn 549
             :::
Db  1504 CGTGAAGCAGGATTTAGTTATTCCCATGCAGGACTCGAGTGGTAACAGACTAGCTAGAGACAAT 1563

Qy   550 GlnLeuArg---------LysGlnLeuGluAlaIleIleAlaThrAspProLeuAsn 565
             :::|||
Db  1564 GAATTAAGAGAAAAATGATAAAGACAGCTCCGAGACAATTTGTACAGCATCCTCTATCT 1623

Qy   566 ProLeuThrAlaGluAspLysProGluPheArgTyrGluSerIleLeuLysAspAsp 585
             :::|||
Db  1624 GGAATCACTCAGCAAGAGAAGAATTTTCTGTGAGCAAGGCCACAGACTATTTGTCTAACTATC 1683

Qy   586 ProLysAlaTyrProLysPheSerSerValLysTrpGlyGlnGlnIleLeuValAla 605
             :::|||
Db  1684 CCCGAAATTGCTTCATGTTGCCACCTTCATTTTGGGATTGGGAACCTCTAGAATGAAGTAGCT 1743
```

CC   polymer is located at a predetermined position on the solid support, and
CC   the array comprises nucleic acid polymers which are specific for less
CC   than 100 genes other than the selected genes. The method is useful for
CC   determining tumour characteristics in a tissue sample taken from a
CC   patient. The present sequence represents a human lipid-associated gene
CC   related cDNA sequence, which is used in the exemplification of the
CC   present invention.
XX
SQ   Sequence 3424 BP; 1134 A; 618 C; 709 G; 963 T; 0 other;

Alignment Scores:
Pred. No.:   Length: 3424
Score: 2.95e-129   Matches: 1466.50
Percent Similarity: 51.52%   Conservative: 387
Best Local Similarity: 33.62%   Mismatches: 206
Query Match: 25.33%   Indels: 396
DB: Gaps: 163
                                                        24
                                                        40

US-09-974-573-1 (1-1102) x ABL59523 (1-3424)

Qy   19 ArgArgArgArgMetLysProArgSerThrAlaAlaSerLeuSerSerMetLysLeuIle   38
Db   1 AGGATCAGAACAATGCCTCCAAGACCATCAGTGACCTGTGGGCATCCACTGATG   60

Qy   39 Pro--------IleGluPheValLeuProThrSerGlnArgAsnThrLysThrPro   54
Db   61 CCCCCAGAATCCTAGTGACAATGTTTACTACCAAATGGATGATGTGACT--------   111

Qy   55 GluThrAlaLeuLeuHisValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnVal   74
Db   112 --------TTAGAATGCCTCCGTGAGGCTACCATTAGTAACTATAAAGCATGAACTA   159

Qy   75 TrpLeuArgAlaLeuGluThrSerValSerAlaSerAlaAspPheTyrHisArgLeuGlyProAsp   94
Db   160 TTTAAAGAAGCAAGAAAATACCCTC----------------CATCAACTTCTTCAAGAT   204

Qy   95 HisPheLeuLeuLeuTyrGlnLysGlyGlnTrpTyrGluIleTyrAspLysTyrGln   114
Db   205 GAATCTTCTTACATTTCGTAAGTGTTACCCAAGAAGCAGAAAGGGAAGAATTTTTTGAT   264

Qy   115 ValValGlnThrLeuAspCysLeuArgTyrTrpLysValLeuHisArgSerProGlyGln   134
Db   265 GAAACAAGACGACTTTGTGATCTTCGGCTTTTTCAACCATTT----------   306

Qy   135 IleHisValValGlnArgHisAlaProSerGluGluThrLeuAlaPheArgArgGlnLeu   154
Db   307 TTAAAGTAATTGACCAGTAGGCAACCGTGAAGAAAGATC--CTCAATCGAGAAATT   363

Qy   155 AsnAlaLeuLeuGlyTyrAspValTyrAspValSerAsnValHisAspAspGluLeuGlu   174
Db   364 GGTTTTGCTATCGGCATGCCAGTGTGCGAATTCAATTGATATGGTTAAAGATCCTGAAGTACAG   423

Qy   175 PheThrArgArgLeuValThrProArgMetAlaGluValAlaGlyValAlaGlyAsp----   192
Db   424 GACTTCCGAAGAGAAATTCTTAATGTTGTTAAAGAAGAGCTGTGGGATCTTAGGAT   483

Qy   193 ----------ProLysLeuTyrAlaMetHisProValThrSerLysPro---Leu   207
Db   484 TCACCTCATAGTAGAGCAATGATATGTCTATCCGCCACATGAGAATCTTCACCAGAGCTG   543

Qy   208 ProGluTyrLeuLeuLysIleThrAsnAsnCysValPheValIle----------   224
Db   544 CCAAGACCACATATATAATAAATTGGATAGAGGCCAAATATAGTGTGATTTGGGTAATA   603

Qy   225 ----------HisArgSerThrThrSerGlnThrIleLeuValSerAlaAspAspThrPro   241
Db   604 GTTTCTCCAAATAATGACAAGACAGAAGTATACTCTGAAAATCAACCATGACTGTGCCA   663

Qy   242 GlyThrIleLeuGlnSerPhePheThrLysMetAlaLysSerLeuMetAspIle   261
Db   664 GAACAAGTAATTGCTGAAGCAATCAGGAAA------AAAACTAGAAGTATGTTGCTATCA   717

Qy   262 ProGluSer----------GlnAsnGluArgPheValLeuArgValCys   275

Qy   954 IleSerGluThrGlyLysAsnLeuPheHisAspPheGlyHisIleLeuGlyGlyAsnTyrLys   973
Db 2767 GTTAAAGATGATGGACAACTGTTCATATAGAATTTGGATCACAAGAAG   2826

Qy   974 SerPheLeuGlyIleAsnLysGluGlyValProPheValLeuArgValProPheAspPheLeuPhe   993
Db 2827 AAAAAATTGGTTATAAACGAGAGCGGCGTGCCGTTGTTTTGACACCAAGATTCTTAATA   2886

Qy   994 ValMetGlyThrSerGlyLysLys------ThrSerLeuHisPheGlnLysPheGlnAsp   1011
Db 2887 GTGATTAGTAAGGAGGAGCCAAGAATGACACAAGAGACAAGAGAATTTGAGAGGTTTCAGGAG   2946

Qy 1012 ValCysValLysAlaTyrLeuAlaLeuArgHisHisThrAsnLeuLeuIleLeuLeuPhe   1031
Db 2947 ATGTGTTACAAGCCTTATCTAGCTATTCGGCAGCATGCCAATCCTCTTCATAAAATCTTTC   3006

Qy 1032 SerMetMetThrGlyMetProGlnLeuThrSerLysGluAspIleGluTyrIle   1051
Db 3007 TCAATGATGACTGGCCTCTGGAATGCCAGAACCTGCAATCTTTTGATGATATTGCATACATT   3066

Qy 1052 ArgAspAlaLeuThrValGlyLysSerGluGluAspAlaLysLysTyrPheLeuAspGln   1071
Db 3067 CGAAAGACCCTAGCTTTAGATAAAACTGAGCAAGGCTTTGGAGTATTCATGAAACAA   3126

Qy 1072 IleGluValCysArgAspLysGlyTrpThrValGlnPheAsnTrpPheLeuHisLeuVal   1091
Db 3127 ATGAATGATGCACCATGGTGGCTGGACAACAAAAATGGATTGGATCTTCCACACAATT   3186

RESULT 11
ABL59523
ID   ABL59523   standard; cDNA; 3424 BP.
XX
AC   ABL59523;
XX
DT   16-JUL-2002   (first entry)
XX
DE   Human phosphatidylinositol-3-kinase catalytic alpha cDNA SEQ ID NO:23.
XX
KW   Human; phosphatidylinositol-3-kinase catalytic alpha; enzyme;
KW   tumour; lipid associated gene; lipid metabolism; lipid synthesis;
KW   chromosome 3q26.3; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200227028-A1.
XX
PD   04-APR-2002.
XX
PF   27-SEP-2001; 2001WO-US30366.
XX
PR   28-SEP-2000; 2000US-0676052.
XX
PA   (ATAI-) ATAIRGIN TECHNOLOGIES INC.
XX
PI   Skinner MK, Patton JL, Chaudhary J;
XX
DR   WPI; 2002-402054/43.
XX
PT   Identifying tumor characteristics in a tissue sample taken from a
PT   patient, involves determining the copy number or expression level of
PT   genes associated with lipid metabolism, synthesis or action -
XX
PS   Example 1; Page 82-83; 111pp; English.
XX
CC   The present invention describes a method for identifying tumour
CC   characteristics, comprising measuring a copy number or expression level
CC   of at least two genes associated with lipid metabolism, synthesis, or
CC   action in cells from a patient tissue sample, and comparing the results
CC   with a copy number or expression level of the genes in a normal cell.
CC   Also described is an array of nucleic acid polymers immobilised on a
CC   solid support, comprising a solid support, at least two different nucleic
CC   acid polymers which are each specific for a different gene associated
CC   with lipid metabolism, synthesis or action, where each nucleic acid

This page contains a nucleotide/protein sequence alignment (Qy query vs. Db database) printed in landscape orientation. The alignment consists of paired rows labeled "Qy" and "Db" with flanking position numbers and match symbols (`|`, `:`). Representative position numbers and translated reading frames include:

```
1665 ATGGAGTCACAGACACTATTGTCTAACTACCCGAAATTCACCCAAATTGCTTCTGTC 1724
 595 rValLysTrpGlyGlnGlnGluIleValIleValAlaLysThrTyrGlnLeuLeuAlaLysArgGl 615
1725 TGTTAAATGGAATTCTAGAGATGAAGTAGCCCAGATGTATTGCTTG---------- 1770
 615 uValTrpAspGlnSerAlaLeuAspValGlyLeuThrMetGlnLeuLeuAspCysAsnPh 635
 ...
 923 aAlaValGluArgPheValTyrserCysAlaGlyLYrCysValAlaThrPheValLeuGl 943
2688 AGCCATTGACCTGTTTACACGTTCATGTCGTAGCTACCTTCATTTTGGG 2747
```

(The remainder of the page continues the same alignment format with Qy/Db sequence pairs and numeric coordinates.)

PT   compound   -

XX

PS   Example 1; Page 55-60; 85pp; English.

XX

CC   The present invention relates to identifying a modulator of the

CC   phosphatidylinositol 3-kinase (PI3K; pi10delta) enzyme that binds to

CC   the catalytic subunit via a SH3 domain-containing polypeptide such as

CC   LASP-1. Also described are methods of assaying the specific binding

CC   affinity of the PI3-kinase binding partner. Such modulators are useful

CC   for the treatment of diseases characterised by the undesirable or

CC   excessive activity of PI3kdelta. For example the modulators can be used

CC   for inhibiting the growth or proliferation of cancer cells

CC   (e.g. malignant neoplasms of lymphoid and reticuloendothelial tissues,

CC   Hodgkin's lymphoma, leukaemias), inflammatory diseases (e.g. rheumatoid

CC   arthritis), ophthalmic disorders (e.g. allergic conjunctivitis),

CC   autoimmune diseases (e.g. systematic lupus erythematosus), inflammatory

CC   bowel diseases (e.g. chronic inflammatory bowel disease), inflammatory

CC   dermatoses (e.g. contact dermatitis; central or peripheral nervous

CC   system inflammatory disorders (e.g. meningitis), bacterial pneumonia,

CC   and Type I diabetes mellitus. The present sequence encodes for human

CC   pi10alpha isoform of PI3k.

XX

SQ   Sequence 3424 BP; 1134 A; 618 C; 709 G; 963 T; 0 other;

Alignment Scores:

Pred. No.:   Length: 3424

Score: 2.95e-129   Matches: 387

Percent Similarity: 1466.50   Conservative: 206

Best Local Similarity: 51.52%   Mismatches: 396

Query Match: 33.62%   Indels: 163

DB: 25.33%   Gaps: 40

                     24

US-09-974-573-1 (1-1102) x AAS14365 (1-3424)

```
Qy    19 ArgArgArgMetLysProArgSerThrAlaAlaSerLeuSerMetGluLeuIle  38
             :::  ||||||||||||||||||||||||||||||||||||||||
Db     1 AGGATCAGAAGAACAATGCCTCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG  60

Qy    39 Pro--------IleGluPheValLeuProThrSerGlnArgAsnThrLysThrPro  54
             ::: ||||||| ::||||||||
Db    61 CCCCCAGAATCCTAGTGGAATGTTTACTACCAAATGAAATGGATGATAGTGACT-------  111

Qy    55 GluThrAlaLeuLeuHisValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnVal  74
             ||||||||   :::  ||||||||||
Db   112 --------TTAGAATGCCTCCGTGGAGCTACATTAGTAACTATAAGCATGAACTA  159

Qy    75 TrpLeuArgAlaLeuGluThrSerValSerAlaAspPheTyrHisArgLeuGlyProAsp  94
             :::  ||| |||||||||
Db   160 TTTAAAGAAGCAAGAAAATACCCTCTC----------CATCAACTTCTTCAAGAT  204

Qy    95 HisPheLeuLeuLeuTyrGlnLysLysGlyInTrpTyrGluIleTyrAspLysTyrGln  114
             :::::: ||||||||||
Db   205 GAATCTTCTTACATTTCGTAGTGTTACCCAAGAAGCAGAAGGAAGAATTTTTGAT  264

Qy   115 ValValGlnThrLeuAspCysLeuArgTyrTrpLysTrpLysHisArgSerProGlyGln  134
             |||||||||||||  ||||
Db   265 GAAACAAGACCGACTTTGTGATCTTCGGCTTTTTCACCCATT----------  306

Qy   135 IleHisValValGlnArgHisAlaProSerGluThrLeuAlaPheGlnArgGlnLeu  154
             ::: ||||||  :::  ||||||
Db   307 TTAAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATC---CTCAATCGAGAAATT  363

Qy   155 AsnAlaLeuIleGlyTyrAspValThrAspValSerAsnValHisAspLysGlyLeuGlu  174
             ||| :::  ||||||
Db   364 GGTTTTGCTATCCGCATGCCAGTGCCAATTGATTGATGGTTAAAGATCCTGAAGTACAG  423

Qy   175 PheThrArgArgLeuValThrProArgMetAlaGluValAlaGlyArgAsp---------  192
             ::::::: ||||||
Db   424 GACTTCCGAAGAAAATATTCTTAATGTTGTAAAGAAGCTGTGGGATCTTAGGGATCTTAAT  483

Qy   193 --------ProLysLeuTyrAlaMetHisProValThrSerLysPro---Leu  207
             ::::: |||||||||||
Db   484 TCACCTCATAGTAGAGCAATGTAGTCTATCCGCCACATGTAGAATCTTCACCAGAGCTG  543
```

The left column (rotated, reading bottom-to-top):

```
Qy   943 YIleGlyAspArgHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeuPheHisIl  963
             ||||||||||       :::  ||||||||||
Db  2748 AATTGGAGATCGTCACAATAGTAACATCATGTGAAAGACGATGGACAACTGTTCATAT  2807

Qy   963 eAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLysGluArgVa  983
             ||||||||   ::||||||||
Db  2808 AGATTTGGACACTTTTGGATCACAAGAAGAAAAAATTTGGTTATAAACGAGAACGTGT  2867

Qy   983 lProPheValLeuThrProAspPheLeuPheValMetGlyThrSerGlyLysLys-----  1001
             ||||||  :::::
Db  2868 GCCATTTGTTTGACACAGGATTTCTTAATAGTGATTAGTAAGGAGGCCAAGAATGCAC  2927

Qy  1002 -ThrSerLeuHisPheGlnLysPheGlnAspValCysValLysAlaTyrLeuAlaLeuAr  1021
             ||| ||||||||||
Db  2928 AAAGACAAGAGAATTGAGAGGTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCG  2987

Qy  1021 gHisHisThrAsnLeuLeuIleLeuLeuPheSerMetMetLeuMetThrGlyMetProGl  1041
             |||||||||||
Db  2988 ACAGCATGCCAATCTCTCATAAATCTTTTCCAATGAATGCTTGGCTCTCGGAATGCCAGA  3047

Qy  1041 nLeuThrSerLysGluArgAspIleGluTyrIleArgArgAlaLeuThrValGlyLysSerGl  1061
             ||| :::||||||
Db  3048 ACTACAAATCTTTTGATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGA  3107

Qy  1061 uGluAspAlaLysLysTyrPheLeuAspGlnIleGluValCysArgAspLysGlyTrpTh  1081
             ||| ||||||||||
Db  3108 GCAAGAGGCTTTGGAGTATTTCATGAAACAAATGAATGCACATCATGGTGCTCGGAC  3167

Qy  1081 rValGlnPheAsnTrpPheLeuHisLeuVal  1091
             ||| :::
Db  3168 AACAAAAATGGATTGGGATCTTCCACACAATT  3198
```

RESULT 12

AAS14365

ID   AAS14365 standard; cDNA; 3424 BP.

XX

AC   AAS14365;

XX

DT   12-MAR-2002 (first entry)

XX

DE   cDNA encoding human pi10alpha isoform of PI3-kinase.

XX

KW   Human; phosphatidylinositol 3-kinase; PI3K; pi10alpha isoform;

KW   LASP-1; cancer; inflammatory disease; ophthalmic disorder; SH3 domain;

KW   autoimmune disease; inflammatory bowel disease; bacterial pneumonia;

KW   Type I diabetes mellitus; cytostatic; immunosuppressive; ss.

XX

OS   Homo sapiens.

XX

FH   Key   Location/Qualifiers

FT   CDS   13..3219

FT   /*tag= a

FT   /product= "pi10alpha isoform of PI3-kinase"

XX

PN   WO200185986-A2.

XX

PD   15-NOV-2001.

XX

PF   10-MAY-2001; 2001WO-US15065.

XX

PR   10-MAY-2000; 2000US-203346P.

XX

PA   (ICOS-) ICOS CORP.

XX

PI   Sadhu C;

XX

DR   WPI; 2002-075252/10.

DR   P-PSDB; AAU09687.

XX

PT   Identifying a modulator of pi10delta polypeptide binding to SH3

PT   domain-containing polypeptides e.g. LASP-1, comprising allowing the

PT   binding partners to interact in the presence and absence of a test

```
Qy   520 LeuAspAsnTyrCysHisProIleAlaLeuProLysHisArgProThrProAspProGlu  539
                       :::   ||:|     ||||||||
Db  1486 ATTGAACAGCA--TGCCAATTGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGC  1544

Qy   540 -GlyAspArgValAlaGluMetProAsnGlnLeuArg---------         LysGlnLe  555
                       :::  |||||||
Db  1545 AGGACTAGTAACAGACAGCTAGCTAGAGAGCAAATGAATTAAGGAGAAAATGACAAGAACAGAGCT  1604

Qy   555 uGluAlaIleIleuAlaThrAspProLeuAsnProLeuThrAlaGluAspLysGluLeuLe  575
                       :::: ||||| ||||||||||||
Db  1605 CAAAGCAATTTCTACACGAGATCCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCT  1664

Qy   575 uTrpHisPheArgTyrGluSerLeuLysAspProLysAlaTyrProLysLeuPheSerSe  595
                       :::  :::
Db  1665 ATGGAGTCACAGACACATTGTAACTATCCCGAAATTGCTTCTGTC  1724

Qy   595 rValLysTrpGlyGlnGluIleuIleTyrGlnLeuAlaLysThrTyrGlnLeuLeuAlaLysArgGl  615
                       |||  :::||||||||||||||||
Db  1725 TGTTAAATGGAATTCTAGAGATGAAGTAGCCCAGATGTATTGCTTG----------------  1770

Qy   615 uValTrpAspGlnSerAlaLeuAspValGlyLeuThrMetGlnLeuLeuAspCysAsnPh  635
                       :::: |||||||||||||||
Db  1771 -GTAAAAGATTGGCTCCAATCAACCTGAACAGGCTATGGAACTTCTGACTGTAATTA  1829

Qy   635 eSerAspGluAsnValArgAlaIleAlaValGlnLysLeuGluSer---LeuGluLysAs  654
                       |||  :::
Db  1830 CCCAGATCCTATGGTTCGAGGTTTCGGTGCTTGGAAAAATATTAACAGATGA  1889

Qy   654 pAspValLeuHisTyrLeuLeuGlnLeuuValGlnAlaValLysPheGluProTyrHisAs  674
                       :::  ||||||
Db  1890 CAAACTTCTCAGTATTTAATTCAGCTAGTACAGGTCCTAAAATATGAACAATATTTGGA  1949

Qy   674 pSerAlaLeuAlaArgPheLeuuLeuGlyLysArgGlyLeuArgAsnLysArgIleGlyHisPh  694
                       :::: ||||||||||||||||||
Db  1950 TAACTGCTTGTGTGAGATTTTTACTGGAAGAAAGCATTGACTAGTCAAAGGAATTGGGCACTT  2009

Qy   694 eLeuPheTrpPheLeuArgSerGluIleAlaGlnSerArgHisTyrGlnArgPheAl  714
                       :::: ||||||||||||||||
Db  2010 TTTCTTTTGGCATTTAAAATCTGAGATG--CACATAAAACAGTTAGCCAGAGGTTTGG  2066

Qy   714 aValIleLeuGluAlaTyrLeuArgGlyCysGlyThrAlaMetLeuHisAspPheThrGl  734
                       :::: ||||||||||||
Db  2067 CCTGCTTTGGAGTCCTATTGTCGTGCATGTGGATGTATTTGAAGCAC---CTGAATAG  2123

Qy   734 nGlnValGlnValIleAspMetLeuGlnLeuLysValThrIleAspIleLysSerLeuSerAl  754
                       :::: ||||||
Db  2124 GCAAGTCGAGGCAATGCAATGACAAAAGCTCATTAACTTAACT---GACATT-------CTCAAACA  2174

Qy   754 aGluLysTyrAspValSerSerGlnValIleSerGlnLeuLysGlnLeuGluAsnLe  774
                       :::: |||||||||||||
Db  2175 GGAGAGGAAGGATGAAACACAAAAGGTA------CAGATGAAGTTTTAGTGAGCAAAT  2228

Qy   774 uGlnAsn-------LeuAsnLeuProSerPheArgValProTyrAspProGlyLe  791
                       :::: :::
Db  2229 GAGGCGGCCACCGAGATTCATGGATGCCCTACAGGGCTTGCTGTCTCCTCTAAACCCTGCTCA  2288

Qy   791 uLysAlaGlyAlaLeuValIleLeuGluLysCysLysValMetAlaSerLysLysProLe  811
                       :::: |||||||
Db  2289 TCAACTAGGAAACCTCAGGCTAAAGAGTGTCGAATTATGTTCTTCTGCAAAAAGGCCACT  2348

Qy   811 uTrpLeuGluPheLysCysAlaAspProThrAlaLeuSer---------         -As  825
                       :::: ||||||
Db  2349 GTGGGTTGAATTGGGAG------AACCCAGAACATCATGTCAGAGTTACTGTTTCAGAACA  2402

Qy   825 nGlnIleLeuArgIleMetGluSerIleTrpGluThrAspLeuGlnAspMetLeuIleIle  845
                       :::: |||
Db  2403 TGAG--ATCACATTTAAAAATGGAAAATCTGCAAAATACAAGGTCTTGAATGTT  2453

Qy   845 uGlnIleLeuLeuArgMetGlyLeuTyrCysIleSerThrGlyMetIleGlyMetIleGlyLeuLeuValLysAspAl  865
                       :::: ||||||||||||
Db  2454 TCAAATATTCGTATTATGAGAAAATCTGCAAAATACAAGGTCTTGAATGTT  2513

Qy   865 uProTyrGlyCysIleSerThrGlyLeuMetIleGlyMetIleGlyMetIleGlyIleLeuValLysAspAl  885
```

```
Qy   208 ProGluTyrLeuLeuLysLysIleThrArgAsnCysValPheIleValIle--------  224
                       ||:::::::||:|       :::  ||||||
Db   544 CCAAAGCACATATATAAATTGGATAGAGGCCAAATAAATAGTGGTGATTTGGGTAATA  603

Qy   225 --------HisArgSerThrGlnThrIleLeuLysValSerAlaAspAspThrPro  241
                        |||
Db   604 GTTTCTCCAAATAATGACAAGCAGAAGTATACTTCTGAAAATCACCATGACTGTGTGCCA  663

Qy   242 GlyThrIleLeuGlnSerPhePheThrLysMetAlaLysLysSerLeuMetAspIle  261
                       :::::: ||| :::
Db   664 GAACAAGTAATTGCTGAAGCAATCAGGAA----AAAACTAGAAGTAATGTTGCTATCA  717

Qy   262 ProGluSer------------GlnAsnGluArgAspPheValLeuArgValCys  275
                       :::
Db   718 TCTGAACAATTAAAAACTCTGTGTTTAGATATCAGGGCAAGTACATTTAAAAGTGTGT  777

Qy   276 GlyArgAspGluTyrLeuValGlyValGlyGluThrProIleLeuLysAsnPheGlnTrpValArgGln  295
                       ||| :::
Db   778 GGATGTGATGAATTACTTCCTAGAAAAATATCCTCGAGTCAGTATAAGTATATAAGAGAGC  837

Qy   296 CysLeuLysAsnGlyGluGluIleHisLeuValLeuValLeuAspThrProProAspProAlaLeu  315
                       :::
Db   838 TGTATAAATGCTTGGGAGGATG----------------CCCAATTG  867

Qy   316 AspGluValArgLysGlu--------GluTrpProLeuValAspAspCysThrGly  331
                       ||| :::
Db   868 AAGATGATGGCTAAAGAAGCCCTTATTCTCAACTGCCAATG------GACTGTTTTACA  921

Qy   332 ValThrGlyTyrHisGlyGlnLeuThr---------         IleHisGlyLysAspHis  346
                       ::: ||||||
Db   922 ATGCCATCTCATTCCAGACGCATTCCACAGTCCACCATATGGAATGGAGAA  975

Qy   347 GluSerValPheThrValSerLeuuTrpAspCysAspPheArgValLys--------  364
                       :::: :::
Db   976 -----ACATCTACAAAAATCCCTTGGGTTATAAAATAGAGCACTCAGAATAAAAATTCTT  1029

Qy   365 --------IleArgGlyIleAspIleProValLeuProArgThr  376
                       |||
Db  1030 TGTGCAACCTACGTGAATCTAAAATATTCGAGACATTGAC------  1068

Qy   377 AlaAspLeuThrValPheValGluAlaAsnIleGlnTyrGlyGlnLeuCysGln  396
                       :::: :::
Db  1069 --------AAGATTTATGTTCGAACAGGTATCTCACCATGGAGGAGGAGAACCCTTATGTGAC  1119

Qy   397 ArgArgThrSerProLysProPheThrGluGluValLeuuLeuValLeuTrpLeuGluPhe  416
                       ||:::
Db  1120 AATGTGAACACTCAAAGAGTACCTTGTTCCAATCCCAGGTGGAATGAATGGCTGAATTAT  1179

Qy   417 SerIleLeuLysAspLeuProLeuLysGlyThrLeuAlaLeuAsnAsnIleTyrCysGly  436
                       ||||||
Db  1180 GATATACATTCCGATCTTCCTGGTGCTGCTTGCGACTTTGCACTTTGCCATT---TGC  1233

Qy   437 LysAlaProAlaLeuSerGlyLysLysThrSerAlaGluMetProSerProGluSerLysGly  456
                       :::
Db  1234 --------TCTGTTAAAGGCCCGAAAAGGGTGCT------------AAAGAG  1263

Qy   457 LysAlaGlnLeuLeuTyrTyrValPheValValAsnLeuLeuLeuIleAspHisArgPheLeuArg  476
                       :::
Db  1264 GAACACTGTCCATTGGCATGGGAAATAAAACTTGTTGATTACACAGACACTCAGTA  1323

Qy   477 HisGlyGluTyrValLeuHisMetTrpGlnLeuSerGlyGlyLysGlyAspGlnGlySer  496
                       |||:::
Db  1324 TCTGGAAAAAATGGCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGAT----TTG  1377

Qy   497 PheAsnAlaAspLysLeuThrSerAlaThrAsnProAspLysGluAsn--------  512
                       :::: :::
Db  1378 CTGAACCCTATTGGTGTTACT--GGATCAAAATCCAAATAAAGAAACTCCAATGCTTAGAG  1434

Qy   513 --------SerMetSerIleSerIleLeu------  519
                       |||:::
Db  1435 TTGGAGTTTGACTGGTTGCAGTGTCGTGTAAGTTCCCAGATATGTCAGTG------  1485
```

Db 2514 ::|||||||||||||||||| :::|||||||||:: |||||
         ACCTTATGGTGTCTGTCAATCGGTGACTGTGTGGGGACTTATTGAGGTGGTGCGAAATTC 2573

Qy   885 aThrThrIleAlaLysIleGlnGlnSerThrValGlyAsnThrGlyAla-----PheLy 903

Db 2574 TCACACTATTATGCAAATT---CAGTTGCAAAGGCGGCTTGAAAGGTGCACTGCAGTTCAA 2630

Qy   903 sAspGluValLeuSerHisTrpLeuLysGluLysCysProIleGluGluLysPheGlnAl 923

Db 2631 CAGCCACCACACTACACAGTGGCTCAAAGACAGAACAAA---GGAGAAATATATGATGC 2687

Qy   923 aAlaValGluArgPheValTyrSerCysAlaGlyTyrCysValAlaThrPheValLeuGl 943

Db 2688 AGCCATTGACCTGTTTACACGTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTTGGG 2747

Qy   943 yIleGlyAspArgHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeuPheHisIl 963

Db 2748 AATTGGAGATCGTCACAATAGTAACATCATGGTGAAAGACGATGGACAACTGTTTCATAT 2807

Qy   963 eAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLysGluArgVa 983

Db 2808 AGATTTTGGACACTTTTTGGATCAACAAGAAGAAAAATTGGTTATAAACGGAGAACGTGT 2867

Qy   983 lProPheValThrProAspPheLeuPheValMetGlyThrSerGlyLysLys----- 1001

Db 2868 GCCATTTGTTTTGACACAGGATTTCTTAATAGTGATAGTAGAAAGAGGCCCAAGAATGCAC 2927

Qy 1002 -ThrSerLeuHisPheGlnLysAspValCysValLysSerAlaTyrLeuAlaLeuAr 1021

Db 2928 AAAGACAAGAGATTTGAGAGGTTCAGGAGATGGTTACACGGCTTATCTAGCTATTCG 2987

Qy 1021 gHisHisThrAsnLeuLeuIleLeuPheSerMetMetLeuMetThrGlyMetProGl 1041

Db 2988 ACAGCACGCAATCTCTTCATAAATCTTTCTCAATGATGCTGGCTCTGGAATGCCAGA 3047

Qy 1041 nLeuThrSerLysGluLysIleGluTyrIleArgAspAlaLeuThrArgValGlyLysSerGl 1061

Db 3048 ACTACAAATCTTTTGATGACATCTTTGCCATACATTCGAAAGACCCCTAGCCTTAGATAAAACTGA 3107

Qy 1061 uGluAspLysLysTyrPheLeuAspCysGlnIleGluValCysArgAspLysLysGlyTrpTh 1081

Db 3108 GCAAGAGGCTTTGGAGTTATTTCATGAAACAAATGAAATGATGCACATCATGGTGGCTGGAC 3167

Qy 1081 rValGlnPheAsnTrpPheLeuHisVal 1091

Db 3168 AACAAAAATGGATTGGATCTTCCACACAATT 3198

RESULT 13
AQ51155

CC   Southern blot analysis was performed using a bovine cDNA probe contg.
CC   a fragment of a PI3-kinase-encoding sequence and human cDNA isolated
CC   from a cDNA library constructed from mRNA isolated from the human
CC   cell line KG1a. Positive clones were sequenced to give the human
CC   PI3 kinase p110 sequence shown. This sequence has 95 percent
CC   homology with the bovine sequence. The domain encoding residues 19-
CC   100 of human p110 is sufficient to encode the kinase which will
CC   associate with the p85 kinase subunit. The gene may be used to
CC   provide a protein with PI3 kinase activity, and is useful for
CC   screening for (ant)agonists of PI3 kinase activity which could be
CC   useful for stimulation or inhibition of cell proliferation and hence
CC   prophylaxis or therapy. Platelet or neutrophil activity or blood
CC   glucose levels can be controlled using the kinase.
CC   See also AAQ51156, AAQ59012-23 and AAQ57522-3.
CC   (Updated on 09-JAN-2003 to add missing OS field.)
CC   (Updated on 25-MAR-2003 to correct PN field.)
CC   (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ   Sequence 3207 BP; 1028 A; 581 C; 680 G; 918 T; 0 other;

Alignment Scores:
Pred. No.:   39

Score: 3.33e-129   Length: 3207
                       1465.50   Matches: 382
Percent Similarity: 51.40%   Conservative: 204
Best Local Similarity: 33.51%   Mismatches: 405
Query Match: 25.31%   Indels: 149
DB: 14   Gaps: 39

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Qy   23 MetLysProArgSerThrAlaAlaSerLeuSerMetGluIleuPro--------- 39
            ||| ::: |||||| ||::|
Db   1 ATGCCTCCAAGACCATCACCAGGTGAACTGTGGGGCATCCACTTGATGCGCCCCCAAGAATC 60

Qy   40 ---IleGluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeu 58
                 ::: :::|||||
Db   61 CTAGTAGAAATGTTACTACCAAATGGGATGATAGTGACT---------------- 99

Qy   59 LeuHisValAlaAlaGlyHisGlyAsnValGluGlnValGluMetLysAlaGlnValTrpLeuLysArgArgAla 78
            |||:   :: :::::::||||
Db   100 TTAGAATGCCTCCGTGAGGCTACGTTAATAACGATAAAGCATGAACTATTTAAAGAAGCA 159

Qy   79 LeuGluThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeu 98
                 || |||
Db   160 AGAAAATACCCCTC----------------CATCAACTTCCTTCAAGATGAATCTTCTTAC 204

Qy   99 LeuTyrGlnLysLysGlnGlnIleTyrGluIleTyrAspTyrGlnValValGlnThr 118
            ||:   :::
Db   205 ATTTTCGTAAGTGTTACCCAAGAACAGAAAGGGAAGAATTTTTGATGAAACAACGA 264

Qy   119 LeuAspCysLeuArgTyrTrpLysTrpLeuHisArgSerProGlyGlnIleHisValVal 138
            || ::::
Db   265 CTTTGTGACCTTCGGCTTTTTCAACCCTTT----------TTAAAAGTAATT 306

Right-hand alignment column:

```
                                                                                                      :::::: |||||
Qy        AATATAAACTGTTTGATTACACAGATACTCTAGTATCTGAAAAATGGCTTGAATCTT  1335
Db   1276                                                                                              504

Qy   485  TrpGlnLeuSerGlyLysGlyGluAspGlnGlySerPheAsnAlaAspLysLeuThrSer
Db   1336 TGGCAGTACCTCATGGACTAGAAGAT---TTGCTGAACCCATTGGTGTTACT---  1386

Qy   505  AlaThrAsnProAspLysGluAsnSerMetSerIleSerIleLeuLeuLeuAspLysAsnTyrCys  524
Db   1387 GGATCAAATCCAAATAAAGA---ACTCCATGTTTAGAGTTGGAGTTGACTGGTTCAGC  1443

Qy   525  HisProIleAlaLeuProLysHisArgProThrProGluProGluValGlyAspArgVal---  543
Db   1444 AGTGTGGTAAAGTTCCAGATATGTCAGTAGTCAGTGATTGAAGAGCATGCCAATGGTCTGTATCC  1503

Qy   544  ---ArgAlaGluMetProAsn  549
Db   1504 CGTGAAGCAGGATTTAGTATTATTCCATGCACAGGACGTAACAGACAGTAGTGAGACAAT  1563

Qy   550  ---LysGlnLeuGluAlaIleLeuIleAlaThrAspProLeuAsn  565
Db   1564 GAATTAAGAGAAAAATGATAAAGAACAGCCTCCGAGCAATTGTACACGAGATCCTCTATCT  1623

Qy   566  ProLeuThrAlaGluAspLysGluLeuLeuTrpHisPheArgTyrGluSerLeuLysAsp  585
Db   1624 GAAATCACTGAGCAAGAAGAGATTTTCTGTGGAGCCACAGACACTATTGTAACTATC  1683

Qy   586  ProLysAlaTyrProLysPheSerSerValLysTrpGlyGlnGlnIleGlnIleValAla  605
Db   1684 CCCGAAATTCACCCAAATTGCTTCGTTCGTTGTTAAATGGACTCTAGAGATGAAGTAGCT  1743

Qy   606  LysThrTyrArgLeuLeuLeuAlaLysArgGluValTrpAspGlnSerAlaValGly  625
Db   1744 GTAAAAGATTGGCCTCCAATCAAGCCTGAA  1788

Qy   626  LeuThrMetGlnLeuLeuAspCysAsnPheSerArgAspGluAsnValAlaIleAlaVal  645
Db   1789 CAGGGTCATGGAGCTCGGACTGCAATTACCCAGATCCATGGTTCGGAGTTTTGCTGTT  1848

Qy   646  GlnLysLeuGluSer---LeuGluAspAspAlaValHisTyrLeuGlnLeuGlnLeuVal  664
Db   1849 CGGTGCTTAGAAAAATATTTAACAGATGACAAACTTTCTCAGTACTAATTCAGCTAGTA  1908

Qy   665  GlnAlaAlaValLysAspPheThrGlnGlnValAspSerAlaLeuAlaLeuArgPheLeuLeuLysArg  684
Db   1909 CAGGTACTAAAATATGAACAGTATTTGGATAACCTGCTTGTGAGATTTTACTCAAAAA  1968

Qy   685  GlyLeuArgAsnLysArgIleGlyHisTrpPheLeuProLeuLeuArgSerGluIleIleAla  704
Db   1969 GCGTTAACTAACTCAAAGAGATCGGTCACTTTTCTTTTGGGCATTTAAAATCTGAGATG---  2025

Qy   705  GlnSerArgHisTyrGlnAsnArgPheAlaValIleLeuGluAlaTyrLeuArgGlyCys  724
Db   2026 CACAATAAAAACAGTAGTCAGTGGTTTGGCCTGCTTTTGGAGTCCTATTGCCGTGCATGT  2085

Qy   725  GlyThrAlaMetLeuHisAspArgPheThrGlnInValGlnInValLeuGlnInMetLeuGlnLys  744
Db   2086 GGGGATGTATCGAAGCAC---CTTAATAGGCAAGTTGAGGCTATGGAAAAGCTCATTAAC  2142

Qy   745  ValThrIleAspLysSerLeuSerArgAlaGluLysTyrAspValSerSerGlnValIle---  764
Db   2143 TTGACT---GACATT---CTCAAACAAGAGAGAAGGATGAAACACAAAGGTA---  2190

Qy   765  SerGlnLeuLysGlnLysLysGlnInLeuGluAsnLeuGlnAsn---------LeuAsnLeuProGln  781
Db   2191 ---CAGATGAAGTTTTAGTTGAGCAAATGCGGCCACCAGATTCATGGATGCTCTCCAG  2247

Qy   782  SerPheArgValProTyrAspTyrProGlyLeuLysAlaGlyInValAlaLeuValIleGluLysCys  801
Db   2248 GGCTTCTTCGTCTCCTCAAACCTGTCTCATCAGCTGGAAATCTCAGGCTGGGAAATCTCAGGAGTGT  2307

Qy   802  LysValMetAlaSerLysProLeuPheLysGluPheLeuTrpLeuGlyGlyThr  821
```

Left-hand alignment column:

```
Qy   139  GlnArgHisAlaProSerGluGluThrLeuAlaPheGlnLeuAsnAlaLeuIle  158
Db   307  GAACCAGTAGGCAACCGTGAAGAAAAGATC---CTCAATCGAGAAGATACTCTAGTATCTGTCTATC  363

Qy   159  GlyTyrAspValThrAspValSerAsnValHisAspArgGluLeuGluPheThrArg  178
Db   364  GGCATGCCAGTGTGTGAATTGATATGGTTAAAGATCCAGAGAAGACTACCAGGACTTCCGAAGA  423

Qy   179  ArgLeuValThrProPheArgMetAlaGlyValAlaGlyArgAsp---  192
Db   424  AATATTCTCAATGTTGTAAAGAGCTGTGGATCTTAGGGATCTTAATTCACCTCATAGT  483

Qy   193  ProLysLeuTyrAlaMetHisProTrpValThrSerPro--LeuProGluTyrLeu  211
Db   484  AGAGCAAATGTATGTTTATCCTCCAAATGTAGAATCTTCACCCAGAACTGCCAAAGCACATA  543

Qy   212  LeuLysLysIleThrAsnAsnCysValPheIleValIle---------His  225
Db   544  TATAATAAATTGGATAAACGGCAAATAATATAGTGTGATTTGGGTAATAGTTTCTCCAAAT  603

Qy   226  ArgSerThrSerGlnThrIleLeuLysValSerAlaAspAspThrProGlyThrIleLeu  245
Db   604  AATGACAAACAGAAGTATACTCTGAAAATCAACCATGACTGTGTGCCAGAACAAGTAATT  663

Qy   246  GlnSerPhePheThrLysMetAlaLysLysLysSerLeuMetAspIleProGluSer---  264
Db   664  GCTGAAGCAACAGGAAA-----AAAACTCGAAGTAGTGTTGCTATCATCGTGAACAACTA  717

Qy   265  ---------GlnAsnGluArgAspPheValLeuArgValCysGlyValArgAspGlu  279
Db   718  AAACTCTGTGTTTAGAATATCAGGGCAAGTATATTTAAAGTGTGTGGATGTGATGAA  777

Qy   280  TyrLeuValGlyGluThrProIleLeuLysAsnPheGlnInTrpValArgGlnCysLeuLysAsn  299
Db   778  TACTTCCTAGAAAAATAATCCTCTGAGTCAGTAGTATAAGTATAAGAAGCTGTATAATGCTT  837

Qy   300  GlyLeuGluIleHisLeuValLeuAspThrProProAlaLeuAspAspValArg------  319
Db   838  GGGAGGATGCCCAATTTGATGCTG--------------ATGGCTAAAGAAAGCCTC  879

Qy   320  LysGluGluTrpProLeuValAspAspCysThrGlyValThrGlyTyrHisGluGlnLeu  339
Db   880  TATTCTCAACTGCCAATG-----GACTGTTTTACAATGCCATCATATTCCAGACGCCATC  933

Qy   340  Thr--------IleHisGlyLysAspHisGluSerValPheThrValSerLeu  354
Db   934  TCCCAGGCTACGGCCATATATGAATGGAGAA-----ACATCTACAAAATCCCTT  981

Qy   355  TrpAspCysSerAspArgLysPheArgValLys--------  364
Db   982  TGGGTTATAAATAGTGCACTCAGAATAAAAAATTCTTTGTGCAACCTATGTGAATGTAAAT  1041

Qy   365  IleArgGlyIleLeuAspIleProValLeuProArgThrAlaAspLeuThrPheValGlu  384
Db   1042 ATTCGAGACATTGAC---------------------AAGATTTATGTTCGA  1071

Qy   385  AlaAsnIleGlnIleTyrGlyGlnInValLeuCysGlnInArgArgThrGlnLysPhe  404
Db   1072 ACAGGTATCTCAAACGGAGGAGAACCCTATG---CTTAATAGGCAAGTTGAGGCTATGGAAAAGCTCATTAAC  1131

Qy   405  ThrGluGluValLeuTrpAsnValTrpProLeuPheSerIleLysIleLysAspLeuPro  424
Db   1132 TGTTCCAATCCCAGGTGAATTGGCTGAATTGCATGGTGAATTACGATATACAATTCCTGATCTTCCT  1191

Qy   425  LysGlyAlaLeuLeuAsnLeuGlnIleTyrCysGlyLysLysGlyAlaProAlaLeuSerGlyLys  444
Db   1192 CGTGCTGCCGACTTTGCCTTTGCCTTT-TGT-----TCTGTTAAAGGCCGA  1236

Qy   445  ThrSerAlaGluMetProSerProGluSerLysLysGlyLysAlaGlnInLeuLeuTyrTyrVal  464
Db   1237 AAGGGTGCT------------AAAGAGGAACACTGTCCATTGGCCTGGGGGA  1275

Qy   465  AsnLeuLeuIleLeuAspHisArgPheLeuLeuArgGlyHisGlyLeuGluThrTyrValValLeuHisMet  484
```

```
Db  2308  CGAATTATGTCTTCTGCAAAAAGGCCACTGTGGTTGAATTGGGAG------AACCCAGAC  2361
                                                              ::::::|||||
Qy   822  AlaLeuSer-------------------AsnGluThrLeuGlyIleIlePheLysHisGly   835
          :::|||
Db  2362  ATCATGTCAGAATTACTCTTCAGAACAGAG--------ATCACTTTAAAAAATGGG  2412

Qy   836  AspAspLeuArgAsnMetLeuIleLeuGlnIleLeuArgIleMetGluSerIleTrp   855
          |||||||||||||||||||
Db  2413  GATGATTTACGGCAAGATATGCTAACCCTTCAGATTATTCGGCATATGGAAATATCTGG  2472

Qy   856  GluThrGluSerLeuAspLeuCysLeuLeuProTyrArgGlyCysIleSerGluThrGlyAspLys   875
          :::  :::
Db  2473  CAAAATCAAGGTCTTGATCTTCGAATGTTACCTTATCGAGGTCGTCAATCCGTGACTGT  2532

Qy   876  IleGlyMetIleGluIleValLysAspAlaThrThrIleAlaLysLysGlnSerThr   895
          |||||
Db  2533  GTGGGACTTATCGAGTCGGTGGTGGAGAAATTCTCACACTATAATGCAGATT---CAGTGTAAA  2589

Qy   896  ValGlyAsnThrGlyAla------PheLysAspGluValSerHisTrpLeuLysGlu   913
          |||||
Db  2590  GGAGGCCTGAAAGTGCACTGCAGTTTAACAGCCACACCTCATCAGTGGCTCAAAGAC  2649

Qy   914  LysCysProIleGluGluLysPheGlnAlaAlaAlaValGlnArgPheValTyrSerCysAla   933
          |||    :::
Db  2650  AAGAACAAG--GGGAAATATAATGATGGGCCATGATTGTTTACACGATCATGTGCT  2706

Qy   934  GlyTyrCysValAlaThrPheValLeuGlyIleGlyAspArgHisAsnAspAsnIleMet   953
          |||||||||
Db  2707  GGATATTGTGTTGCCACCTTCATTTTGGGAGATCGTCACAATAGTAATATCATG  2766

Qy   954  IleSerGluThrGlyAsnLeuPheHisIleAspPheGlyHisIleLeuGlyAsnTyrLys   973
          :::  |||||||  :::  :::
Db  2767  GTTAAAGATGATGGACAACTGTTTCATATAGATTTTGGACACTTTTGGATCACAAGAAG  2826

Qy   974  SerPheLeuGlyIleAsnLysGluArgValProPheValLeuThrProAspPheLeuPhe   993
          |||||||||
Db  2827  AAAAAATTTGGTTATAAACGAGAGCGCGTCCCGTTTGTTTTGACACAAGATTTCTTAATA  2886

Qy   994  ValMetGlyThrSerGlyLys------ThrSerLeuHisPheGlnLysPheGlnAsp  1011
                              :::       :::
Db  2887  GTGATGAGTTGAAAGGAGCCCAAGAATGCACAAGACAAGAGAATTTGAGGAGGTTTCAGGAG  2946

Qy  1012  ValCysValLysAlaTyrLeuAlaLeuArgHisHisThrAsnLeuLeuIleIleLeuPhe  1031
          :::||||||  |||||
Db  2947  ATGTGTTACAAGGCTTATCTAGCTATTCGGCACCATTCGACAATCTTCATAAAATCTTTTC  3006

Qy  1032  SerMetMetLeuMetThrGlyMetProGlnLeuThrSerLysGluAspIleGluTyrIle  1051
          |||
Db  3007  TCAATGATGCTTGGCTCTGGAATGCCAGAACTGACTTCCAATCTTTTGATGATTGCCATACATT  3066

Qy  1052  ArgAspAlaLeuThrValGlyLysSerGluGluAspAlaLysLysTyrPheLeuAspGln  1071
          ||||||  :::||||||
Db  3067  CGAAAGATGCCCTAGTTGAGTTGGATAAAACTGAGCAAGGCTTTGGAGTATTCATGAAACAA  3126

Qy  1072  IleGluValCysArgAspLysProLysThrValGlnTrpPheLeuAsnTrpPheLeuHisLeuVal  1091
          :::||||||  :::
Db  3127  ATGAATGATGCACACACATGGTGGCGGGACAACAAAAAAATGGATTGGATCTTCCACACATT  3186
```

RESULT 14
AAQ51156

Alignment Scores:

Pred. No.:	14		
Score:	1.1e-128	Length:	3412
Percent Similarity:	1460.50	Matches:	385
Best Local Similarity:	51.53%	Conservative:	206
Query Match:	33.57%	Mismatches:	394
DB:	25.22%	Indels:	163
		Gaps:	40

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```
Qy   23  MetLysProArgThrAlaAlaSerLeuSerMetGluLeuIlePro---------  39
         |||||| :::|||        ||||||||||
Db    1  ATGCCTCCAAGACCATCATCAGGTGAACTCAGGTGAACTGTGGGGCATCCACTTGATGCCCCCAAGAATC  60

Qy   40  ---IleGluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeu  58
            :::  |||||:|||
Db   61  CTAGTGGAATGTTTACTTACCAAATGGAATGATGACT---------------------  99

Qy   59  LeuHisValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnValTrpLeuArgArgAla  78
         ||| :::|
Db  100  TTAGAATGCCTCCGTGAGGCTACATTAGTAACTATAAAGACATATAAAGAAGAAGCA  159

Qy   79  LeuGluThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeu  98
         ||:::|||:|||
Db  160  CATCAACTTCTTCAAGATGAATGTTCTTAC---------------------------------  204
```

```
Qy   421 LysAspLeuProLysGlyAlaLeuLeuAsnGlnIleTyrCysGlyLysAlaProAla 440
             ||||||||||||     ::|||||||||       |||
Db  1180 CCTGATCTTCCTCGTGCTGCTGAACTTTGCCTTTCATT---TGC------------TCT 1224

Qy   441 LeuSerGlyLysThrSerAlaGluMetProSerProGluSerLysGlyLysAlaGlnLeu 460
             :::  :::|:    |||          :::|||||||||
Db  1225 GTTAAAGGCCGAAAGGGTGCT---------------------AAAGAGGAACACTGTCCA 1263

Qy   461 LeuTyrTyrValAsnLeuLeuIleAspHisArgPheLeuLeuArgHisGlyGluTyr 480
             :::    |||||||| ::                     :::   |||||
Db  1264 TTGGCATGGGAGAAATATAAACTTGTTTGATTACACAGACCACTCTAGTATCTGGAAAAATG 1323

Qy   481 ValLeuHisMetTrpGlnLeuSerGlyLysGlyLysGlyAspGlnGlySerPheAsnAlaAsp 500
             ||||||||     |||||||||   |||:::
Db  1324 GCTTGAATCTTTGGCCAGTACCTCAGTGGATTAGAAGAT------TTGCTGAACCCTATT 1377

Qy   501 LysLeuThrSerAlaThrAsnProAspLysGluAsn 512
             :::::||||| :::
Db  1378 GGTGTTACT---GGATCAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAGTTTGAC 1434

Qy   513 ----------------------SerMetSerIleSerIleLeuLeuAspAsnTyr 523
                                    |||  ::::    :::
Db  1435 TGGTTCAGCAGTGTGGTAAAGTCCCAGATATGTCAGTG--------ATTGAAGAGCA- 1484

Qy   524 CysHisProIleAlaLeuProLysHisArgProThrProAspProGlu--GlyAspArgVa 543
             :::   |||||||||||:::|||   ::|||         :::
Db  1485 TGCCAATTGGTCTGTATCCGAAGCAGGAGATTTCCACGCAGGACTGAGTAA 1544

Qy   543 lArgAlaGluMetProAsnGlnLeuArg--------------------LysGlnLeuGluAlaIleIl 559
             :::   :::|||:::||||||:||                        :::
Db  1545 CAGACTAGCTAGAGACAATGAATTAAGGGAAAATGACAAAGACAGCTCAAAGCAATTTC 1604

Qy   559 eAlaThrAspProLeuAsnProLeuThrAlaGluAspLysGluLeuLeuTrpHisPheAr 579
             :::    |||||| :::|||   :::
Db  1605 TACACGAGATCCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTATGGAGTCACAG 1664

Qy   579 gTyrGluSerLeuLysAspProLysAlaTyrProLysLeuPheSerSerValLysTrpGl 599
             |||   |||||||||||||   :::
Db  1665 ACACTATTGTGTAACTATCCCCAAATTCTACCCAAATTGCTTCTGTGTTAAATGGAA 1724

Qy   599 yGlnGlnGluIleValIleAlaLysThrTyrGlnLeuLeuAlaLysArgGluValTrpAspGl 619
             :::::|||||||||||||:::|||||||||::: 
Db  1725 TTCTAGAGATGAAGTAGCCCAGATGATTGCTTG--------GTAAAAGATTG 1769

Qy   619 nSerAlaLeuAspValGlyLeuThrMetGlnLeuLeuAspCysAsnPheSerAspGluAs 639
             :::
Db  1770 GCCTCCAATCAAACCTGAACAGGCTATGATGAACTTCTGGACTGTAATTACCCAGATCCTAT 1829

Qy   639 nValArgAlaAlaIleAlaAlaValGlnLysLeuGluSer----LeuGluAspAspValLeuHi 658
             :::|||:::|||
Db  1830 GGTTCGAGGTTTTGCTGTTGCTGCTGTCCTGGAAAAATATTAACAGATGACAAACTTTCTCA 1889

Qy   658 sTyrLeuGlnLeuValGlnAlaValLysPheGluProTyrHisAspSerAlaLeuL 678
             :::||||||||||
Db  1890 GTATTTAATTCAGCTAGTACACAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGT 1949

Qy   678 aArgPheLeuLeuLysArgGlyLeuArgAsnLysArgIleGlyHisPheLeuTrpPh 698
             :::
Db  1950 GAGAGTTTTTACTGAAGAAAGCATTGACTAATCAAAGGATTGGCACTTTTCTTTTGGCA 2009

Qy   698 eLeuArgSerGluIleAlaGlnSerArgHisTyrArgGlnArgPheAlaValIleLeuGl 718
             :::
Db  2010 TTTAAAATCTGAGATG---CACAATAAAACAAGTAGCCAGAGGTTTGGCTGCTTTTGGA 2066

Qy   718 uAlaTyrLeuArgGlyCysGlyThrAlaMetLeuHisAspPheThrGlnGlnValGlnva 738
             :::::||||||||||:::       :::::
Db  2067 GTCCTATTGTGCTGCATGTGGGATGATTGAAGCAC---CTGAATAGGCAAGTCGAGGC 2123

Qy   738 lIleAspMetLeuGlnLeuValThrIleGluProIleAspIleLysSerLeuSerLysTyrAs 758
             ::: |||
Db  2124 AATGGAAAAGCTCATTAACTTAACT------GACATT------CTCAAACAGGAGGAAGGA 2174

Qy   758 pValSerSerGlnValIleSerGlnLeuLysGlnLeuAsnLeuAsn--------- 776
```

```
Qy    99 LeuTyrGlnLysLysGlyGlnThrTrpTyrGluIleTyrAspLysTyrGlnValValGlnThr 118
             ||||||||   :::     :::
Db   205 ATTTCGTAAGTGTACCCAAGAAGCAGAAGGGAGAATTTTTGATGAAACAAGACGA 264

Qy   119 LeuAspCysLeuArgTyrTrpLysTrpLysValLeuHisArgSerProGlyGlnIleHisValVal 138
             |||||| ||||||:::         ::: :::
Db   265 CTTTGTGATCTTCGGCGTTTTCAACCATTT-------TTAAAGTAATT 306

Qy   139 GlnArgHisAlaProSerGluGluThrLeuAlaPheGlnArgGlnLeuAsnAlaLeuIle 158
             :::|||||||||:::   |||||||||||||
Db   307 GAACCAGTAGGCAACCGTGAAGAAAAGATC---CTCAATCGAGAAATTGGTTTTGCTATC 363

Qy   159 GlyTyrArgAspValThrArgSerAsnValHisAspAspGluLeuGluPheThrArgArg 178
             |||||||||:::|||||||||     |||||||||   :::
Db   364 GGCATGCCAGTGTGCGAAATTGATATGTTAAAGATCCTGAAGTACAGGACTTCCGAAGA 423

Qy   179 ArgLeuValThrProArgMetAlaGlyMetAlaGlyValAlaGlyArgAsp--------- 192
             :::::::
Db   424 AATATTCTTAATGTTGTAAAGAAGCTGTGGATCTTAGGGATCTTAATTCACCTCATAGT 483

Qy   193 ProLysLeuTyrAlaMetHisProTrpValThrSerLysPro---LeuProGluTyrLeu 211
             :::
Db   484 AGAGCAATGTATGTCTATCCCCACATGTAGAATCTTCACCAGAGTCCAAAGCACATA 543

Qy   212 LeuLysLysIleThrAsnAsnCysValPheIleValIle------------His 225
             :::
Db   544 TATAATAAATTGGATAGAGGCCAAATAATAAGTGGTGATTTGGGTAAATAGTTTCTCCAAAT 603

Qy   226 ArgSerThrThrSerGlnThrIleLysValSerAlaSerAspThrProGlyThrIleLeu 245
             ||| :::   :::::::
Db   604 AATGACAAGCAGAGATATACTCTGAAAATCAACCATGACTGTGTGCCAGAACAAGTAATT 663

Qy   246 GlnSerPhePheThrLysMetAlaLysSerLeuMetAspIleProGlySer-- 264
             :::
Db   664 GCTGAAGCAATCAGGAAA------AAAACTAGAAGTATGTTGCTATCATCTGAACAATTA 717

Qy   265 ----------GlnAsnGluArgAspPheValLeuArgValCysGlyTyrArgAspGlu 279
             :::
Db   718 AAACTCTGTCGTTTAGAATATCAGGGCAAGTACATTTTAAAGTGTGGATGATGAA 777

Qy   280 TyrLeuValGlyGluThrProIleLysAsnPheGlnTrpValArgGlnCysLeuLysAsn 299
             :::      :::
Db   778 TACTTCCTAGAAAAATATCTCTGAGTCAGTATAGATAAGTAATAGAAGCTGTATAATGCTT 837

Qy   300 GlyGluGluIleHisLeuValLeuAspThrProProAspProAlaLeuAspGluValArg 319
             |||
Db   838 GGGAGGATG----------------------------CCCAATTTGAAGATGATGGCT 867

Qy   320 LysGlu--------GluTrpProLeuValAspCysAspThrGlyValThrGlyTyr 335
             |||||||      :::  :::
Db   868 ACAAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATAAAAATTCTTTGTGCCAACCTAC 921

Qy   336 HisGluGlnLeuThr------IleArgGlyIleLeuAspIleProValLeuProLeuThr 350
             ||||||||||||
Db   922 TCCAGACGCATTCCACAGTCACCATATGGAATGGAGAA------ACATCT 969

Qy   351 ThrValSerLeuTrpAspTrpAspCysAspSerArgLysPheArgValLys----------- 364
             :::
Db   970 GGGAGGATG----------------------------------CCCAATTTGAAGATGATGGCT 1029

Qy   365 ----------IleArgGlyIleLeuAspIleProValLeuProArgThrAlaAspLeuThr 380
             :::
Db  1030 GTGAATCTAAATATTCGAGACATTGAC------------------------AAG 1059

Qy   381 ValPheValGluAlaAsnIleGlnTyrGlyGlnInValLeuCysGlnArgArgThrSer 400
             :::::||||:::     :::
Db  1060 ATTTATGTTGCAACAGGTATCTCCATGGAGAGAACCCTTATGTGACAATGTGAACACT 1119

Qy   401 ProLysProPheThrGluGluValLeuTrpAsnValTrpLeuGluPheSerIleLysIle 420
             :::
Db  1120 CAAAGAGTACCTTGTTCCAATCCCAGGTGAATGAATTGGCTGAATTATGATATATACATT 1179
```

```
ID   AAC65690 standard; DNA; 3213 BP.
XX
AC   AAC65690;
XX
DT   16-FEB-2001 (first entry)
XX
DE   Human PI3 kinase p110beta DNA.
XX
KW   Human; pI3 kinase P110 beta; antisense inhibition; primer; cytostatic;
KW   antiinflammatory; antiinfective; ds.
XX
OS   Homo sapiens.
XX
PN   US6133032-A.
XX
PD   17-OCT-2000.
XX
PF   09-SEP-1999;   99US-0392350.
XX
PR   09-SEP-1999;   99US-0392350.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Monia BP, Cowsert LM;
XX
DR   WPI; 2000-686014/67.
DR   P-PSDB; AAB11124.
XX
PT   Antisense compound 8-30 nucleobases in length targeted to a start codon
PT   of the coding region of human PI3 kinase p110beta, useful for
PT   inhibiting the expression of the human polynucleotide -
XX
PS   Example 1; Column 43-50; 34pp; English.
XX
CC   This invention describes a novel antisense compound (I) 8-30 nucleobases
CC   in length targeted to a start codon or nucleobases 4-3174 of the coding
CC   region of human PI3 kinase p110beta (II), in which (I) specifically
CC   hybridizes with and inhibits the expression of (II). The products of the
CC   invention have cytostatic, antiinflammatory and antiinfective activity.
CC   (I) is useful for inhibiting the expression of (II) in human cells or
CC   tissues. The antisense compound can be utilized for diagnostics,
CC   therapeutics, prophylaxis and as research reagents and kits. The
CC   antisense compounds may also be useful prophylactically, e.g. to prevent
CC   or delay infection, inflammation or tumor formation. The antisense
CC   compounds are useful for research and diagnostics, because these
CC   compounds hybridize to nucleic acids encoding (II).
XX
SQ   Sequence 3213 BP; 979 A; 612 C; 704 G; 918 T; 0 other;

Alignment Scores:
Pred. No.:                                Length:          3213
Score:                  1.32e-118         Matches:         1354.50
Percent Similarity:     49.60%            Conservative:    361
Best Local Similarity:  31.81%            Mismatches:      202
Query Match:            23.39%            Indels:          407
DB:                     21                Gaps:            165
                                                           37

US-09-974-573-1 (1-1102) x AAC65690 (1-3213)
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```
Db  2175 :::            |||      |||||||     ...CAGATGAAGTTTTAGTTGAGCAAATGAGGCGACCAGA 2228
Qy   777 ---LeuAsnLeuProGlnSerPheArgValProTyrAspProGlyLeuLysLysAlaGlyAl 795
Db  2229 TTTCATGGATGCCCTACAGGGCTTGCTGTCCTCCTAAACCCTGCTCATCAACTAGGAAA 2288
Qy   795 aLeuValIleGluLysCysLysValMetAlaSerLysLysValProLeuTrpLeuGluPh 815
Db  2289 CCTCAGGCTTAAAGAGTGTCGAATTATGTCTTCTGCAAAAAGGCCACTGTGGTTGAATTG 2348
Qy   815 eLysCysAlaAspProThrAlaLeuSer------------AsnGluThrIleGl 829
Db  2349 GGAG------AACCCAGACATCATGTCAGAGTTACTGTTTCAGAACATGAG------ 2394
Qy   829 yIleIlePheLysHisGlyAspAspArgGlnMetMetLeuLeuGlnIleLeuLeuAr 849
Db  2395 -ATCATCTTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACACTTCAAATTATTCG 2453
Qy   849 gIleMetGluSerIleTrpGluThrGluSerLeuAspLeuCysLeuLeuProTyrGlyCy 869
Db  2454 TATTATGGAAAATATCTGGCAAATCAAGGTCTTGATCTTCGAATGTTACCTTATGGTTG 2513
Qy   869 sIleSerThrGlyLysIleGlyMetIleGluIleValLysLysAspAlaThrThrIleAl 889
Db  2514 TCTGTCAACTGGTACTGTTGTGGGACTTATTGGAGGTGGTGCGAAATTCTCACACTATTAT 2573
Qy   889 aLysIleGlnSerThrValGlyAsnThrGlyAla------PheLysAspGluValLe 907
Db  2574 GCAAATT---CAGTGCAAGGGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACACT 2630
Qy   907 uSerHisTrpProLeuLysGluLysGlyProIleGluGlyGluProPheGlnIleAlaAlaAlaValGluAr 927
Db  2631 ACATCAGTGGCTCAAAGACAAGACAAA--GGAGAAATATATGATGCAGCCATTGACCT 2687
Qy   927 gPheValTyrSerCysAlaGlyTyrCysValAlaTyrPheValLeuGlyTyrIleGlyTyrAspAr 947
Db  2688 GTTTACACGTTCATGTCATGTCGTCGGATACTGTGTAGCTACCTTCATTTGGGAATTGGAGATCG 2747
Qy   947 gHisAsnAspAsnIleMetIleSerGluHisGlyThrGlyAsnLeuPheHisIleAspPheGlyHi 967
Db  2748 TCACAATAGTAACATCATGATGGTGAAAGACGATGGACAACTGTTTCATATAGATTTTGGACA 2807
Qy   967 sIleLeuGlyAsnTyrLysSerPheLeuGlyIleIleAsnLysGluArgValProPheValLe 987
Db  2808 CTTTTGGATCACAAGAGAAAAAATTTGGTTATAAACAGAACGTGTGCCATTTGTTTT 2867
Qy   987 uThrProAspPheLeuPheValMetGlyThrSerGlyLysLys-----ThrSerLeuHi 1005
Db  2868 GACACAGGATTTCTTAATAGTGATTGATTAGTAAAGGAGCCACAAAGACCAACAGAGA 2927
Qy  1005 sPheGlnLysPheGlnAspLeuCysValLysSerValLeuAlaTyrLeuAlaLeuArgHisHisThrAs 1025
Db  2928 ATTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCGACAGCCATGCCAA 2987
Qy  1025 nLeuLeuIleIleLeuPheSerMetMetLeuMetThrGlyMetProGlnLeuThrSerLy 1045
Db  2988 TCTCTTCATAAATCTTTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAAATCTTT 3047
Qy  1045 sGluAspIleGluTyrIleGluArgAspAlaLeuThrValGlyLysSerGluGluValAspAlaLy 1065
Db  3048 TGATGACATTGCATCATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTT 3107
Qy  1065 sLysTyrPheLysGlnIleLeuGluValCysArgAspLysGlyTrpThrValGlnPheAs 1085
Db  3108 GGAGTATTTCATGAAACAAATGAAGAATGATGCCACATCATGGTGGCTGACAACAAAAATGGA 3167
Qy  1085 nTrpPheLeuHisLeuVal 1091
Db  3168 TTGGATCTTCCACACAATT 3186
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Qy    30 AlaSerLeuSerMetGluLeuIleProIleGluPheValLeuProThrSerGlnArg 49
Db    64 TCACAGATAGCATCTGATGGCTCCATCCTGTGGATTTCCTTTGCCACTCGG------ 117

Qy    50 AsnThrLysThrProGluThrAlaLeuLeuHisValAlaGlyHisGlyAsnValGluGln 69
Db   118 ------------ATTTATCCAGTTGGAGGTACCTCGGGAAGCTACCATTCTTAT 162

Qy    70 MetLysAlaGlnValTrpLeuArgAlaLeuGluGluThrSerValSerAlaAspPheTyrHis 89
Db   163 ATTAAGCAGATGTTATGGAAGCAAGTTCACAATTACCCAAATG------------ 204

Qy    90 ArgLeuGlyProAspHisPheLeuLeuTyrGlnLysGlyGlnTrpTyrArgGluIle 109
```

RESULT 15
AAC65690

```
Db
205 --------------------------------------TTCAACCTCCTATGATAATGACTCCTATATGTTTGCATGT 246
Qy
110 TyrAspLysTyrGlnValValGlnThrLeuAsp--------------Cys------ 121
Db
247 GTGAATCAGACTGCTGTATATGAGGAGCTTGAAGATGAAACACGAAGACTCTGTGATGTC 306

Qy
122 ----------LeuArgTyrTrpLysValLeuHisArgSer------ProGlyGlnIleHis 136
Db
307 AGACCTTTTCTTCCAGTTCCAAATTAGTGACAAGAAGTGTGTGACCCAGGGGA------ 360

Qy
137 ValValGlnArgHisAlaProSerGluGluThrLeuAlaPheGlnArgGlnLeuAsnAla 156
Db
361 ----------------------AAATTAGACTCAAAAATTGGAGTC 384

Qy
157 LeuIleGlyTyrAspValThrAspValSerArgAsnValHisAspAspGluLeu---GluPhe 175
Db
385 CTTATAGGGAAAAGTCTGCATGAAATTTGATTCCTTGAAGGATCCTGAAGTAAATGAATTT 444

Qy
176 ThrArg------ArgArgLeuValThrProArgMetAlaGluValAlaGlyValAlaArgAsp--- 192
Db
445 CGAAGAAAAATGCCCAAATTCAGCGAGGAGAAAAATCCGTCACTTGTGGGGATTGTCTTGG 504

Qy
193 ---ProLysLeuTyrAlaMetHisProTrpValThrSerLysProGluTyrTyrLeu 211
Db
505 ATGGGACTCGGCTAAAACAAACAAACATATCCACCAGAGCGATGAACCATCCCTGAAAACTTA 564

Qy
212 LeuLysLysIleThrAsnAsnCysValPheIleValIleHisArgSerThrThrSerGln 231
Db
565 GAAGATAAACTTTATGGGGAAACTTCATCGTAGCTGTTCATTTGAAAACTGCCAGGAC 624

Qy
232 ------ThrIleLysValSerAlaAspThrProGlyThrIleLeuGlnSerPhePhe 249
Db
625 GTGTTAGTTTCAAGTGTCTCCCAATAATGAATCCTATCAAAGTAAATGAA------ 675

Qy
250 ThrLysMetAlaLysLysLysSerLeuMetAspIleProGluSerGlnAsnGluArgAsp 269
Db
676 TTGGCAAAATCCAAAAACGTTTGACTATTCATGGGAAGAAGATGAAGTTAGCCCCTATGAT 735

Qy
270 PheValLeuArgValCysGlyGluTyrGluProIleLysProIleGluThrProLysAsn 289
Db
736 TATCGTGTTGCAAGTGAACAGTTCAGCGGGGAGAGTGAGATGCTTGAATCATCCAATTCAG 795

Qy
290 PheGlnTrpProValArgGlnGlnCysLysLeuLysAsnGlyGluGlnIleHisLeuValLeuAspThr 309
Db
796 TTCCAGTATATCCCGGAACTGTGTGATGACAGAGCCCTGCCCATTTTATACTT---- 849

Qy
310 ProProAspProLeuAspPheLysGluGluArgLysGluGluLeuTrpProLeuValAspAspCys 329
Db
850 --------------------------GTGGAATGC 858

Qy
330 ThrGlyValThrGlyTyrHisGlyGln------LeuThrIleHisGlyHisGlu 347
Db
859 TGCAAGATCAAGAAAAATGATGAACAAGAAATGATTGCCATAGAGAGGTGCCCATAAATCGA 918

Qy
348 SerValPheThrValSerLeu---------------- 354
Db
919 AATTCATCTAAATCTTCCTTCCTTACCACCCAAAGAAAAACACGAATTATTTCTCATGTT 978

Qy
355 TrpAspCysSerAspArgLysPheArg--ValLysIleArgGlyIleAspIleProValLeu 373
Db
979 TGGGAAAATAACACACCCTTTCCAAATTGTCTTGGGTAAGGGA----------AATAAACTT 1029

Qy
374 ProArgThrAlaAspLeuThrValPheValGluAsnIleGlnTyrGlyGlnValVal 393
Db
1030 AACACAGAGGAAACTGTAAAAGTTCATGTCAGGGCTCGTCTTTTCCATGGTACTGAGCTC 1089

Qy
394 LeuLysGlnArgArgThrProLys--ProPheThrGluGluValLeuValLeuAspValVal 412
Db
1090 CTGTGTAAAACCATCGTAAAGGTTATCAGGAGTACTGAGCTTTCATTATTTGGAATGAA 1149

Qy
413 TrpLeuGluPheSerIleLysLysGluGluLysProLeuGluAspGluLeuTrpLeuAspGlnIleLeuGln 432
Db
1150 CCACTGAATTTTGATATTAATAATTTTGATACTTACCAAGAATGGCTTCGATTATGTTTGCT 1209
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Qy
433 IleTyrCysGlyLysGlyAlaProAlaLeuSerGlyLysThrSerAlaGluProSerPro 452
Db
1210 GTTTAT---GCAGTTTGGATAATAAAGTAAAAACGAAGAAAAACATTATTAATCCC 1266

Qy
453 ------------GluSerLysGlyLyLysAlaGlnLeuLeuTyrTyr----------ValAsn 465
Db
1267 TCTAAATATCAGACACCATCAGGAAAGCTGGAAAAGTGCATTATCCTGAGCGTGGGTAAAT 1326

Qy
466 LeuLeuLeuIleAspHisArgPheLeuArgHisGlyTyrValLeuHisMetTrp 485
Db
1327 ACGATGGTTTTGACTTAAGGACAATTGAGAACTGGACATAATATTACACAGCTGG 1386

Qy
486 GlnLeuSerGlyLysGlyLysGlyGlnGlyGlySerPheAsnAlaAspLysLeu---- 502
Db
1387 ------------------TCTTCATTT---CCTGATGAACTCGAAGAAATG 1416

Qy
503 --------ThrSerAlaThrAsnProAspLysGluAsnSerMetSerIleSer 517
Db
1417 TTGAATCCAATGGACTGTTCAAACAAATCCATATACTGAAAATGCAACAGCTTTGCAT 1476

Qy
518 IleLeuLeu--AspAsnTyrCysHisProIleAlaLeuPro------------ 530
Db
1477 GTTAAATTTCCAGAGAAATAAAAAACAACCTTATTATTACCCTCCCTTCGATAAGATTATT 1536

Qy
531 ---LysHisArgProThrProProGlyGluGlyAspArgValAlaAlaGluMetProAsn 549
Db
1537 GAAAAGGCAGCTGAGATTGCAAGCAGTAGTGCTAATGGTCAAGTCGAGGTGGAAAA 1596

Qy
550 GlnLeuArgLysGlnLeuLeuGluAlaIleAlaIleAlaThrAspAsnProLeuAsnProLeuThrAla 569
Db
1597 AAGTTCTTCCTGTATTGAAAGAAATCTTGGACACAGGGATCCCTTGTCTCAACTGTGTGAA 1656

Qy
570 GluAspProLysGluLeuLeuTrpHisPheArgTyrGluSerLeuLys--AspProLysAla 588
Db
1657 AATGAAAATGGATCTTATTGGCACTTTGCGCAAGAACGTGCCGAGAGATTTCCCACAATCA 1716

Qy
589 TyrProLysPheSerSerValLysTrpGlyValGlnGlnGluIleLeuValAlaAlaLysThrTyr 608
Db
1717 CTGCCAAAATTACTGCTGTCAATCAAGTGAATAAACTTGAGGATGTTGCT---------- 1767

Qy
609 GlnLeuLeuAlaLysArgGluValTrpAspGlnSerGlnArgAlaLeuAspValLeuThrMet 628
Db
1768 CAGCTTCAGGCGCGTCGTCCAGATTTGGCCCTAAA------CTGCCCCCCGGGAGGCCCTA 1821

Qy
629 GlnLeuLeuAspCysAsnPheSerGluAsnValLeuHisTyrLeuLeuGlnLeuLysLys 648
Db
1822 GAGCTTCTGGATTTCAACTATCCAGACCAGTACGTTCGAATATGCTGTAGGCGTTGCCTG 1881

Qy
649 GluSerLeuGluAspAspAspValLeuHisThrTyrLeuLeuGlnGlnLeuGlnLysAlaLeuVal 668
Db
1882 CGACAGATGAGTGATGAGAACTTTCTCAATATCTTTACAACTGGTGCAAGTGTTAAAA 1941

Qy
669 PheGluProTyrHisAspSerPheAlaLeuValIleLeuLysProPheLeuLysArgGlyLeuArgAsn 688
Db
1942 TATGAGCCTTTTCCTGATTGTGCCCTCTGTTCCTATTAGAAAGAGACACTTGGTAAT 2001

Qy
689 LysArgIleGlyHisGlyHisPheLeuPheTrpPheLeuLeuArgSerGluLeuAlaGlnSerArgHis 708
Db
2002 CGGAGGGATAGGGCAGTTCATTTTGGCATCTTAGGTCACAAGTG----------CAC 2049

Qy
709 --------TyrGlnProTyrHisAspProPheGluAlaTyrLeuProLeuGlyCysGly 725
Db
2050 ATTCCTGCTGCTCCAGTACAATTTGGTGCCATCCTGAGCATACTGCCCGGGA---AGT 2106

Qy
726 ThrAlaMetLeuHisAspPheThrGlnGlnLeuValGlnValIleAspMetLeuGlnLeuLysVal 745
Db
2107 GTGGGGCCACATGAAAGTGCTTCTAAGCAGGTTGAAGCACTCAATAAGTTAAAAACTTTA 2166

Qy
746 Thr------------IleAspIleLysSerLeuSerArgAlaGluLeuTyrArgAspValSerSerGlnVal 763
Db
2167 AATAGTTTAATCAAACTGAATGCCTGAAGTAAACAGAGCCAAAGGGAAGGAGGCCATG 2226
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Qy    764 IleSerGlnLeuLysGlnLys-------------LeuGluAsnLeuGlnAsnLeuAsn 778
          :::||||||||                     ||||||||:::
Db   2227 CATACCTGTTTAAAACAGAGTGCTTACCGGGAAGCCCTTCTGACCTGCAGTCA------ 2280

Qy    779 LeuProGlnSerPheArgValProTyrAspProGlyLeuLysAlaGlyAlaLeuValIle 798
          |||  :::  ||||||||||||:::
Db   2281 -------CCCTGAACCCATGTGTTATCCTCTCCAGAACTCTATGTT 2319

Qy    799 GluLysCysLysValMetAlaSerLysLysProLeuTrpLeuPheGluLysCysAla 818
          ||||||||||   :::|||||||||||   :::
Db   2320 GAAAAGTGCAAATACATGGATTCCAAATGAAGCCCTTTGTGGCTGGTATAC-------- 2370

Qy    819 AspProThrAlaLeuSerAsnGluThrIleGlyTyrIleIlePheLysHisGlyAspAspLeu 838
          :::       :::::||||||||||:::||||||||||:::|||||||||
Db   2371 AATAACAAGGTATTTGGTGAGGATTCAGTTGGAGTGATTTTTAAAAATGGTGATGATTTA 2430

Qy    839 ArgGlnAspMetLeuLeuGlnIleLeuArgIleMetGluSerIleTrpGluThrGlu 858
          :::||||||   :||||||:::|||||||:::||||||:::
Db   2431 CGACAGGATATGTTGACACTCCAAATGTTGCGTTGAGGGATTACTCTGGAAGAAGCT 2490

Qy    859 SerLeuAspCysLeuLeuProTyrGlyCysIleSerGlyThrGlyAspLysIleGlyMet 878
          ||||||||||:::||||||||||||||||   :::
Db   2491 GGTTTGGATCTTGCCTTATGTCCTTAGCAACAGGAGATCGCTCTGGCCTC 2550

Qy    879 IleGluIleValLysAspAlaThrThrIleAlaLysValIleGln-------GlnSerThrVal 896
          ||||||   :::   ||||||||||
Db   2551 ATTGAAGTTGTGAGACACCTCTGAAACAATTGCTGACATTCAGCTGACAGTAGCAATGTG 2610

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Qy    917 IleGluGluLysPheGlnAlaAlaAlaValGluArgPheValTyrSerCysAlaGlyTyrCys 936
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Qy    937 ValAlaThrPheValLeuGlyTyrIleGlyAspArgHisAsnAspAsnIleMetIleSerGlu 956
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                    GenCore version 5.1.6
            Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on:        February 15, 2004, 02:16:17 ; Search time 148 Seconds
                                    (without alignments)
                             3286.515 Million cell updates/sec

Title:        US-09-974-573-1
Perfect score: 5790
Sequence:     1 MELENTEQPVVLREDNRRRR........QFNWFLHLVLGIKQGEKHSA 1102

Scoring table: BLOSUM62
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Searched:     569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters:      1139956

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
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-DB=Issued_Patents_NA -QMT=fastap -SUFIX=rni -MINMATCH=0.1 -LOOPCL=0
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-MODE=LOCAL -CUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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Database :    Issued_Patents_NA:*
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     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
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Result No.	Score	% Query Match	Length	DB	ID	Description
1	5726	98.9	3808	2	US-08-916-917-3	Sequence 3, Appli
2	5726	98.9	3808	2	US-08-972-631-3	Sequence 3, Appli
3	5726	98.9	3808	2	US-08-972-629-3	Sequence 3, Appli
4	5726	98.9	3808	2	US-08-972-630-3	Sequence 3, Appli
5	5726	98.9	3808	2	US-08-672-211-3	Sequence 3, Appli
6	5726	98.9	3808	3	US-09-225-170-3	Sequence 3, Appli
7	5534	95.6	5162	3	US-08-916-917-13	Sequence 13, Appli
8	5534	95.6	5162	3	US-09-225-170-13	Sequence 13, Appli
9	5499.5	95.0	4137	2	US-08-817-090B-3	Sequence 1, Appli
10	5440	94.0	4134	2	US-08-817-090B-1	Sequence 1, Appl
11	1465.5	25.3	3207	1	US-08-162-081B-35	Sequence 35, Appl
12	1465.5	25.3	3207	2	US-08-780-872-35	Sequence 35, Appl
13	1465.5	25.3	3207	3	US-09-085-957-35	Sequence 35, Appl
14	1460.5	25.2	3240	1	US-08-162-081B-34	Sequence 34, Appl
15	1460.5	25.2	3240	2	US-08-780-872-34	Sequence 34, Appl
16	1460.5	25.2	3240	3	US-09-085-957-34	Sequence 34, Appl
17	1460.5	25.2	3412	1	US-08-162-081B-32	Sequence 32, Appl
18	1460.5	25.2	3412	2	US-08-780-872-32	Sequence 32, Appl
19	1460.5	25.2	3412	3	US-09-085-957-32	Sequence 32, Appl
20	1354.5	23.4	3213	3	US-09-392-350-1	Sequence 1, Appli
21	1352.5	23.4	5220	2	US-08-777-405A-1	Sequence 1, Appli
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26	1349.5	23.3	3387	4	US-09-194-640A-29	Sequence 2, Appli
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40	322.5	5.6	2451	3	US-09-055-699-29	Sequence 29, Appl
41	322.5	5.6	2451	4	US-09-273-565-29	Sequence 29, Appl
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                              ALIGNMENTS

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; Sequence 3, Application US/08916917
; Patent No. 5856132
; GENERAL INFORMATION:
;  APPLICANT: Stephens, Len
;  APPLICANT: Hawkins, Phillip Thomas
;  APPLICANT: Braselmann, Sylvia
;  TITLE OF INVENTION: G-BETA-GAMMA REGULATED
;  TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
;  NUMBER OF SEQUENCES: 14
;  CORRESPONDENCE ADDRESS:
;  ADDRESSEE: Pennie & Edmonds, LLP
;  STREET: 1155 Avenue of the Americas
;  CITY: New York
;  STATE: NY
;  COUNTRY: USA
;  ZIP: 10036-2811
;  COMPUTER READABLE FORM:
;  MEDIUM TYPE: Diskette
;  COMPUTER: IBM Compatible
;  OPERATING SYSTEM: Windows
;  SOFTWARE: FastSEQ for Windows Version 2.0b
;  CURRENT APPLICATION DATA:
;  APPLICATION NUMBER: US/08/916,917
;  FILING DATE: 15-AUG-1997
;  CLASSIFICATION: 435
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: 08/672,211
;  FILING DATE: 27-JUN-1996
;  ATTORNEY/AGENT INFORMATION:
;  NAME: Abrams, Samuel B
;  REGISTRATION NUMBER: 30,605
;  REFERENCE/DOCKET NUMBER: 8549-0006-999
;  TELECOMMUNICATION INFORMATION:
;  TELEPHONE: 650-493-4935
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;   TELEFAX:  650-493-5556
;   TELEX:    66141 PENNIE
;   INFORMATION FOR SEQ ID NO:  3:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  3808 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS:  single
;     TOPOLOGY:  linear
US-08-916-917-3

Alignment Scores:
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Score:                 5726.00       Matches:        1090
Percent Similarity:    99.46%        Conservative:      6
Best Local Similarity: 98.91%        Mismatches:        6
Query Match:           98.89%        Indels:            0
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US-09-974-573-1 (1-1102)  x  US-08-916-917-3 (1-3808)
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Db 2909 GTTCTCGGAATAGGGGACAGACGGAACGACAATATTATGATCTCAGAAACCAGGAAATCTTA 2968

Qy 961 PheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLys 980
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Db 2969 TTTCATATTGATTTCGGACACATTCTTGGGAATTACAAAAGTTTCCTGGGCATTAATAAA 3028

Qy 981 GluArgValProPheValLeuThrProAspPheLeuPheValMetGlyThrSerGlyLys 1000
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Db 3029 GAGAGGGTGCCATTTGTGCTAACCCCAGACTTCCTGTTTGTGATGGGGACTTCTGGAAAG 3088

Qy 1001 LysThrSerLeuHisPheGlnLysPheGlnAspValCysValAlaTyrLeuAlaLeu 1020
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Db 3089 AAGACAAGTCTACACTTCCAGAAATTCCAGGATGTCTGCGTCGCGTTACCTAGCCCTT 3148

Qy 1021 ArgHisHisThrAsnLeuLeuIleIleLeuPheSerMetLeuMetThrGlyMetPro 1040
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Db 3149 CGTCATCACACAAACCTACTGATCATCCTCTTCTCCATGCTGATGACAGGAATGCCC 3208

Qy 1041 GlnLeuThrSerLysGluAspAspIleGluTyrIleArgAspAlaLeuThrValGlyLysLysSer 1060
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Db 3209 CAGTTAACCAGCAAAGAAGAGACATTGAATACATTCGGGATGCCCTCACAGTGGGCAAAAGT 3268

Qy 1061 GluGluAspAspAlaLysTyrTyrPheLeuAspGlnIleGluValCysArgAspLysGlyTrp 1080
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Db 3269 GAGGAGGATGCTAAAAGTATTTTCTGGATCAGATTGAAGTTGCAGAGACAAAGGATGG 3328

Qy 1081 ThrValGlnPheAsnTrpPheLeuHisLeuValLeuGlyIleLysGlnGlyGluLysHis 1100
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Db 3329 ACCGTGCAGTTTAACTGGTTTCTTACATCTTGTTCTTGGCATCAAACAAGGGGAGAAGCAT 3388

Qy 1101 SerAla 1102
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Db 3389 CCCGCA 3394

RESULT 2
US-08-972-631-3
; Sequence 3, Application US/08972631
; Patent No. 5856133
; GENERAL INFORMATION:
;   APPLICANT: Stephens, Len
;   APPLICANT: Hawkins, Phillip T.
;   TITLE OF INVENTION: G-BETA-GAMMA REGULATED
;   TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
;   NUMBER OF SEQUENCES: 10
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Pennie & Edmonds
;   STREET: 2730 Sand Hill Road
;   CITY: Menlo Park
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94025
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/972,631
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/672,211
;   FILING DATE: 27-JUN-1996
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Halluin, Albert P.
;   REGISTRATION NUMBER: 25,277
;   REFERENCE/DOCKET NUMBER: 8549-0005-999
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415)854-3660
;   TELEFAX: (415)854-3694
;   INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 3808 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: unknown
;   MOLECULE TYPE: cDNA
US-08-972-631-3

Alignment Scores:
Pred. No.:   0   Length: 3808
Score: 5726.00   Matches: 1090

Percent Similarity:	99.46%	Conservative: 6
Best Local Similarity:	98.91%	Mismatches: 6
Query Match:	98.89%	Indels: 0
DB:		Gaps: 2

US-09-974-573-1 (1-1102) x US-08-972-631-3 (1-3808)

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Db     89 ATGGAGCTGGAGAACATGATGAACAGCCCGGCACCCGGGTGCTGAGAGAGGACAACGGCCGCAGGCGT  148

Qy     21 ArgArgMetLysProArgSerThrAlaAlaSerLeuSerSerMetGluLeuIleProIle  40
Db    149 CGGAGGATGAAGCCGCGCAGCACCGGAGCCAGCCTGTCCTCCATGGAGCTCATCCCCATC  208

Qy     41 GluPheValLeuProThrSerGlnAsnThrLysThrProGluThrAlaLeuLeuHis  60
Db    209 GAGTTTGTGTTTGGCCACCAGCCAGCCAACACCAAGACCCCGGAAACGGCACTGCTGCAC  268

Qy     61 ValAlaGlyHisGlyAsnValGluGluMetLysAlaGlyInValTrpLeuArgAlaLeuGlu  80
Db    269 GTGGCCGGCCACGGCAATGTGGAAGAGATGAAGGCCCAGGTGTTGCGCGCGCTGGAG  328

Qy     81 ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTyr  100
Db    329 ACGAGCGGTTCTGGGACTTCTACCACCGGCTTGGGCCCGACCACTTCCTCCTGGTTTC  388

Qy    101 GlnLysLysSerGlyGlnTrpTyrGluIleTyrAspLysTyrGlnValValGlnThrLeuAsp  120
Db    389 CAGAGAGAGGGGGAGGTGTACGAGATCTATGACAAGTACCAGGTGGTGCAGACCCTGAC  448

Qy    121 CysLeuArgTyrTrpLysTrpLysLysProGlyGlnIleHisValValGlnArg  140
Db    449 TGCCTGCGCTACTGGAGGTGTTCACCGAGATCCACGTGGTCAGGCGG  508

Qy    141 HisAlaProSerGluGluThrGluGlnPheGlnArgGlnLeuAsnAlaAlaLeuGlyTyr  160
Db    509 CACGGCGCCCTCGGAGGAGACATTGGCCTTCCAGCGCGCAGCTCCAACGCGCCTCATCGGTAC  568

Qy    161 AspValThrAspValSerAsnValHisAspAspGluGluLeuLysAspProLeuTyrArgArgLeu  180
Db    569 GACGTCACCGACGTCAGCAACGTGCATGACGATGAGCTGAAGCTTTACGCCGCCGCTG  628

Qy    181 ValThrProArgMetAlaGlyValAlaGlyAlaGlyLysAspAspProLysLeuTyrAlaMetHisPro  200
Db    629 GTCACCCCCGGACATGGCCGGCGAGGTGGCCGGCCGGCCCAAGCTTTACGCCATGCACCCC  688

Qy    201 TrpValThrSerLysProLeuProGluTyrLeuProLysLysIleThrAsnAsnCysVal  220
Db    689 TGGGTGACATCCAAGCCCCTCCCTGAGTACCTTCTGAAGAAGATCACTAACACTGCGTC  748

Qy    221 PheIleValIleHisArgSerThrThrSerGlnThrIleLysValSerAlaAspAspThr  240
Db    749 TTCATCGTCATTCACCGCAGCACCACCAGCCAGACCATCAAGGTCTCGGCCGATGACACC  808

Qy    241 ProGlyThrIleLysThrPhePheThrLysMetAlaLysLysSerLeuMetAsp  260
Db    809 CCAGGGACCATCAAGACGTTCTTTACCAAGATGGCCAAGAAGAAATCTCCTGATGGAT  868

Qy    261 IleProGluSerGlnAsnGluArgAspPheValArgGlnPheValArgAspGluTyr  280
Db    869 ATCCCTGAGAGCCAGAACGAACCAGACGGGACTTTGTGCGTCGCGCTCGTAGGAGGTGTAC  928

Qy    281 LeuValGlyGluThrProLeuGluLysPheGlnAsnPheGlyCysLeuLysAsnGly  300
Db    929 CTGGTGGGGTGAGACGTGAGAAGTTTCAGTGGGTGAGGCAGTGCCTCAAGAATGGG  988

Qy    301 GluGlnIleHisLeuValLeuValAspAspProProAlaLeuAspGluValArgLys  320
Db    989 GAGCAGATTCACCTTGTGCTGGAAGATTTGAAATTTGAACCATGACAGTGCCCTAGCCAGATT  1048

Qy    321 GluGluTrpProLeuValAspAspCysThrGlyValThrGlyTyrHisGluGlnLeuThr  340
Db   1049 GAAGAGTGGCCGCTGGTGGATGACTGCACGGGAGTCACTGGCTACCACGAGCAGCTGACC  1108

Qy    341 IleHisGlyLysAspHisGluSerValPheThrValLeuSerLeuTrpAspCysArgLys  360
Db   1109 ATCCACGGCAAGGACCATGAAAGTGTTCACGTGTCCCTGTGGGACTGTGACCGCAAG  1168

Qy    361 PheArgValLysIleAspIleGlyIleLeuAspPheProArgLeuProArgThrAlaAspLeuThr  380
Db   1169 TTCAGGGTCAAAATCGATATCGGCCATTGATAATCCCGTCCTGCCCCGGACCGCTGACCTCACG  1228

Qy    381 ValPheValGluAlaAsnIleGlyTyrGlyGlnValLeuCysGlnValArgArgThrSer  400
Db   1229 GTGTTTGTGGAGGCAAACATCCAGTATGGGCAGGTGCTTTGCCAAAGGAGAACCAGC  1288

Qy    401 ProLysProPheThrGluValLeuValLeuTrpAsnValTrpLeuTrpLeuGluPheSerIleLeuLysHis  420
Db   1289 CCCAAACCCTTCACGGAGGAGGTGCTCTGGAACGTGTGGCTTGAGTTCAGTATTAAAATC  1348

Qy    421 LysAspLeuProLysGlyValAlaLeuLeuAsnLeuIleLeuTyrCysGlyLysAlaProAla  440
Db   1349 AAAGACTTACCCAAAGGGGTCTCTGCAACCTCCAGATCTACTGCGGCAAAGCTCCAGCA  1408

Qy    441 LeuSerGlyLysThrSerAlaGlnMetProSerProGluSerLysGlyLysLysAlaGlnLeu  460
Db   1409 CTGTCTGGCAAGACCTCTGCACAGATGCCCAGTCCCGAGTCCAAAGGCAAAGCTCAGCTT  1468

Qy    461 LeuTyrTyrValValAsnLeuLeuLeuHisArgGluLeuArgHisGlyHisGlyGluTyr  480
Db   1469 CTGTACTATGTCAACCTATTGCTGATAGACCACCGCCTTCCTCCTCGCGCATGGGAGTAT  1528

Qy    481 ValLeuHisMetTrpGlnLeuSerGlyLysGlyGluAspGlnGlySerPheAsnAlaAlaAsp  500
Db   1529 GTGCTCCACATGTGGCAGTTATCCCGGAAGGGGAAGACCAAGGGAGCTTCAATCCGGAC  1588

Qy    501 LysLeuThrSerAlaThrAsnProLysProLysHisArgProHisProProGluGly  520
Db   1589 AAGCTCACGTCGGGAACCACCCAGCCCTGCCAAGACTCAATGTCCATCTCCATTCTTCTG  1648

Qy    521 AspAsnTyrCysHisProIleAlaGluMetProAsnGlnLeuArgLeuArgTrpHisPro  540
Db   1649 GACAATTACTGCCACCCTATAGCCTTCGCCAAGCAATCAGCTTCGGAAGCAATCATAGCC  1708

Qy    541 AspArgArgAlaArgMetAlaGluAlaGlyLysLeuLeuGluAlaIleIleAla  560
Db   1709 GACCGGGTTCGGGCAGAAATGCCCAATCGCTTCGGAAGCTGGCTTGTCGAGGCAATAGGG  1768

Qy    561 ThrAspProLeuAsnProLeuThrArgAlaLysLysGluLeuTrpHisArgTyr  580
Db   1769 ACGGATCCGCTTAACCCACTCACGAGCGAAGCAGAAAGCTCCTGGCATTTCAGATAT  1828

Qy    581 GluSerLeuLysLysAspProLysLysAlaTyrProLysLeuPheSerSerValLysTrpGlyGln  600
Db   1829 GAAAGCTCAGGATCCAAAGCGTATCCTAAGCTCTTTAGCTCGGTGAAATGGGGACAG  1888

Qy    601 GlnGlyIleLeuAlaLysThrTyrGlnLeuLeuAlaAlaLysArgGluValTrpAspGlnSer  620
Db   1889 CAAGGAATTTTGGCCAAGACCTACCAATTATTAGCCGCAAAGGGAGGTCTGGATCGCAGT  1948

Qy    621 AlaLeuAspAspValGlyLeuThrMetGlnLeuLeuLeuAspCysAsnPheSerAsnVal  640
Db   1949 GCTTTGGATGTTGGGCAAACATACCAGCTGCTGCTGGATGTGCCACTTCCATTACCTG  2008

Qy    641 ArgAlaIleAlaValGlnLeuSerLeuGluAspAspAspValLeuHisTyrLeu  660
Db   2009 AGAGCCATTGCAGTCGAGTCCAGAAACTGGAGAGCTTGGAGGATGATGACGTGCTG  2068

Qy    661 LeuGlnLeuValGlnAlaValLysAspGluPheGlyProTyrHisAspSerAlaLeuAlaArgPhe  680
Db   2069 CTCCAGCTGGTGCAGGCTGTGAAATTGAACCATGACAGTGCCCTAGCCAGATTT  2128

Qy    681 LeuLeuLeuArgGlyLeuArgAsnLysArgIleGlyHisPheLeuTrpPheLeuArg  700
Db   2129 CTGCTGCTGAAGCGTGGGTTTAAGAAACAAGAGAATTGGTCACTTCTTGTTTGTTCTTGAGA  2188
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Qy  701 SerGluIleAlaGlnSerArgHisTyrGlnGlnArgPheAlaValIleLeuGluAlaTyr 720
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Db 2189 AGTGAGATTGCCCAGTCACATCAGCAGAGGTTTGCAGTGATCCTGGAAGCCTAC 2248

Qy  721 LeuArgGlyCysThrAlaMetLeuHisAspPheThrGlnGlnValGlnValIleAspAsp 740
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Db 2249 CTGAGGGGCTGTGGCACAGCCATGCTGCACGACTTCACCCAGCAAGTCCAAGTAATTGAC 2308

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Db 2369 TCCCAAGTTATTTCCCAACTTAAGCAAAAGCTTGAAAACCTACAGAAATTTGAATCTCCC 2428

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Db 2489 TGTAAAGTGATGGCCTCCAAGAAGAAGCCCCTGTGGCTTGAGTTTAAATGTGCCGATCCT 2548

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Db 2549 ACGGCTCTCAATGAAACAATTGGAATTATCTTAAACACGGTGACGATCTGCGCCAA 2608

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Db 2669 GATCTGTGCCTCCTGCCATATGGCTGCATTTCAACTGGTGACAAAATAGGAATGATCGAG 2728

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Db 2729 ATCGTGAAGGACGCCACGACAATCGCCAAAATTCAGAACAGCACAGTGGGCAACACGGGT 2788

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Db 2789 GCCTTTAAAGATGAAGTCCTGAGTCACTGGCTCAAAGAAAAATGCCCCATTGAAGAAAAG 2848

Qy  921 PheGlnAlaAlaValGlnArgPheValTyrSerCysAlaGlyTyrCysValAlaThrPhe 940
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Qy  961 PheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLys 980
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2969 TTTCATATTGATTTCGGACACATCTTGGAAATTACAAAAGTTTCCTGGGCATTAATAAA 3028

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Qy 1021 ArgHisHisThrAsnLeuIleLeuIleLeuPheSerMetMetLeuMetThrGlyMetPro 1040
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Db 3149 CGTCATCACACAAACCTACTGATCATCCTTTCCATGATGCTGATGACAGGAATGCCC 3208

Qy 1041 GlnLeuThrSerGlyGluAspIleGluTyrIleArgAspAlaLeuThrValGlyLysSer 1060
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Db 3269 GAGGAGGATGCTAAAAAGTATTTTCTGGATCAGATTGAAGTTTGCAGAGACAAAGGATGG 3328

Qy 1081 ThrValGlnPheAsnTrpPheLeuHisLeuValLeuGlyIleLysGlyGluLysHis 1100
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Db 3329 ACCGTGCAGTTAACTGGTTCTTACATCTTGGTTCTTGGCATCAACAAGGGGAGAAGCAT 3388

Qy 1101 SerAla 1102
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Db 3389 CCCGCA 3394
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RESULT 3
US-08-972-629-3

; Sequence 3, Application US/08972629
; Patent No. 5859201

GENERAL INFORMATION:

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  APPLICANT: Stephens, Len
  APPLICANT: Hawkins, Phillip T.
  TITLE OF INVENTION: G-BETA-GAMMA REGULATED
  TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
  NUMBER OF SEQUENCES: 10
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Pennie & Edmonds
    STREET: 2730 Sand Hill Road
    CITY: Menlo Park
    STATE: California
    COUNTRY: USA
    ZIP: 94025
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/972,629
    FILING DATE:
  CLASSIFICATION:
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/672,211
    FILING DATE: 27-JUN-1996
  ATTORNEY/AGENT INFORMATION:
    NAME: Halluin, Albert P.
    REGISTRATION NUMBER: 25,277
    REFERENCE/DOCKET NUMBER: 8549-0005-999
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (415)854-3660
    TELEFAX: (415)854-3694
INFORMATION FOR SEQ ID NO: 3:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 3808 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: unknown
    MOLECULE TYPE: cDNA
US-08-972-629-3
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Alignment Scores:

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Pred. No.:              0              Length:        3808
Score:            5726.00             Matches:       1090
Percent Similarity: 99.46%            Conservative:     6
Best Local Similarity: 98.91%         Mismatches:       6
Query Match:        98.89%            Indels:           0
DB:                     2             Gaps:             0
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US-09-974-573-1 (1-1102) x US-08-972-629-3 (1-3808)

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Qy    1 MetGluLeuGluAsnTyrGluGlnProValLeuArgGluAsnArgArgArgArg 20
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Qy   21 ArgArgMetLysProArgSerThrAlaSerLeuSerMetGluLeuIleProIle 40
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Qy  401 ProLysProPheThrGluValValLeuTrpAsnValTrpLeuGluPheSerIleLysIle 420
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Db 1289 CCCAAACCCTTCACGGAGGAGGTGGTGCTTCTGGAACGTGTTGGCTTGGAGTTCAGTATTAAAAATC 1348

Qy  421 LysAspLeuProLysGlyAlaLeuLeuAsnLeuGlnIleTyrCysGlyLysAlaProAla 440
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Qy  441 LeuSerGlyLysThrSerAlaGluMetProSerProSerLysGlyLysAlaGlnLeu 460
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Db 1409 CTGTCTGGCAAGACCTCTGCAGAGATGCCCAGTCCGAGTAAAGGCAAAGCTCAGCTT 1468

Qy  461 LeuTyrTyrValAsnLeuLeuIleAspHisArgPheLeuArgHisGlyGluTyr 480
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Qy  481 ValLeuHisMetTrpGlnLeuSerGlyLysGlyAspGlnGlySerPheAsnAlaAsp 500
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Qy  501 LysLeuThrSerAlaThrAsnProAspLysGluAsnSerMetSerIleSerIleLeuLeu 520
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Qy  541 AspArgAlaArgAlaGluMetProAsnGlnLeuLysGlnLeuGlnLeuAlaIleIleAla 560
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Qy  561 ThrAspProLeuAsnProLeuThrAlaGluAlaThrSerGluLeuTrpHisPheArgTyr 580
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Qy  581 GluSerLeuLysAspProLysAlaTyrProLysLeuPheSerSerValLysTrpTyrGln 600
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Db 1829 GAAAGCCTGAAGGATCCCAAAGCGTATCCTAAGCTCTTTAGCTCGGTGAAATGGGGACAG 1888

Qy  601 GlnGluLeuValAlaLysGlyTyrLeuThrMetGlnAsnLeuLeuAspCysTyrAsnVal 620
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Db 1889 CAAGAAATTGTGGCCAAAGGTTAACCTAACCATTATTAGCTGACTCGGATGAAAACGTG 1948

Qy  621 AlaLeuAlaLeuAlaValGlyGlyLeuThrHisArgIleGlyHisPheLeuTyrLeu 640
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Db 1949 GCTTTGGATGTGGGGTTAACGAGTCTCCAGTCTGCACTTCTGCTCCATTACCTG 2008

Qy  641 ArgArgValAlaArgAsnArgGlnSerAspAspAspValAlaLeuHisTyrLeu 660
            |||||||||||||||||||||||||||||||||||||||||||
Db 2009 AGAGCCATTGCCAGTCTCCAGAAACTGGAGAACTGGAGGAGGTTGAGGATGACTGCCAGAGT 2068

Qy  661 LeuGlnLeuValGlnAlaValLysProGluGluHisAspLysAlaLeuAspArgPhe 680
            |||||||||||||||||||||||||||||||||||||||||||||||
Db 2069 CTCCAGCTGGTCCAGGCTGTGAAATTGAAATTGAACCATACCATGACAGTGCCCTAGCCAGGATTT 2128

Qy  681 LeuLeuLysArgGlyLeuArgAsnLysArgIleGlyHisGlyHisPheTrpPheLeuArg 700
            |||||||||||||||||||||||||||||||||||||||||||||||
Db 2129 CTGCTGAAGCGTGGTTTAAGAAACAAGAGAATTGGTCACTTCTGTTTTGGTTCTTGAGA 2188

Qy  701 SerGluIleAlaGlnSerArgHisTyrGlnAsnArgPheAlaValIleLeuGluAlaTyr 720
            |||||||||||||||||||||||||||||||||||||||||||||||
Db 2189 AGTGAGATTGCCCAGTCCAGGCACTATCAGAACAGAGTTTGCAGTCCTGGAAGCCTAC 2248

Qy  721 LeuArgGlyCysGlyThrAlaMetLeuHisAspPheThrGlnGlnValIleLeuAsp 740
            |||||||||||||||||||||||||||||||||||||||||||
Db 2249 CTGAGGGGCTGTGGCACCAGCATGCTGCACGACTTCACCCAGCAAGTAATTGAC 2308

Qy  741 MetLeuGlnLysValThrIleLeuAspIleLysSerLeuLysSerAlaGluGlyLysTyrValSer 760
            |||||||||||||||||||||||||||||||||||||||||||||||
Db 2309 ATGTTACAAAAAGTCACCATTCTGGACATTAAATCGCTTCTCTGCTGAAAAATGACGTCAGT 2368
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Db  149 CGGAGGATGAAGCCGGCACGGCAGCCAGCCTGCCTCCATGAGAGCTCATCCCCATC 208
Qy   41 GluPheLeuProThrSerGlnThrLysThrProGluThrAlaLeuLeuHis
            |||||||||||||||||||||||||||||||||||||||||
Db  209 GAGTTTGTTTGGCCACCAGCGCAACACCAGAGACCCCGAAACGGCACTGCTGCAC 268
Qy   61 ValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnAsnValTrpLeuArgAlaLeuGlu 80
            :::::|||||||||||||||||||||||||||||||||||||||||
Db  269 GTGGCCGGCCACGGCAATGTGGAGCAGATGAAGGCCCAGGTGTTGTTGCGGCGCTGGAG 328
Qy   81 ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTyr 100
            |||:::::::::::::::::::::::::::::::
Db  329 ACGAGCGTTTCTGGACTTCTACCACCGGTTCGGCCCGACCACTTCCTCCTGGTCTTC 388
Qy  101 GlnLysLysGlyGlnThrTrpTyrGluIleTyrArgLysAspLysTyrArgGlnValValGlnThrLeuAsp 120
            |||||||||||||||||||||||||||||||||||||||||
Db  389 CAGAAGAAGGGGAGTGTACAGAATTATGACAAGTACCAGGTGTGCAGACCCTGGAC 448
Qy  121 CysLeuArgArgTyrTrpLysTrpValGlyLeuHisArgSerProGlyGlnIleHisValValGlnArg 140
            |||||||||||||||||||||||||||||||||||||||||||
Db  449 TGCCTGCGCTACTGGAGAGTGTGCAACCGCAGCCCGGGACAGATCCACGTGGTCCAGCGG 508
Qy  141 HisAlaProSerGluGluThrLeuValAlaPheGlnLeuArgGlnLeuAsnAlaLeuIleGlyTyr 160
            |||||||||||||||||||||||||||||||||||||||||||
Db  509 CACGCGCCCTCGGAGGAGACATTGGCCTTCCAGCGCTCCAGCTCAACGCCCTCAAGGCTAC 568
Qy  161 AspAspValThrAspAlaValSerAlaAsnValHisAspAspGlyLeuGluGlyPheGluGluLeuLysArgArgLeu 180
            |||||||||||||||||||||||||||||||||||||||||||||||
Db  569 GACGTCACCGACGCTCAGCAACGCAGCAAGGTGCATGATGACGGTGGAGTTCACGCGGCGCCGCCTG 628
Qy  181 ValThrProArgMetAlaAlaGluGlyGlyAlaValAlaGlyProLeuTyrLeuAlaMetHisPro 200
            |||||||||||||||||||||||||||||||||||||||||||
Db  629 GTCACCCCGCCGCATGGCCGAGGTGGCCCGGCCCGCCAAGTTTTACGCCCATGCACCCC 688
Qy  201 TrpValThrSerLeuProLeuProGluTyrProGluTyrLeuLeuLeuLysLysLysThrAsnAsnCysVal 220
            |||||||||||||||||||||||||||||||||||||||||||
Db  689 TGGGTGACATCCAAGCCCCTCCCTGAGTACCCTGAGTACCTGAGAGATCACTAACAACTGCGTC 748
Qy  221 PheIleIleHisArgSerThrThrSerGlnIleThrIleLeuGluLysValSerAlaAspAspThr 240
            |||||||||||||||||||||||||||||||||||||||||||
Db  749 TTCATCGTCATTCACCGCAGCACCACCAGCCAGATGGCCAAGATAACCATCAAGGTCTCGCGGCGATGACACC 808
Qy  241 ProGlyThrIleLeuGlnSerPhePheThrTyrProThrValArgGlnLeuArgAspGluThr 260
            |||||||||||||||||||||||||||||||||||||||||||
Db  809 CCAGGCACCATCCTCCCAGAGCTTCTTTACCAAGATGGCCAAGAGAAATCCTGATGGAT 868
Qy  261 IleProGluSerGlnLeuArgAspAspLysProGluPheValCysLeuArgArgGlyGluGlyTyr 280
            |||||||||||||||||||||||||||||||||||||||||||
Db  869 ATCCCTGGGGAGCTCAAGAACAGAGAGACTTTGTGTGCCTGCGCTCGCGGCGGGATGAGTAC 928
Qy  281 LeuValGlyLysGluHisGluHisValLeuGluAspLeuLeuAspProAlaAlaProAspGlnLeuAsnGly 300
            |||||||||||||||||||||||||||||||||||||||||||
Db  929 CTGGTGGGTGAGCAGCGTGAGCATGTGCTGGAGGACCTGCTCGACCCTGCAGCTCCAGAATGGG 988
Qy  301 GluGluIleHisLeuValLeuAspAspGluLeuLysLysTyrProAlaAlaValAspGluAspAspValLysArgLys 320
            |||||||||||||||||||||||||||||||||||||||||||
Db  989 GAGGAGATTCACCTTGTGCTGGACAGTGAACTGCGGATAGTGCCCTGAGCGAGTGAGGAAG 1048
Qy  321 GluLeuTrpProProLeuValAspAspCysThrGlyValThrArgGlyTyrTyrHisGlyGlnLeuGlnLeuThr 340
            |||||||||||||||||||||||||||||||||||||||||||
Db 1049 GAAGAGTGGCCGCCGGTGATGATGGCACACACCGAGTCACTGGCTACCGAGCAGCCAGCTCACC 1108
Qy  341 IleHisGlyLysLysAspHisGlySerValPheThrValPheIleProProGluGlnTrpArgArgGly 360
            |||||||||||||||||||||||||||||||||||||||||||
Db 1109 ATCCACGGCAAGGACCATGAAAGTGTGTTCACCGTGTCCCTGGGACTGTGACCGGCAAG 1168
Qy  361 PheArgValLysAsnArgGlyIleIleGluAspIleAspHisTyrGlyGlnValAlaAspLeuThr 380
            |||||||||||||||||||||||||||||||||||||||||||
Db 1169 TTCAGGGTCAAAAACAGAGGCATTGAATTCCCTGTCCTCCTGCTGCACCTCACG 1228
Qy  381 ValPheGluValAlaAsnIleGlnAsnTyrGlyGlnLeuValLeuCysGlnArgArgArgThrArgSer 400
            |||||||||||||||||||||||||||||||||||||||||||
Db 1229 GTGTTTGAGGTGGCCAAACATCACCCAGTATGGCGCCAAGTGCCTTTGCCAAAGGGAGAACCAGCC 1288
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US-08-972-630-3
; Sequence 3, Application US/08972630
; Patent No. 5869271
; GENERAL INFORMATION:
;-  APPLICANT: Stephens, Len
;-  APPLICANT: Hawkins, Phillip T.
;-  TITLE OF INVENTION: G-BETA-GAMMA REGULATED
;-  TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
;-  NUMBER OF SEQUENCES: 10
;-  CORRESPONDENCE ADDRESS:
;-    ADDRESSEE: Pennie & Edmonds
;-    STREET: 2730 Sand Hill Road
;-    CITY: Menlo Park
;-    STATE: California
;-    COUNTRY: USA
;-    ZIP: 94025
;-  COMPUTER READABLE FORM:
;-    MEDIUM TYPE: Floppy disk
;-    COMPUTER: IBM PC compatible
;-    OPERATING SYSTEM: PC-DOS/MS-DOS
;-    SOFTWARE: PatentIn Release #1.0, Version #1.30
;-  CURRENT APPLICATION DATA:
;-    APPLICATION NUMBER: US/08/972,630
;-    FILING DATE:
;-    CLASSIFICATION:
;-  PRIOR APPLICATION DATA:
;-    APPLICATION NUMBER: US 08/672,211
;-    FILING DATE: 27-JUN-1996
;-  ATTORNEY/AGENT INFORMATION:
;-    NAME: Halluin, Albert P.
;-    REGISTRATION NUMBER: 25,277
;-    REFERENCE/DOCKET NUMBER: 8549-0005-999
;-  TELECOMMUNICATION INFORMATION:
;-    TELEPHONE: (415)854-3660
;-    TELEFAX: (415)854-3694
; INFORMATION FOR SEQ ID NO: 3:
;-  SEQUENCE CHARACTERISTICS:
;-    LENGTH: 3808 base pairs
;-    TYPE: nucleic acid
;-    STRANDEDNESS: single
;-    TOPOLOGY: unknown
;-  MOLECULE TYPE: cDNA
US-08-972-630-3

Alignment Scores:
Pred. No.:                           0           Length:        3808
Score:                          5726.00          Matches:       1090
Percent Similarity:              99.46%          Conservative:     6
Best Local Similarity:           98.91%          Mismatches:       6
Query Match:                     98.89%          Indels:           0
DB:                                   2          Gaps:             0

US-09-974-573-1 (1-1102) x US-08-972-630-3 (1-3808)
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Qy    1  MetGluLeuGlnTyrGlyGlnProValValLeuArgGluAspAsnArgArgArgArg  20
Db   89  ATGGAGCTGGAGAACTATGAACAGCCCGTGGTGCTGAGAGAGGACAACCGCCGAGGCGT  148

Qy   21  ArgArgMetLysProArgSerThrAlaAlaSerLeuSerMetGluSerArgIleProIle  40
Db  149  CGGAGGATGAAGCCGCGCAGCACGGCAGCCTGTCCTCCATGGAGTCCAGGATCCCCATC  208

Qy   41  GluPheValLeuProThrSerGlnArgAsnThrTyrProGluThrAlaLeuLeuHis  60
Db  209  GAGTTTGTTTTGCCCACCAGCCAGCCGCAACACCAAGACCCCCGAAACGGCACTGCTGCAC  268

Qy   61  ValAlaGlyHisGlyAsnValGluHisMetLysAlaGlnValTrpLeuArgAlaLeuGlu  80
Db  269  GTGGCCGGCCACGGCAATGTGGAGCAATGAGAAGGCCCAGGTGTTGTTGCGCGCTGGAG  328

Qy   81  ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTyr  100
Db  329  ACGAGCGTTTCTTGGGACTTCTCACCACCGGTTCGCCCGACCACTTCCTCCTGGTCTTC  388
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Qy   761  SerGlnValIleSerGlnLeuLysGlnLeuGluAsnLeuGlnAsnLeuAsnLeuPro  780
Db  2369  TCCCAAGTTATTTCCCAACTTAAGCAAAGCTTGAAAACCTACAGAATTTGAATCTCCCC  2428

Qy   781  GlnSerPheArgValProTyrAspProGlyLeuLysAlaGlyValAlaLeuValIleGluLys  800
Db  2429  CAAAGCTTTAGAGTCCCTATGATCCTGGACTGCTGAAAGCCGGGCACTGGTGATCGAAAA  2488

Qy   801  CysLysValMetAlaSerLysLysProLeuTrpLeuGluPheLysCysAlaAspPro  820
Db  2489  TGTAAAGTGATGGCCTCCAAGAAGAAGCCCCTGTGGCTTGAGTTTAAATGTGCCGATCCT  2548

Qy   821  ThrAlaLeuSerArgAsnGluThrIleGlyIleIleLysGlyHisGlyAspSerLeuArgGln  840
Db  2549  ACGGCTCTCATCAAATGAAACAATTGGAATTATCTTTAAACACGGTGACGATCTGCGCCAA  2608

Qy   841  AspMetLeuIleLeuGlnIleLeuArgIleMetGluSerIleTrpGluThrGluSerLeu  860
Db  2609  GACATGCTTATTTTACAGATTCTACGAATCATGGAGTCAATTGGGAGACCGAGAATCTTTG  2668

Qy   861  AspLeuCysLeuLeuProTyrGlyCysIleSerThrGlyAspLysIleGlyMetIleGlu  880
Db  2669  GATCTGTGCCTCCTGCCATATGGCTGCATTTCAACTGGTGACAAAATAGGAATGATCGAG  2728

Qy   881  IleValLysAspAlaThrIleAlaLysThrIleAlaLysSerThrValGlyAsnThrGly  900
Db  2729  ATCGTGAAGGACGCCACAGACAGCCAAAATCGCCAAAATCAGCAAAGCACAGTGGGCAACACGGGT  2788

Qy   901  AlaPheValAspGluValLeuSerHisTrpLeuLysGluGluLysLysCysProIleGluGluLys  920
Db  2789  GCCTTTAAAGATGAAGATCCCTGAGTCACTGGCTCAAAGAAGAAATGCCCTATTGAAGAAAAG  2848

Qy   921  PheGlnAlaAlaValGlnArgPheValTyrSerCysAlaGlyTyrCysValAlaThrPhe  940
Db  2849  TTTCAGGCAGCTGTGGAGAGATTTGTTTATTCCTGCGCAGGCTACTGTGTGGCAACCTTT  2908

Qy   941  ValLeuGlyIleGlyAspArgHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeu  960
Db  2909  GTTCTCGGAATAGGCGACAGAGCACAATGACAATATTATGATCTCAGAAACAGGAAATCTA  2968

Qy   961  PheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLys  980
Db  2969  TTTCATATTGATTTCGGACACATTCTTGGAAATTACAAAAGTTTCCTTGGCATTAATAAA  3028

Qy   981  GluArgValProPheValLeuThrProAspPheLeuPheValMetGlyThrSerGlyValLys  1000
Db  3029  GAGAGGGTGCCATTTGTGCTAACCCCAGACTTCCTGTTTGTTGTGATGGGGACTTCTGGAAAG  3088

Qy  1001  LysThrSerLeuHisPheGlnLysPheGlnValAspGlnIleIleGluValGlyArgArgLeuAlaLeu  1020
Db  3089  AAGACAAGTCTACACTTCCAGAAATTTCAGGATGTCTCGTCAAGGGTTACCTAGCCCTT  3148

Qy  1021  ArgHisHisThrAsnLeuLeuIleLeuLeuPheSerMetMetLeuMetThrGlyMetPro  1040
Db  3149  CGTCATCACACAAACCTACTGATCATCCTCTTCTCCATGATGCTCATGACAGGAATGCCC  3208

Qy  1041  GlnLeuThrSerLysGluAspProIleGluTyrIleArgAspAlaLeuThrValGlyLysSer  1060
Db  3209  CAGTTAACCAGCAAAGAAGACAATTGAAATACATTCGGGATGCCCTCACAGTGGGCAAAAGT  3268

Qy  1061  GluGluAspAlaLysLysTyrPheLeuAspGlnIleIleGluValCysArgAspAspGlyTrp  1080
Db  3269  GAGGAGGATGCTAAAAAGTATTTTCTGGATCAGATTGAAGTTTGCAGAGACAAAGGATGG  3328

Qy  1081  ThrValGlnPheAsnTrpPheLeuHisLeuValLeuGlyIleLysGlnGlyGluLysHis  1100
Db  3329  ACCGTGCAGTTTAACTGGTTCTTACATCTTGTTCTTGGCATCAAACAAGGGGAGAAGCAT  3388

Qy  1101  SerAla  1102
Db  3389  CCCGCA  3394
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RESULT 4

Left column

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Qy  101 GlnLysGlyGlnTrpTyrGluIleTyrAspLysTyrGlnValValGlnThrLeuAsp 120
        |||||||||  ||::|  ||||||||||||||||||||||||||||||||||||||||
Db  389 CAGAAGAGGGGGAGTGGTACGAGATCTATGACAAGTACCAGGTGGTGCAGACCCTGGAC 448

Qy  121 CysLeuArgTyrTrpLysValLeuValAspSerProGlyGlnIleHisValValGlnArg 140
        ||||||||||||||||||  :||
Db  449 TGCCTGCGCTACTGGGAGGTGTTGCACCGGAGATCCAGGCCCGGGATCCGTGGTCCAGCGG 508

Qy  141 HisAlaProSerGluGluThrLeuAlaPheGlnArgGlnLeuAsnAlaLeuIleGlyTyr 160
        ||||||||||||
Db  509 CACGCGCCCTCCGGAGGAGACAATTGGCCTTCCAGCGCGCAACCCCTCAACCGCCATCGGCTAC 568

Qy  161 AspValThrAspValSerAsnValHisAspAspGluLeuPheThrArgArgLeu 180
Db  569 GACGTCACCGACGTCAGCAACGTGCATGACGATGAGCTGGAGTTCACGCGGCCGCTG 628

Qy  181 ValThrProArgMetAlaAlaGluValAlaAlaGlyTyrArgAspProLysLeuTyrLeuTyrArgAlaMetHisPro 200
Db  629 GTCACCCCGCGCATGGCCGAGGTGGCCGCGGGTTACCGCGACCCCAAGCTTTACCTGTATCGTGCCATGCACCCC 688

Qy  201 TrpValThrSerLysProLeuProGluTyrLeuLysLeuLysLysIleThrAsnAsnCysVal 220
Db  689 TGGGTGACATCCAAGCCCCTCCCTGAGTACCTTCTGAAGAAGAAATCTCGGCCGATGACACC 748

Qy  221 PheIleValIleHisArgSerThrThrSerGlnThrIleThrLysLysValSerValSerAlaAspAspThr 240
Db  749 TTCATCGTCATTCACCGCAGCACCACCAGCCAGACCATCACCAAGAAGGTCTCGGCCGATGATGGAT 808

Qy  241 ProGlyThrLeuGlnSerPheThrLysMetAlaLysAlaLysSerLeuMetAsp 260
Db  809 CCAGGCACCCTCCAGAGCTTCTTACCAAGATGGCCAAGGCCAAGAGCCTGATGGAT 868

Qy  261 IleProGluSerGlnAsnGluArgAspPheValLeuArgValCysGlyArgAspGluTyr 280
Db  869 ATCCCTGAAAGCCAGAACGAACGGGACTTTGTGCTCGCGTCTGCGGCGGGATGACGTAC 928

Qy  281 LeuValGlyLeuThrProIleLysProIleLysAsnPheGlnTrpValArgGlnCysLeuLysAsnGly 300
Db  929 CTGGTGGGTGAGACGCCCATCAAAAATTTCCAGTGGGTGAGGCAGTGCCTCAAGAATGGG 988

Qy  301 GluLeuIleHisLeuValLeuValAspThrProProAspProAlaLeuAspGluLeuAspGluValAlaArgLys 320
Db  989 GAGCTGATTCACCTTGTCTGGACACTCCTCCAGACCCTGGGGACTGTGACGGAGAAG 1048

Qy  321 GluGluThrProProLeuValAlaAspCysTyrSerTyrValThrGlyValThrGlyTyrHisGluGlnLeuThr 340
Db 1049 GAAGAGTGGCCGCTGGTGGTCGATGACTGCACGGAGAGTCACTGGCTACCACGAGCAGCTGACC 1108

Qy  341 IleHisGlyLysAspHisGluSerValPheThrValSerLeuPheTrpAspCysArgArgLys 360
Db 1109 ATCCACGGCAAGGACCATGAAAGTGTTCACCGTGTCCCTGTTTGGGACTGTGACCGGAAG 1168

Qy  361 PheArgValLysLysArgGlyIleTyrIleAspPheIleGlyProValLeuProValArgThrAlaAspLeuThr 380
Db 1169 TTCAGGGTCAAAAATCAGAGGCATTGATATTCCCGTTCCTCCTGTCCCCCGACCGCTGACCCTCACG 1228

Qy  381 ValPheValGluAlaGluAlaAsnIleGlyThrTyrGlyGlnGlnGlnValLeuGlnValLysLeuCysGlnAsnArgArgThrSer 400
Db 1229 GTGTTTGTGGAGGCAGAAGCAAACATCGGCATGTGGCAGCAAGTCCTTTGCCAAGGAGAACCAGC 1288

Qy  401 ProLysProPheThrGluGluValLeuLeuTrpAsnValPheAsnLeuGluProSerIleLeuLysIle 420
Db 1289 CCCAAACCCTTCACTGAGGAAGTGCTTCTGTGGAACGTGTCCAACCTTGAGCCCTCAGATTATTAAAATC 1348

Qy  421 LysAspLeuProLysGlyAlaLeuLeuLeuAsnLeuGlnIleLeuTyrCysGlyGlyLysAlaProAla 440
Db 1349 AAAGACTTACCCAAAGGGGCTCTGCTCCTGAACCTCCAGATTCTACTGCGGCGAAAGCTCCAGCA 1408

Qy  441 LeuSerGlyLysThrSerAlaGluGluMetProSerProGluSerLysGlyGlyLysAlaGlnLeuLeu 460
Db 1409 CTGTCTGGGAAGACCTCTGCAGAAGAGATGCCCAGCCCTGAGTCTAAAGGTGGCCTTGAGTTTAAATGCCCAATCCT 1468
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Right column

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Qy  461 LeuTyrTyrValAsnLeuLeuLeuIleAspHisArgPheLeuArgHisGlyGluTyr 480
Db 1469 CTGTACTATGTCAACCTATTGCTGATAGACCACCGCTTCCTCCGGCCATGGGAGTAT 1528

Qy  481 ValLeuHisMetTrpGlnLeuSerGlyLysGlyGluProGlnLysGluPheAsnAlaAsp 500
Db 1529 GTGCTCCACATGTGGCAGTTATCCGGGAAGGGGGAAGACCAAGGGAGCTTCAATGCCGAC 1588

Qy  501 LysLeuThrSerAlaThrAsnProAspLysGluAsnSerMetSerIleSerIleLeuLeu 520
Db 1589 AAGTTCACGTCGGAACCAACCCGGACAAGGAGGACTCAATGTCCATTCCATTCTTCTG 1648

Qy  521 AspAsnTyrCysHisProIleAlaLeuProLysHisArgProAspProGlyGly 540
Db 1649 GACAATTACTGCCACCCCATAGCCTTGCCTAAGCATCGGCCTGACCCTGGAGGG 1708

Qy  541 AspArgValAlaGlyLysMetProAsnGlnAsnLeuArgLysGlnLeuGlnLeuAlaIleIleAla 560
Db 1709 GACCGGGTTCCGGGCAAAATGCCCAATCAGCTTCGGAAGCAACTGGAGGCAATCATAGCC 1768

Qy  561 ThrAspProLeuAsnProLeuThrArgAlaGluAspLysGluLeuLeuTrpHisPheArgTyr 580
Db 1769 ACGGATCCGTTAACCCACCTGAGCACTGAAGACAAAGAACTGCTCTGGCATTTCAGATAT 1828

Qy  581 GluSerLeuLysAspProLysAlaTyrProLysLeuPheSerSerValLysTrpGlyGlnSer 600
Db 1829 GAAAGCCTGAAGGATCCCAAAGCGTATCCCAAGGCTCTTTAGCTCGGTGAAATGGGGACAG 1888

Qy  601 GlnGluIleValAlaAlaLysThrTyrTyrGlnLeuLeuAlaLeuAlaLysArgGluValTrpAspGlnSer 620
Db 1889 CAAGAAATTGTGGCCAAACATACCAATTATTAGCCAAAAGGGAGGTCTGGATCCAGAGT 1948

Qy  621 AlaLeuAspAspValGlyLeuThrMetGlnLeuLeuAsnAspCysAsnPheSerAspGluAsnVal 640
Db 1949 GCTTTGGATGTGGGGGTTAACCATGCAGCTCCTGGACTGCAACTTCTCGGATGAAAACGTG 2008

Qy  641 ArgAlaIleAlaValGlnLysLeuLeuGluSerLeuGluAspAspAspValLeuHisTyrArgLeu 660
Db 2009 AGAGCCATTGCAGTCCAGAAACTGGAGAGTCTTGGAGGATGATGACGTGCTCCATTACCTG 2068

Qy  661 LeuGlnLeuValGlnAlaValLysSerPheGluProTyrHisAspSerAlaLeuAlaArgPhe 680
Db 2069 CTCCAGCTGGTCCAGGCTGTGAAATTTGAACCATACCATGACAGTGCCCTAGCCAGATTT 2128

Qy  681 LeuLeuLeuArgGlyLeuAsnLysArgIleGlyHisPheLeuProTrpPheLeuArg 700
Db 2129 CTGCTGAAGCGGTGGTTAAGAACAAGAGAATTGGTCACTCTTGTTTGTTCTTGAGA 2188

Qy  701 SerGluIleAlaGlnSerArgHisTyrGlnAsnArgPheAlaValIleLeuGluLeuAlaTyr 720
Db 2189 AGTGAGATTGCCCAGTCCAGCCACTATCAGCAGAGGTTTGCAGTCCTGGAAGCCTAC 2248

Qy  721 LeuArgGlyCysGlyTyrThrAlaMetLeuHisAspPheThrGlnValGlnIleAspAsp 740
Db 2249 CTGAGAGGGCTGTGGCACTGGCCCATGCTGCACGACTTCACCCAGCAAGTCCAAGTAATTGAC 2308

Qy  741 MetLeuGlnLysValThrIleLysSerLeuSerLeuAspGluAlaGluLysSerTyrAspValSer 760
Db 2309 ATGTTACAAAAAGTCACCATTAAATCGCTTTCGCTCTGTGAAAAGATGACGTCAGT 2368

Qy  761 SerGlnValIleLeuSerGlnLysLeuGluGlnAsnLeuAsnLeuAsnLeuPro 780
Db 2369 TCCCAAGTTATTTCCAACTTAAGCAAAGGTTGAAAACTTACAGATTTGAAATCTCCCC 2428

Qy  781 GlnSerPheArgValProTyrAspProGlyLeuLysAlaGlyValIleLeuGluLysLys 800
Db 2429 CAAAGCTTTAGAGTTCCCTATGATCCTGGACTGAAAGCCGGGACTGGTGATCAGAAA 2488

Qy  801 CysLysValMetAlaSerLysLysProLeuTrpGluPheLysCysAlaAspPro 820
Db 2489 TGTAAAGTGATGGCCTCCAAGAAGAGCCCCTTGTGGGAGTTTAAATGCGCCGATCCT 2548

Qy  821 ThrAlaLeuSerAsnGluThrIleGlyTyrIleGlyIleIlePheLysHisPheLysHisGlyAspLeuArgGln 840
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STATE: California
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,211
FILING DATE: 27-JUN-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,277
REFERENCE/DOCKET NUMBER: 8549-0005-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)854-3660
TELEFAX: (415)854-3694
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3808 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
US-08-672-211-3

Alignment Scores:
Pred. No.:   0   Length: 3808
Score: 5726.00   Matches: 1090
Percent Similarity: 99.46%   Conservative: 6
Best Local Similarity: 98.91%   Mismatches: 6
Query Match: 98.89%   Indels: 0
DB: 2   Gaps: 0

US-09-974-573-1 (1-1102) x US-08-672-211-3 (1-3808)

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Qy     1 MetGluLeuGluAsnTyrGluGlnProValLeuArgGluAspAsnArgArgArgArg     20
Db    89 ATGGAGCTGGAGAACTATGAACAGCCCGTGCTGCGAGAGGAGGACAACCGCCAGGCGT    148

Qy    21 ArgArgMetLysProArgSerThrAlaAlaSerLeuSerMetGluLeuIleProIle     40
Db   149 CGGAGGATGAAGCCCCGGTCCACGGCGGCCAGCCTGTCCATGGAGCTCATCCCCATC    208

Qy    41 GluPheValLeuProThrSerGlnArgAsnThrLysThrProGlyThrAlaLeuLeuHis     60
Db   209 GAGTTTGTTTTGCCAACCAGCCAGCGCAACACCAAGACCCCGAAACGGCACTGCTGCAC    268

Qy    61 ValAlaAlaGlyHisGlyAsnValGluGlnMetLysAlaAlaGlnValTrpLeuArgAlaLeuGlu     80
Db   269 GTGGCCGCGGGCCACGGCAATGTGGAGCAAATGAAGGCCCAGGTGTTGTTGCGGGCGCTGGAG    328

Qy    81 ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisProLysLeuArgLeuLeuTyr    100
Db   329 ACGAGCGTTTCTTGGACTTCTACCACCGGTTCGGCCCCGACCACCCTCCTGGTCTTC    388

Qy   101 GlnLysLysGlyGlnTrpTyrGlnIleTyrGluTyrThrGlnValValGlnThrLeuAsp    120
Db   389 CAGAAGAAGGGGGAGTGGTACGAGATCTATGAGTACACCAGGTGCAGACCCTGGAC    448

Qy   121 CysLeuArgTyrTrpLysValLeuHisArgSerProGlyGlnIleHisValValGlnArg    140
Db   449 TGCCTGCGCTACTGGGAGGTGTTGCACCGGAGCCCCGGGCAGATCCACGTGGTCCAGCGG    508

Qy   141 HisAlaProSerGluThrLeuAlaPheLeuArgGlnLeuAsnAlaLeuIleGlyTyr    160
Db   509 CACGGGCCCTCGGAGACAGCATTGGCCTTCCAGCTGCAGCTTCAAGCCCTCATCGGCTAC    568

Qy   161 AspValThrAspValSerAsnValHisAspAspArgGluGluThrArgArgLeu    180
Db   569 GACGTCACCGACGTCAGCAACGTGCATGAGCTGGAGTTCACGCGCGCGCCCCTG    628
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[Lower portion - sequence alignment, read bottom-to-top for page flow]

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Db  2549 ACGGCTCATCAAATGAACAATTGGAATTATCTTTAAACACGGTGACCATCTGCGCCAA  2608

Qy   841 AspMetLeuIleLeuGluGlnIleLeuGluArgIleMetGluSerIleTrpGluSerLeu   860
Db  2609 GACATGCTTATTTTACAGATTCTACGAATCATGAGTCCCATTTGGGAGACCGAATCTTTG  2668

Qy   861 AspLeuCysLeuLeuProTyrGlyTyrCysLeuGlyProTyrGlyAspLysIleGlyTyrMetIleGlu   880
Db  2669 GATCGTGTGCCTCCTGCATTCGACTGGTGACAAAATAGGAATGATCAG  2728

Qy   881 IleValLysAspAlaThrThrIleAlaLysIleGlnGlnSerThrValGlyTyrAsnThrGly   900
Db  2729 ATCGTGAAGGACGACGCCACGACAATCGCCAAAATTCAGCAAGACAGTGGGCAACACCGGT  2788

Qy   901 AlaPheLysAspGluValLeuSerHisTrpLeuLysGluHisTrpGlyGluGlyLys   920
Db  2789 GCCTTTAAAGATGAAGTCCTGAGTCACTGGCTCAAAGAAAAATGCCCATTGAAGAAAAG  2848

Qy   921 PheGlnAlaAlaAlaValGluArgPheValTyrSerCysAlaGlyTyrCysValAlaThrPhe   940
Db  2849 TTTCAGGCAGCTGTGGAGAGATTGTTTATTCCTGTGCCGGCTACTGTGTGGCAACCTTT  2908

Qy   941 ValLeuGlyTyrIleGluGlyTyrAsnAspAsnIleMetIleSerGluThrGlyLysAsnLeu   960
Db  2909 GTTCTCGGAATAGGCGACAGACAACAATGACAATTATGATCTCAGAAAACAGAAATCTA  2968

Qy   961 PheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLys   980
Db  2969 TTTCATATTGATTTCGGACACATTCTTGGGAATTACAAAAGTTTCCTGGGCATTAATAAA  3028

Qy   981 GluArgValProPheValLeuThrProAspPheLeuPheValMetGlyThrSerGlyLys  1000
Db  3029 GAGAGGGTGCCATTTGTGCTAACCCCAGACTTCCTGTTTGTGATGGGGACTTCTGGAAAG  3088

Qy  1001 LysThrSerLeuHisPheGlnLysPheGlnAsnAspValCysValLysAlaTyrLeuAlaLeu  1020
Db  3089 AAGACAAGCTCACACTTCCAGAAATTTCAGAATGACGTGTGCGTCAAGGCTTACCTAGCCCTT  3148

Qy  1021 ArgHisThrAsnLeuIleLeuIleLeuPheSerMetMetLeuMetThrGlyMetPro  1040
Db  3149 CGTCATCACAAACCTACTGATCATCCTTTCTCCATGATGCTGATGACAGGAATGCCC  3208

Qy  1041 GlnLeuThrSerLysGluLysProIleIleArgIleGluAspAlaLeuArgValGlyLysSer  1060
Db  3209 CAGTTAACCAGCAAAGAGAAGCCAATACAATTCGGGATGATGCCCTGCACAGTGGCAAAAGT  3268

Qy  1061 GluGluAspAlaAlaLysTyrPheLeuLeuAspGlnIleGluVaCysArgGlyAspLysGlyTrp  1080
Db  3269 GAGGAGGATGCTAAAAGTATTTTCTGGATCAGATTGAAGTTTGCAGAGACAAAGGATGG  3328

Qy  1081 ThrValGlnPheAsnTrpPheLeuHisLeuValLeuGlyIleLysGlnGlnGluLysHis  1100
Db  3329 ACCGTGCAGTTTAACTGGTTCCTTACATCTTGTTCCTGGCATCAAACAAACAGGGAGAAGCAT  3388

Qy  1101 SerAla  1102
Db  3389 CCCGCA  3394
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RESULT 5
US-08-672-211-3
; Sequence 3, Application US/08672211
; Patent No. 5874273
GENERAL INFORMATION:
APPLICANT: Stephens, Len
APPLICANT: Hawkins, Phillip T.
TITLE OF INVENTION: G-BETA-GAMMA REGULATED
TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 2730 Sand Hill Road
CITY: Menlo Park

Qy   541 AspArgValArgAlaGluMetProAsnGlnLeuArgLysGlnLeuGluAlaAlaIleIleAla 560
             ||||| ||| ||||||||||||||||| |||||||||||| |||
Db 1709 GACCGGGTTCGGGAGAAATGCCCAATCAGCTTCGGAGCAACTGGAGGCAACTCATAGCC 1768

Qy   561 ThrAspProLeuAsnProLeuThrAlaGluAspLysGluLeuLeuTrpHisPheArgTyr 580
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Db 1769 ACGGATCCGCTTAACCCACTCACCGCAGAAGACAAAGAACTGCTCTGGCATTTCAGATAT 1828

Qy   581 GluSerLeuLysAspProLysAlaTyrProLysLeuPheSerSerValLysTrpGlyGln 600
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Db 1829 GAAAGCCTGAAGGATCCCAAAGCGTATCCTAAGCTCTTTAGCTCGGTGAAATGGGGACAG 1888

Qy   601 GlnGluIleValAlaLysThrTyrGlnLeuLeuAlaLysArgGluValTrpAspGlnSer 620
             ||||||||||| |||||
Db 1889 CAAGAGATTGTGGCCAAAACATACCAATTATTAGCCAAAAGGGAGGTCTGGGATCAGAGT 1948

Qy   621 AlaLeuAspValGlyLeuThrMetGlnLeuLeuAspCysAsnPheSerAspGluAsnVal 640
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Db 1949 GCTTTGGATGTGGGGTTAACCATGCAGCTCCTGGACTGCAACTTCTCGGATGAAAACGTG 2008

Qy   641 ArgAlaAlaIleAlaAlaValGlnLysLeuLeuGluSerLeuGluAspAspAspValHisTyrLeu 660
             |||||||||| |||
Db 2009 AGAGCCATTGCAGCTGTCCAGAAACTGGAGAGCTTGGAGGATGATGACGTGCCATTACCTG 2068

Qy   661 LeuGlnLeuValGlnAlaValLysPheGluProTyrHisAspSerAlaLeuAlaArgPhe 680
             |||||||||||
Db 2069 CTTCCAGCTGGTCCAGGCTGTGGAAATTTGAACCATACCATGACAGTGCCCTAGCCAGATTT 2128

Qy   681 LeuLeuLysArgGlyLeuValArgAsnLysArgIleGlyHisGlyLeuPheTrpPheLeuArg 700
             ||||||||||
Db 2129 CTGCTGAAGCGTGGTTTAAGAACACAAGAGAATTGGTCACTTCTTGTTTGGTTCTTGAGA 2188

Qy   701 SerGluIleAlaGlnSerArgHisTyrArgGlnAsnArgPheHisLeuValIleLeuGluAlaTyr 720
             |||||||||||
Db 2189 AGTGAGATTGCCCAGTCTAGGCACTATCAGCAGAACCGTTTCGATGATCCTGGAAGCCTAC 2248

Qy   721 LeuArgGlyCysGlyThrAlaMetLeuHisAspPheThrGlnGlnValIleLeuAsp 740
             |||||||||||
Db 2249 CTGAGGGGCTGTGGCACAGCCATGCTGCACGACTTCACCCAGCAAGTAATTGAC 2308

Qy   741 MetLeuGlnLysValThrArgIleLeuAspIleLysSerLeuSerLysAlaGluGlyTyrAspLysTyrAspValSer 760
             ||||||||||
Db 2309 ATGTTACAAAAGTCACCATGACATTAAATCGCTCTCTGCTGAAAGTATGACTCAGT 2368

Qy   761 SerGlnValIleSerGlnLeuLeuGlnLysAspValGlnLeuAsnLeuGlnAsnLeuAsnLeuPro 780
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Db 2369 TCCCAAGTTATTTCCCAACTTAAGCAAAAGCTTGAAAAACTACAGAATTTGAATCTCCCC 2428

Qy   781 GlnSerPheArgValProTyrAspProGlyTyrLeuGlyLeuAlaGlyTyrLeuAlaLeuValIleGluLys 800
             |||||||||||
Db 2429 CAAAGCTTTAGAGTTCCCTATGATCCTGGACTCCGAAAGCTGGCACTGGTGATCGAAAAA 2488

Qy   801 CysLysLysValMetAlaSerLysLysAspProLeuTrpLeuGluPheLysCysLysAlaAspPro 820
             |||||||||||
Db 2489 TGTAAGAAAGTGATGGCCTCCAAGAAAGAGCCCCTGTGGCTTGAGTTTAAATGTGGCGATCCT 2548

Qy   821 ThrAlaLeuSerAsnGluThrIleGlyIleIlePheLysHisGlyAspAspLeuArgGln 840
             |||||||||||
Db 2549 ACGGCTCTCATCAAATGAAACATTGGAATATCTTTAAACACGGTGACGATCTGCGCCAA 2608

Qy   841 AspMetLeuIleLeuGluGlnIleLeuGluArgIleMetGluSerIleTrpGluThrGluSerLeu 860
             |||||||||||
Db 2609 GACATGCTTATTTTACAGATTCTACGAATCATGAGAGTCCATTGGGAGACCGAATCTTTG 2668

Qy   861 AspLeuCysLeuProTyrGlyCysIleSerSerThrGlyAspLysProLysMetIleGlu 880
             |||||||||||
Db 2669 GATCTGTGCCTCCCGTGCCCATATGGCTGCATTCAACTGGTGACAAAATAGGAATGATCGAG 2728

Qy   881 IleValLysAspAlaThrThrIleAlaLysIleGlnInSerThrValGlyAsnThrGly 900
             |||||||||||
Db 2729 ATCGTGAAGGACGCCACGACAATCGCCAAAATTCAGCACACGTGGCAACACGGGT 2788

Qy   901 AlaPheLysAspGluValLeuSerHisTrpLeuLysGluLysCysProIleGluGluLys 920

Qy   181 ValThrProArgMetAlaGluValAlaGlyValArgAspProLeuTyrAlaMetHisPro 200
             |||||||||||
Db   629 GTCACCCCGCGCATGGCCGAGGTGGCCGGCGTCCGCGACCCCCTGTACGCCATGCACCCC 688

Qy   201 TrpValThrSerLysProLeuProGluTyrLeuLysLysIleThrAsnAsnCysVal 220
             |||||||||||
Db   689 TGGGTGACATCCAAGCCCCTCCCTGAGTACCTTCTGAAGAAGATCACTAACAACTGCGTC 748

Qy   221 PheIleValIleHisArgSerThrThrSerGlnThrIleLysValAlaSerAlaAspThr 240
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Db   749 TTCATCGTCATTCATCGCAGCACCACCAGCCAGACCATCAAGGTCGCTTCGGCCGATGACACC 808

Qy   241 ProGlyThrIleLeuGlnInSerPhePheThrLysMetAlaLeuValLysLysSerLeuMetAsp 260
             |||||||||||
Db   809 CCAGGCACCATCCTCCAGAGCTTCTTTACCAAGATGGCCAAGAGAAATCTGATGGAT 868

Qy   261 IleProGluSerGlnAsnGluLeuArgAspPheValLeuArgValCysGlyTyrArgAspGluTyr 280
             |||||||||||
Db   869 ATCCCTGAAAGCCAGAACGAACGGGACTTTGTGCTGCGCGTCTGCGGCTACCGGGATGAGTAC 928

Qy   281 LeuValGlyLysThrProIleLeuGluLysPheAsnPheGlnInTrpProValArgGlnCysLeuLysAsnGly 300
             |||||||||||
Db   929 CTGGTGGGTAAGACGCCCATCAAAAAATTTCCAGTGGGTCAGGTGTGCCTCAAGAATGGG 988

Qy   301 GlnGluIleHisGlnValLeuLeuAspThrProProAlaLeuAspAspGluValValArgLys 320
             |||||||||||
Db   989 GAGGAGATTCACCTTGTCTGGACACTCCTCCCAGACCCTGGACGAGGTGAGGAAG 1048

Qy   321 GlyGluTrpProLeuValAspAspaCysThrGlyValThrGlyValThrTyrArgHisGlyGlnLeuThr 340
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Db 1049 GAAGAGTGGCCGCTGGTGGATGACTGCCGCGGGAGTCACCGACAGCTGACC 1108

Qy   341 IleHisSerGlyValAspHisGlyGluSerValPheThrValSerLeuTrpValSerAspCysAspArgGlySer 360
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Db 1109 ATCCACAGCGGCGTGGACCATGGAAAGTGTGTTCACCGTGTCCCTGTGGGACTGTGACCGGAAG 1168

Qy   361 PheArgValLysIleArgGlyTyrIleAspIleProValLeuProValLeuProValAlaAspThrAlaAspLeuThr 380
             |||||||||||
Db 1169 TTCAGGGTCAAAATCAGAGGCTATATTGATATCCCTGTCCTGCCCGGACCTTGCTTCACG 1228

Qy   381 ValPheValGluValAlaAsnIleGlnInTyrGlyValGlnInValLeuCysGlnInArgGlyThrSer 400
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Db 1229 GTGTTTGTGGAGGCAAACATCCAGTATGGGCAGCAAGTCCTTTGCCAAAGGAGAAACCAGC 1288

Qy   401 ProLysProPheThrGluProPheGluValLeuTrpAsnValTrpLeuPheSerIleLysSerIle 420
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Db 1289 CCCAAACCCTTCACGGAGCCGGAGGTTCTCTGGAACGTGTGGCTTTCAGTTTCAGTATTAAAATC 1348

Qy   421 LysAspLeuProLeuGlyAlaAlaLeuLeuAsnLeuGlnInIleTyrCysLysGlyLysAlaProAla 440
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Db 1349 AAAGACTTACCCCTAGGGGGCTCTGCTGCAACCTCCAGATCTACTGGAAGGCAAAGTCCAGCA 1408

Qy   441 LeuSerGlyLysThrSerAlaGluMetProSerProGluSerLysLysLysAlaGlnInLeu 460
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Db 1409 CTGTCTGGCAAGACCTCTGCAGAGATGCCCAGTCCCGAGAGCAAAAGGAGAAACCAAAGCCAAAGCTT 1468

Qy   461 LeuTyrTyrValAsnLeuLeuIleAspGluPheArgLeuLeuArgHisGlyGluTyr 480
             |||||||||||
Db 1469 CTGTACTATGTGAACCTATTGCTCGATGAATTCCGCCTTCCTCCGCGACATGGCGAGTAT 1528

Qy   481 ValLeuHisMetTrpGlnInLeuSerArgAlaGluMetProSerProGlnLysLysGlyGlnInLysSerIleSerAsnAlaAsp 500
             |||||||||||
Db 1529 GTGCTCCACATGTGGCAGTATCCGGAGGGGGAAGACTCCCATGCCAATGCCGAC 1588

Qy   501 LysLeuThrSerAlaThrAsnProAsnAspLysLysGlnLysProGlnInSerMetSerIleSerLeuLeu 520
             |||::|||||
Db 1589 AAGCTCACGTCGGCAACCAACCCGAACGACAAGAAAAAGCAAAAGCCGCAATCGGCCAGGAGGACTCAATGTCCATCTCCTGCTG 1648

Qy   521 AspAsnTyrCysHisProIleAlaLeuProLysHisArgProThrProAspProGluGlyGly 540
             |||||||||||
Db 1649 GACAATTACTGCCACCCCATAGCCTTGCCTAAGCATCGGCCGACTCCCGACCCGGAGGGG 1708

ATTORNEY/AGENT INFORMATION:
    NAME: Abrams, Samuel B
    REGISTRATION NUMBER: 30,605
    REFERENCE/DOCKET NUMBER: 8549-0006-999
TELECOMMUNICATION INFORMATION:
    TELEPHONE: 650-493-4935
    TELEFAX: 650-493-5556
    TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
    LENGTH: 3808 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
US-09-225-170-3

Alignment Scores:
Pred. No.:   0   Length: 3808
Score: 5726.00   Matches: 1090
Percent Similarity: 99.46%   Conservative: 6
Best Local Similarity: 98.91%   Mismatches: 6
Query Match: 98.89%   Indels: 0
DB: 3   Gaps: 0

US-09-974-573-1 (1-1102)   x US-09-225-170-3 (1-3808)

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Qy     21 ArgArgMetLysProArgSerThrAlaAlaSerLeuSerMetGluLeuSerMetGluProIle     40
Db    149 CGGAGGATGAAGCCGCGCAGCACCGCAGCCCTGTCCATGGAGCTCCATCCCCATC    208

Qy     41 GluPheValLeuProThrSerGlnArgAsnThrLysThrProGlyThrAlaLeuLeuHis     60
Db    209 GAGTTTGTTTTGCCACCAGCCAGCGCAACACCAAGACCCCGGAAACGGCACTGCTGCAC    268

Qy     61 ValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnHisValTrpLeuArgAlaLeuGlu     80
Db    269 GTGGCCGGCCACGGCAATGTGGAGAAGATGAAGGCCCAGGTGTGTTGCGGCGCTGGAG    328

Qy     81 ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTyr    100
Db    329 ACGAGCCGTTCTTGGACTTCACCGGTCGGCCCCGACCACTTCCTTCCTTCCTTGGTCTTC    388

Qy    101 GlnLysGlyGlyValGlnTrpTyrGlnIleTyrAspLysTyrGlnThrLeuValGlnThrLeuAsp    120
Db    389 CAGAAGAAGGGCGGAGTGGTACCAGATCTATGACAAGTACCAGGTGGTGCAGACCCTGGAC    448

Qy    121 CysLeuArgTyrTrpLysValLeuHisArgSerProGlyGlnIleHisValValGlnArg    140
Db    449 TGCCTGCGCTACTGGAAGGTGTTGCACCGCAGCCCCGGGCAGATCCACGTGGTCCAGCGCGG    508

Qy    141 HisAlaProSerGluGluThrLeuAlaPheGlnLeuArgGlnLeuAsnAlaAlaLeuIleGlyTyr    160
Db    509 CACGCGCCCTCCGAGGAGACATTGGCCTTCCAGCTGCGACCCCTCAACCCCCTACCGCCTAC    568

Qy    161 AspValThrAspValSerAsnValHisAspAspValCysLeuAsnThrArgArgArgLeu    180
Db    569 GACGTCACCGACGTCAGCAACGTGCACGATGACGTGGAGTTCACGCGGCGCGCCGCCTG    628

Qy    181 ValThrProArgMetAlaGluValAlaGlyValAlaGlyArgAspProLeuTyrAlaMetHisPro    200
Db    629 GTCACCCCGCGCATGGCCGAGGTGGCCGGCCGGCCGACCCCAAGCTTTTACGCCATGCACCCC    688

Qy    201 TrpValThrSerLysProLeuProGluTyrLeuLeuLysIleThrAsnAspAsnCysVal    220
Db    689 TGGGTGACATCCAAGCCCCTCCCTGAGTACCTTTCTGAAGAAGATCACTAACAACTGCGTC    748

Qy    221 PheIleValIleHisArgSerThrThrSerGlnThrLeuLysValSerAlaAspAspThr    240
Db    749 TTCATCGTCATTCACCGCAGCACCACCAGCCAGACCATCAAGGTCTCGGCCGATGACACC    808
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Db   2789 GCCTTTAAAGATGAAGTCCTGAGTCACTCGGCTCAAAGAAAAATGCCCTATTGAAGAAAAG    2848

Qy    921 PheGlnAlaAlaValAlaGluArgPheValTyrSerCysAlaGlyTyrCysValAlaThrPhe    940
Db   2849 TTTCAGGCAGCTGTGGAGAGATTTGTTTATTCCTGTGCCGGCTACTGTGTGGCAACCTTT    2908

Qy    941 ValLeuGlyIleGlyValArgHisAsnAspAlaArgIleSerGluThrGlyAsnLeu    960
Db   2909 GTTCTCGGAATAGGCGACAGACAACAATGACAAATATTATGATCTCAGAAACAGGAAATCTA    2968

Qy    961 PheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLys    980
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Qy    981 GluArgValProPheValLeuThrProAspPheLeuValMetGlyThrSerGlyGlyLys    1000
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Qy   1001 LysThrSerLeuHisPheGlnLysPheGlnAspValCysValIleLysAlaTyrLeuAlaLeu    1020
Db   3089 AAGACAAGTCTACACTTCCAGAAATTTCAGGATGTCTGCGTCAAGGCTTACCTAGCCCTT    3148

Qy   1021 ArgHisHisThrAsnLeuLeuIleIleLeuPheSerMetMetLeuMetThrGlyMetPro    1040
Db   3149 CGTCATCACCACAAACCTACTGACATCATCCTTCTTCCCATGATGCTGATGACAGGAATGCCC    3208

Qy   1041 GlnLeuThrSerLysGluAspIleGluTyrIleArgAspAlaLeuThrValGlyLysLeuLeuSer    1060
Db   3209 CAGTTAACCAGCAAAGAACAGATAGAACATTGAATACATTCGGAGATGCCCTCACAGTGGGCAAAGT    3268

Qy   1061 GluGluAspAlaLysAlaLysTyrPheLeuAsnAlaArgIleGluValCysGlnAspLysGlyTyrTrp    1080
Db   3269 GAGGAGGATGCGTAAAAAAGTATTTTCTGATCAGATTGAAGTTTGCAGAGACAAAGGATGG    3328

Qy   1081 ThrValGlnPheAsnTrpPheLeuHisLeuValLeuGlyIleLysLeuGlyGlnGluLysHis    1100
Db   3329 ACCGTGCAGTTTAACTGGTTCTTACATCTTGTTCTTGGCATCAAAACAGGGGAGGAAGCAT    3388

Qy   1101 SerArg    1102
Db   3389 CCCCGCA    3394
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RESULT 6
US-09-225-170-3
; Sequence 3, Application US/09225170
Patent No. 6017763
GENERAL INFORMATION:
;   APPLICANT: Stephens, Len
;   APPLICANT: Hawkins, Phillip Thomas
;   APPLICANT: Braselmann, Sylvia
;   TITLE OF INVENTION: G-BETA-GAMMA REGULATED
;   TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
;   NUMBER OF SEQUENCES: 14
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Pennie & Edmonds, LLP
;   STREET: 1155 Avenue of the Americas
;   CITY: New York
;   STATE: NY
;   COUNTRY: USA
;   ZIP: 10036-2811
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: Windows
;   SOFTWARE: FastSEQ for Windows Version 2.0b
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/225,170
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/916,917
;   FILING DATE: 15-AUG-1997

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Qy   241  ProGlyThrIleLeuGlnSerPheThrLysMetAlaLysLysSerLeuMetAsp  260
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Db   809                                                             868

Qy   261  IleProGluSerGlnAsnGluArgAspPheValLeuArgValCysGlyArgAspGluTyr  280
          ATCCCTGAAAGCCAGAACGAACGGGACTTTGTGCTGCGCGTCTGCGGCCGGGATGAGTAC
Db   869                                                             928

Qy   281  LeuValGlyGluThrProIleLysAsnPheHisTrpValArgGlnThrCysLeuLysAsnGly  300
          CTGGTGGGTGAGACGCCCATCAAAAATTTCCAGTGGGTGAGGCAGTGCTGCTTCAAGAATGGG
Db   929                                                             988

Qy   301  GluGlnIleHisLeuValLeuAspThrProProAspProAlaLeuAspGluValArgLys  320
          GAGGAGATTCACCTTGTGCTGGACACCCCTCCAGACCCTGGACGAGGTGAGGAAG
Db   989                                                             1048

Qy   321  GluGluTrpProLeuValAspAspCysThrGlyValThrGlyTyrHisGluGlnLeuThr  340
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Db   1049                                                            1108

Qy   341  IleHisGlyLysAspHisGlnSerValPheThrValSerLeuTrpAspTyrAspProCysAspArgLys  360
          ATCCACGGCAAGGACCATCAGAGTGTGTTCACCGTGTCCCTGTGGGACTGTGACCGCAAG
Db   1109                                                            1168

Qy   361  PheArgValLysIleArgGlyTyrIleAspPheProValLeuProArgThrAlaAspLeuThr  380
          TTCAGGGTCAAAATCAGAGGCATTGATATCCCTGTCCTGCCCCGGACCGCTGACCTCACG
Db   1169                                                            1228

Qy   381  ValPheValGlyAlaAsnIleGlnTyrGlyGlnLeuValLeuCysGlnArgThrSer  400
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Db   1229                                                            1288

Qy   401  ProLysProPheThrGluGluLeuTrpAsnValTrpLeuGluPheLeuGluSerIleLysIle  420
          CCCAAACCCTTCACGGAGGAGCTGTGGAACGTGTGGCTTGAGTTCAGTATTAAAATC
Db   1289                                                            1348

Qy   421  LysAspLeuProLysGlyValAlaLeuLeuAsnLeuGlnIleTyrCysGlyGlyLysAlaProAla  440
          AAAGACTTACCCAAAGGGGCTCGCTGCTGAACCTCCAGATCTACTGCGGCAAAGCTCCAGCA
Db   1349                                                            1408

Qy   441  LeuSerGlyLysThrSerAlaGluMetProSerProGluSerLysGlyLysAlaGlnLeu  460
          CTGTCTGGCAAGACCTCTGCAGAATGCCCAGTCCCAGTCCCAAAGGCAAAGCTCAGCTT
Db   1409                                                            1468

Qy   461  LeuTyrTyrValAsnLeuLeuIleAspHisArgPheLeuLeuArgHisGlyGluTyr  480
          CTGTACTACGTGAACCTATTGCTGATAGACCACCGGTTCCTCCTGCGCCATGGCGAGTAT
Db   1469                                                            1528

Qy   481  ValLeuHisMetTrpGlnLeuSerGlyGlyLysGlyGlnLeuAspArgPheAsnAlaAsp  500
          GTGCTCCATGTGGCAGTTATCCGGAGGGGGAAGGGGCAAGGAGCTTCAATGCCGAC
Db   1529                                                            1588

Qy   501  LysLeuThrSerAlaThrAsnProAspAsnProAspLysGluAsnSerMetSerIleLeuLeuLeu  520
          AAGCTCACGTCGGAACCACCCGGAACAAGGAGGACTCAATGTCCATCCCATTCTTCTG
Db   1589                                                            1648

Qy   521  AspAsnTyrCysHisProIleLeuProLysAspHisArgProAspThrProGluGly  540
          GATCGTGCCCATCCTCCTGCCATCAATGGCTGCCATAATCGGCTACCCCTGACCCCAGAAGGG
Db   1649                                                            1708

Qy   541  AlaPheAlaAlaGluValMetProAsnGlnLeuArgLysLysGlnLeuLeuGluAlaIleIleAla  560
          GCCTTTGCAGCTGTGGAAATGCCCAATCAGCTTCGGAAGAAGCAACTGCTGGAAGCAATCATAGCC
Db   1709                                                            1768

Qy   561  ThrAspProLeuAsnProLeuThrAlaAspPheHisProTyr  580
          ACGGATCCCGCTTAACCCACTACAGCTGAAGACAAAGAACTGCTCTGGCATTTCAGATAT
Db   1769                                                            1828

Qy   581  GluSerLeuLysAspProLysAlaTyrProLysAlaPheSerSerValLysTrpGlyGln  600
          GAAAGCCTGAAGGATCCCAAAGCTATCCCAAAGGCTTCTTCTAGCTGTCGGTGAAATGGGGACAG
Db   1829                                                            1888
```

Right column:

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Qy   601  GlnGluIleValAlaAlaLysThrTyrGlnLeuAlaLeuAlaLysArgGluValTrpAspGlnSer  620
          CAAGAAATTGTGGCCGCAAAACATACCAATTATTAGCCAAAAGGGAGGTCTGGGATCAGAGT
Db   1889                                                            1948

Qy   621  AlaLeuAspValGlyLeuThrMetGlnLeuLeuAspLeuLeuAspCysAsnPheSerAspGluAsnVal  640
          GCTTTGGATGTGGGTTACCATGCAGCTCCTGACTGCAACTTCTCGGATGAAAACGTG
Db   1949                                                            2008

Qy   641  ArgAlaIleAlaValGlnLysLysGluSerLeuSerLeuUapAspAspValHisTyrLeu  660
          AGAGCCATTGCAGTCCAGAAGAAGGAGAGCTTGGAGGATGATGACGTGCTCCATTACCTG
Db   2009                                                            2068

Qy   661  LeuGlnLeuValGlnAlaValPheGlnHisProTyrHisAspSerAlaLeuAlaLeuArgPhe  680
          CTCCAGCTGGTGCAGGCTGTGAAATTTGAACCATACCATGACAGTGCCCTAGCCAGATTT
Db   2069                                                            2128

Qy   681  LeuLeuLysGlyLeuArgLysAsnLysArgIleGlyHisPheLeuPheTrpLeuArg  700
          CTGCTGAAGGGCTGGTTTAAGAAACAAGAGAATTGGTCACTTCTTTGGTTCCTTGAGA
Db   2129                                                            2188

Qy   701  SerGluIleAlaGlnSerArgHisTyrGlnAsnArgPheAlaValIleLeuGluAlaAlaTyr  720
          AGTGAGATTGCCCAGTCACGGCACTATCAGAACAGAGGTTTGCAGTGATCCTGGAAGCCTAC
Db   2189                                                            2248

Qy   721  LeuArgCysGlyThrAlaMetLeuHisAspPheThrGlnGlnLnValIleIleAsp  740
          CTGAGGGGCTGTGGCACAGCCATGCTGCACGACTTCACCCAGCAAGTATTGAC
Db   2249                                                            2308

Qy   741  MetLeuGlnLysValThrIleAspIleLysAspIleLysAspIleLysSerAlaGluLysSerTyrAspValSer  760
          ATGTTACAAAAGTCACCATTGACATTGAAAGATATGACGTCAGT
Db   2309                                                            2368

Qy   761  SerGlnValIleSerGlnLysLeuLysGlnLysLysGlnLeuAsnLeuGlnAsnLeuAsnLeuPro  780
          TCCCAAGTTATTTCCCAACTTAAGCAAAAGAGCTTGAAACCTACACAGAATTTGAATCTCCCC
Db   2369                                                            2428

Qy   781  GlnSerPheArgValProTyrArgAspGlyLeuLysGlyAlaLeuAlaLeuAlaLeuValIleGluLys  800
          CAAAGCTTTAGAGTTCCTATGATCCTGACTGGTTTAAATGTGCTGGCACTGGTGATCGAAAA
Db   2429                                                            2488

Qy   801  CysLysLysSerValMetAlaSerLysSerLysLysTrpGluTrpPheLysCysSerAlaAspPro  820
          TGTAAAGTGAATGCTGGCTCCAAGAAGAAGCCCCTGTGGCTTAAATGTTCAAATGTTCCGATCCT
Db   2489                                                            2548

Qy   821  ThrAlaLeuSerArgAsnGluThrIleGlyLyIleIlePheHisGlyAspAspLeuArgArgGln  840
          ACGGCTCTATCAAATGAAACCATTGGAATTATCTTTAAACGGTGACGATCTGCGCCAA
Db   2549                                                            2608

Qy   841  AspMetLeuLeuLeuGlnIleLeuLeuArgIleMetGluSerIleTrpGluTrpGluSerLeuLeu  860
          GACATGCTTATTTTACAGATTCTACGAATCATGGAGTCAATCATGGGAGACCGAATCTTTG
Db   2609                                                            2668

Qy   861  AspLeuCysLeuProTyrGlyCysIleSerSerHisTrpArgThrArgLeuLysLysGlyMetIleGlu  880
          GATCTGTGCCTCCTGCCATATGGCTGCATATCAACTTGCATTCAACTGGTCAAAAATAGGAATCGAG
Db   2669                                                            2728

Qy   881  IleValLysAspAlaThrArgIleAlaLysSerHisSerThrValGlyThrGly  900
          ATCGTGAAGGACGCCACGAGCATCGCCAAAATTCAGCAATGCCAAAGCACACGTGGGCAACACGGGT
Db   2729                                                            2788

Qy   901  AlaPheLysAspGluValGlnLysSerHisTrpLeuLysSerGluLysGluLysLys  920
          GCCTTTAAAGATGAAGTGCAGTCACTGGGTCAAAGAAAAATGCCCTATTGAAGAAGAAAG
Db   2789                                                            2848

Qy   921  PheGlnIleAlaAlaValGlnArgPheValTyrSerCysValAlaAlaThrPhe  940
          TTTCAGGGCGGCTGTGGCAGTCACTGGAGAGATTTGTTTATTCCTGGTGCTGTGTGCAACCTTT
Db   2849                                                            2908

Qy   941  ValLeuGlyIleGlyAspTyrArgHisAsnAspAsnIleMetIleSerGluThrHisValAsnLeu  960
          GTTCTCGGAATAGGCGACAGACAACACAATATTATGATCTCAGAAAACACGAAATCTA
Db   2909                                                            2968

Qy   961  PheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleLeuAsnLys  980
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;
; US-08-916-917-13
STRANDEDNESS: single
TOPOLOGY: linear

Alignment Scores:
Pred. No.:              0          Length:        5162
Score:                  5534.00    Matches:       1049
Percent Similarity:     97.10%     Conservative:  21
Best Local Similarity:  95.19%     Mismatches:    32
Query Match:            95.58%     Indels:        0
DB:                     2          Gaps:          0

US-09-974-573-1 (1-1102) x US-08-916-917-13 (1-5162)

Qy    1 MetGluLeuAsnTyrGluGlnProValLeuArgLeuValLeuAspAsnArgArgArgArg   20
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   84 ATGGAGCTGGAGAACTATAAACAGCCCGTGCTCAGACTGGTGCTGGACAACCGGCGGCGC  143

Qy   21 ArgArgMetLysProArgSerThrAlaAlaSerLeuSerMetGluLeuIleProIle     40
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  144 CGGAGGATGAAGCCGCGGTCTACGGCCGCCAGCCTGTCCATGGAGCTCATCCCCATC    203

Qy   41 GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeuLeuHis   60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  204 GAGTTCGTGCTCCCCACCAGCCAGCGCAAATGCAAGACCCCGAAACGGGCCCTGCTGCAC  263

Qy   61 ValAlaGlyHisGlyAsnValGluGlnMetLysAlaAlaGlnValTrpLeuArgAlaLeuGlu  80
        ||||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db  264 GTGGCCGGCCACGGCAACGTGGAGCAGATGAAGGCCCAGGTGTGGCTGCGAGCGTGGAG   323

Qy   81 ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTyr  100
        :::|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  324 ACCAGCGTGGGCGGCGACTTCTACCACCGGCTGGGACCCGATCACTTCCTCCTGCTCTAT  383

Qy  101 GlnLysGlyGlnTrpTyrAspLysIleTyrAspGluTyrGlnValValGlnThrLeuAsp  120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  384 CAGAAGAAGGGGCAGTGGTACGACATCTACGACGAGTACCAGGTGGTGCAGACTCTGGAC  443

Qy  121 CysLeuArgTyrTrpLysValLeuHisArgSerProGlyIleHisValValGlnArg     140
        ||||||||||||||||||||||||||||||||||||||||||:::||||||||||||||
Db  444 TGCCTGCGCTACTGGAAGGCCACGGAGGCCCCGGGCATCCACGTGGTGCAGCGG       503

Qy  141 HisAlaProSerGluThrLeuAlaPheGlnLeuAsnAlaLeuIleGlyTyr           160
        ||||||||||||:::|||||||||||||||||||||||||||||||||||||
Db  504 CACCCGCCCCTCGAGACGTCCAAGCTCCAGCTGAACGCGCTGATTGGCTAT           563

Qy  161 AspValThrAspValSerAsnValHisAspAspGluLeuGluPheThrArgArgLeu     180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  564 GACGTCACTGACGTCAGCAACGTGCACGACGATGAGCTGGAGTTCACGCGCCGTGGCTTG  623

Qy  181 ValThrProArgMetAlaGluValAlaGlyValAlaGlyTyrArgAspProLysHisPro  200
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  624 GTGACCCCGCGCATGGCGGAGGTGGCCGGCGTGGCCGGCTACCGCGACCCCAAGCACCCG  683

Qy  201 TrpValThrSerLysProLeuProTyrLeuLeuLysLysIleThrAsnAsnCysVal     220
        ||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db  684 TGGGTGACGTCCAAGCCCCTCCCGTACCTGCTGAAGAAGATTACCAACAACTGCATC    743

Qy  221 PheIleValIleHisArgSerThrThrSerGlnThrIleLysValSerAlaAspAspThr  240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  744 TTCATCGTCATTCACCGCAGCACCACCAGCCAGACCATTAAGGTTCACCCGACGACACC   803

Qy  241 ProGlyThrIleLeuGlnSerPhePheThrLysLysMetAlaLysLysLysSerLeuMetAsp 260
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  804 CCCGGGACCATCCTGCAGAGCTTCTTCACCAAGATGGCCAAGAAGAAATCTCTGATGGAT  863

Qy  261 IleProGluSerGlnAsnGluArgAspPheValLeuArgValCysGlyArgAspGluTyr  280
        ||||||||||||||||:::|||||||||||||||||||||||||||||||||||||||||
Db  864 ATTCCCGAAAGCCAAAGCCAAAGGCAACAGGATTTTGTGCTCCGCGTCTGTGGGATGAGTAC 923

Qy  281 LeuValGlyThrProIleLysAsnPheGlnTrpValArgGlnCysLeuLysAsnGly     300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  924 CTGGTGGGCACAACGCCCATCAAAAACTTCCAGTGGGTGAGGCAGTGCCTCAAGAACGGA  983
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Db 2969 ...||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        TTTCATATTGATTCGGACACATTCTTGGGAATTACAAAAGTTCCTGGGCATTAATAAA   3028

Qy  981 GluArgValProPheValLeuThrProAspPheLeuMetGlyThrSerGlyLys        1000
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3029 GAGAGGGTGCCATTTGTGCTAACCCCAGACTTCCGTTTGTGATGGGGACTTCTGGAAAG   3088

Qy 1001 LysThrSerLeuHisPheGlnLysPheGlnLysAspValCysValLysAlaTyrLeuAlaLeu 1020
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3089 AAGACAAGTCTACACTTCCAGAAATTTCAGGATGTCTGCGTCAAGGCTTACCTAGCCCTT   3148

Qy 1021 ArgHisHisThrAsnLeuLeuIleIleLeuLeuLeuPheSerMetMetLeuThrGlyMetPro 1040
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3149 CGTCATCACACAAACCTACTGATCATCCCTTCTCCATGATGCTGACAGGAATGCCC       3208

Qy 1041 GlnLeuThrSerLysGlyAspLeuGluTyrIleGluArgAspAlaLeuThrValGlyLysSer 1060
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3209 CAGTTAACCAGCAAGAGACACATTGAATACATTCGGAGACGCCCTCACAGTGGGCAAAAGT   3268

Qy 1061 GluGluAspAlaLysLysTyrPheLeuAspGlnIleGluValCysArgAspLysAspGlyTrp 1080
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3269 GAGGAGGATGCTAAAAAGTATTTTCTGGATCAGATTGAAGTTTGCAGAGACAAAGGATGG   3328

Qy 1081 ThrValGlnPheAsnTrpPheLeuHisLeuValLeuLeuGlyIleLysGlnGlyLysHis   1100
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3329 ACCGTGCAGTTTAACTGGTTCTTACATCTTGTTCTTGGCATCAAACAAGGGAAGCAT     3388

Qy 1101 SerAla  1102
        ||||||
Db 3389 CCCGCA  3394
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RESULT 7
US-08-916-917-13
; Sequence 13, Application US/08916917
; Patent No. 5856132
GENERAL INFORMATION:
;;  APPLICANT: Stephens, Len
;;  APPLICANT: Hawkins, Phillip Thomas
;;  APPLICANT: Braselmann, Sylvia
;;  TITLE OF INVENTION: G-BETA-GAMMA REGULATED
;;  TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
;;  NUMBER OF SEQUENCES: 14
;;  CORRESPONDENCE ADDRESS:
;;   ADDRESSEE: Pennie & Edmonds, LLP
;;   STREET: 1155 Avenue of the Americas
;;   CITY: New York
;;   STATE: NY
;;   COUNTRY: USA
;;   ZIP: 10036-2811
;;  COMPUTER READABLE FORM:
;;   MEDIUM TYPE: Diskette
;;   COMPUTER: IBM Compatible
;;   OPERATING SYSTEM: Windows
;;   SOFTWARE: FastSEQ for Windows Version 2.0b
;;  CURRENT APPLICATION DATA:
;;   APPLICATION NUMBER: US/08/916,917
;;   FILING DATE: 15-AUG-1997
;;   CLASSIFICATION: 435
;;  PRIOR APPLICATION DATA:
;;   APPLICATION NUMBER: 08/672,211
;;   FILING DATE: 27-JUN-1996
;;  ATTORNEY/AGENT INFORMATION:
;;   NAME: Abrams, Samuel B
;;   REGISTRATION NUMBER: 30,605
;;   REFERENCE/DOCKET NUMBER: 8549-0006-999
;;  TELECOMMUNICATION INFORMATION:
;;   TELEPHONE: 650-493-4935
;;   TELEFAX: 650-493-5556
;;   TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 13:
;;  SEQUENCE CHARACTERISTICS:
;;   LENGTH: 5162 base pairs
;;   TYPE: nucleic acid
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Qy  301 GluGluIleHisLeuValLeuAspThrProProAlaLeuAspProAlaLeuValArgLys 320
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Db  984 GAAGAGATTCACGGTACTGGACACGCCTCCAGACACCCCGGCCCGAGAGGTGAGGAAG 1043

Qy  321 GluGluTrpProLeuValAspAspCysAspThrGlyValThrHisGluGlnLeuThr 340
Db 1044 GAGGAGTGGCCGCTGGTGGACGACGGTTGGACGAGTCACGGAGCAGCTTACC 1103

Qy  341 IleHisGlyLysAspHisGluSerValPheThrValSerLeuTrpAspCysAspArgArgLys 360
Db 1104 ATCCACGGCAAGGACCACGAGAGTGTGTTCACCGTGTTCACCGTGGGGACTGCGACCGCAAG 1163

Qy  361 PheArgValIleArgGlyIleLeuProValLeuProArgValAlaAspLeuThr 380
Db 1164 TTCAGGGTCAAGATCAGAGGCATTGAATCCCCGTTCCTGCCTCGGGAACACCGACCTCACA 1223

Qy  381 ValPheValGluAlaAsnIleGlnThrGlyGlnGlnAsnIleGlnArgArgThrSer 400
Db 1224 GTTTTTGTAGAGGCAAACATCCAGACATGGCACAAGTCCTTTGCCAAGGAGAACCAGC 1283

Qy  401 ProLysProPheThrGluGluValLeuTrpProAsnValTrpLeuGluPheSerIleLysIle 420
Db 1284 CCCAAACCCTTCACAGAGGAGGTGCTGTGGCCAAATGTGTGGCTTGAGTTCAGTATCAAAATC 1343

Qy  421 LysAspLeuProLysSerGlyAlaLeuLeuAsnLeuAsnIleTyrCysGlyLysLysAlaProAla 440
Db 1344 AAAGACTTGCCCAAAGGGCTCTACTGAACCTCAGATCTACTGCGGTAAAGCTCCAGCA 1403

Qy  441 LeuSerGlyLysThrSerAlaGluMetProSerProGluSerLysSerGlyLysLysAlaGlnLeu 460
Db 1404 CTGTCCCAGCAAGGCCTTCGAGAGTCTCGAGAGTAGACACCAGTTCGGCTT 1463

Qy  461 LeuTyrTyrValValAsnLeuLeuLeuLeuAspHisArgPheLeuLeuArgHisGlyGluTyr 480
Db 1464 CTCTATTATGTGGAACCTGCTGCTGCGTAGAGACACCGTTCCTCCCGCGCGTGGAGAATAC 1523

Qy  481 ValLeuHisMetTrpGlnLeuLeuSerGlySerGlyGlnGlnGlnSerPheAsnAlaAsp 500
Db 1524 GTCCTCCCACATGTGGCAGTAATCTGGAAGGGAGAAGACCAAGGAAGCTTCAATGCTGAC 1583

Qy  501 LysLeuThrSerAlaThrAsnProAspLysLysGluAsnSerMetSerIleLeuLeuLeu 520
Db 1584 AAACTTACGTCTGCAACTTCACAGACGAGGAGAACTCAATGTCCATTCCATTCTTCTG 1643

Qy  521 AspAsnTyrCysHisProIleAlaLeuProLysHisArgProThrProAspProGluGly 540
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Qy  541 AspArgValArgAlaGluMetProAsnArgLysGlnLeuLysGlnLeuGlnIleAlaIleIleAla 560
Db 1704 GACCGGGTTCGAGCAGAAAGTGCCCAACCAGCTTCGCAAGCAATTGGAGGCGATCATAGCC 1763

Qy  561 ThrAspProLeuAsnProLeuThrAlaGluLysLysGluLeuLeuLeuLeuTrpHisTyrHisPheArgTyr 580
Db 1764 ACTGATCCACTTAACCCTCTCACAGCAGAGAAAAAGGAGCTATTGCTCTGGCATTTTAGATAC 1823

Qy  581 GluSerLeuLysProLysProArgAlaThrTyrArgProLysLysLeuPheSerSerValLysArgGlyIleGln 600
Db 1824 GAAAGCCTTAAGCACCCAAAAACATACCCCAAAAGAATTCTTCAGTTCAGTTGTGAAGGGGGACAG 1883

Qy  601 GlnIleIleValAlaValGlnLysGlnLysThrTyrGlnLeuLeuAlaLysGluAlaValTrpTrpAspGlySer 620
Db 1884 CAAGAAATTGTGGCAGTAAATGTGGCCCAAAAGCAGAAACATGCCAAGGAAGTCTGGGGACAGT 1943

Qy  621 AlaLeuAspValGlyLeuThrMetGlnLeuLeuAspCysPheSerAsnGluAspAsnVal 640
Db 1944 GCTTTGGATGTGGGTTTAACAATGCAGCTCCTGGACTGCTTCTCCAATGAAGATAATGTA 2003

Qy  641 ArgAlaIleLeuAlaValGlnLysGlnLysSerLeuGluSerLeuAspAspAspValLeuLeuHisTyrLeu 660
Db 2004 AGAGCCATTCTAGCAGTTCAGAAAAAGTTGGAGACGATGATGTTTCTGCATTACCTT 2063
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Qy  661 LeuGlnLeuValGlnAlaValLysPheGluProTyrHisAspSerAlaLeuAlaArgPhe 680
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Qy  681 LeuLeuLysArgGlyLeuArgAsnLysArgIleGlyHisPheLeuPheTrpPheLeuArg 700
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Qy  701 SerGluIleAlaGlnSerArgHisTyrGlnGlnAsnArgPheAlaValIleLeuGluAlaTyr 720
Db 2184 AGTGAGATAGCCCAGTCCAGACACTATCAGCAGAGTTCGCTGTGATTCTGGAAGCCTAT 2243

Qy  721 LeuArgGlyCysGlyThrAlaMetLeuHisAspPheThrGlnGlnValIleGlnValIleAsp 740
Db 2244 CTGAGGGGCTGTGGCACAGCCATGCTGCACGACTTTACCCAACAAGTCCAAGTAATCGAG 2303

Qy  741 MetLeuGlnLysValThrIleAspIleLysSerLeuSerAlaGluLysLysTyrAspValSer 760
Db 2304 ATGTTACAAAAGTCACCCGTTGATATTAAAAGTCTCTGTGCAGAAAAGTATGACGTCAGT 2363

Qy  761 SerGlnValIleSerGlnLeuLysGlnLysLeuGlnLysAsnLeuGlnAsnLeuAsnLeuPro 780
Db 2364 TCCCAAGTTATTTCACAACTAAACAAAAGCTTGAAAAGCTTCAACTCCCC 2423

Qy  781 GlnSerPheArgValProTyrAspProGlyLeuLysAlaGlyAlaLeuValIleGluGluLys 800
Db 2424 GAAAGCTTTAGAGTTCCATATGATCCTGGACTGAAAGCAGGAGCGCTGGCATTGAAAAA 2483

Qy  801 CysLysValMetAlaSerLysLysLysProLeuPheLeuGluTrpPheLysSerGlyAlaAspPro 820
Db 2484 TGTAAAGTAATGGCCTCCAAGAAAAAACCACTATGGCTTGAGTTTAAATGTCGCGATCCT 2543

Qy  821 ThrAlaLeuSerAsnGluThrGlyIleIleGluPheLysHisGlyAspProLeuArgArgGln 840
Db 2544 ACAGCCCTATCAAATGAAACAATGGAATTATCTTTAAACATGGTGACCTGCCGCCAA 2603

Qy  841 AspMetLeuIleLeuGluIleAsnIleLeuLeuArgIleMetGluSerIleThrGluThrGlySerLeu 860
Db 2604 GACATGCTTATTTTACAGATTCTACGATCATGAGGACTGTATTGGAGACTGAATCTTTG 2663

Qy  861 AspLeuCysLeuLeuProTyrTyrGlyCysIleSerSerThrGlyLysMetIleGlu 880
Db 2664 GATCTATGCCTCTGCCTCCTGCCCATATGGTTGCATTTCAACTGGTGACAAAATAGGAATGATCGAG 2723

Qy  881 IleValLysAspAlaThrThrIleAlaLysIleIleGluGlnAsnThrValGlyAsnThrGly 900
Db 2724 ATTGTGAAAGACGCCACGACAATTGCCAAAATTCAGCAAAATACAGTGGGCAACACGGGA 2783

Qy  901 AlaPheLysAspGluValLeuSerHisTrpLeuValSerGlyLysCysProIleGluGluLys 920
Db 2784 GCATTTAAAGATGAAGTCCTGAATCACTGGCTTGTAAGTGGCAAAGAAATCCCCTACTGAAGAAAAG 2843

Qy  921 PheGlnAlaAlaValGluArgPheHisAlaAlaValTyrCysValAlaThrPhe 940
Db 2844 TTTCAGGCAGCAGTGGAGAGATTTGTTATTCCTGCCAGGCACTGTGTGGCAACCTTT 2903

Qy  941 ValLeuGlyIleLeuGlyAspGlyArgHisAsnAspAsnIleSerGluThrMetIleLeuAsnLeu 960
Db 2904 GTTCTTGGAATAGGGACAGGGACGACATATTATGATCACCAGACAGAGAAAACCTA 2963

Qy  961 PheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLys 980
Db 2964 TTTCATATTGACTTCGGGCACATTCTTGGGAATTACAAAAGTTTCCTGGGCATTAATAAA 3023

Qy  981 GluArgValProPheValLeuThrProAspPheLeuPheValMetGlyThrSerGlyLys 1000
Db 3024 GAGAGAGTGCCATTTGTCCTAACCCCTGACTTCCTTTTTGTGATGGGAACTTCGGGAAAG 3083

Qy 1001 LysThrSerLeuHisPheGlnLysPheGlnAspValCysValLysAlaTyrLeuAlaLeu 1020
Db 3084 AAGACAAGCCCACACTTCCAGAAATTCCAGGACGTGTGTGTTAAGGCTTATCTGGCCCTT 3143

Qy 1021 ArgHisIleThrAsnLeuIleIleLeuIleLeuSerMetMetGlyMetPro 1040
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US-09-974-573-1 (1-1102) x US-09-225-170-13 (1-5162)

Qy    1 MetGluLeuGlnAsnTyrGluGlnProValValLeuArgGluAspArgArgArgArg  20
          |||||||||||||||||||||||||||||||||||||||||||
Db   84 ATGGAGCTGCAGAACTATATAAACAGCCCGGTGGTCTGAGAGAGGACAACTGCCGAAGGCGC  143

Qy   21 ArgArgMetLysProArgSerThrAlaAlaSerLeuSerMetGluLeuIleProIle  40
          |||||||||||||||||||||||||||||||||||||||||||
Db  144 CGGAGGATGAAGCCGCGGTCCACCGCAGCCTGTCTCCATGGAGCTCATCCCCATC  203

Qy   41 GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeuLeuHis  60
          ||||||||||||||||:::|||||||||::|||||||||
Db  204 GAGTTCGTGCTGCCCACCAGCCAAATGACGCGCAAAGACCCCGAAGACGCGCTGCAC  263

Qy   61 ValAlaAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnAlaValTrpLeuAlaLeuGlu  80
          ||||||||||||||||||||||||||||||||||||
Db  264 GTGGCCGGCGGCCACGGCCAACGGCAGCAGATGAAGGCCCAGGTGGCTGCGAGCGCTGGAG  323

Qy   81 ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTyr  100
          ||::::|||||||||||||||||||||||||||||||||
Db  324 ACCAGCGTGGCGGCGGACTTCTACCACCGGCTGGGACCCGATCACTTCCTCCTGCTCTAT  383

Qy  101 GlnLysLysGlyInTrpTyrGluIleTyrAspLysTyrGlnValGlnValGlnThrLeuAsp  120
          |||||||||||||||||||||||||||||||||||||||||
Db  384 CAGAAGAAGGGGCAGTGGTACGAGATCTACGACAAGTACCAGGTGGTCCAGACTCTGGAC  443

Qy  121 CysLeuArgTyrTrpLysValLeuHisArgSerProGlyGlnIleIleHisValValGlnArg  140
          |||||||||||||||||||||||||:::::|||||||
Db  444 TGCCTGCGCTACTGGAAGGCCACGACCGGAGCCCGGGCCACCGTGCAGCGG  503

Qy  141 HisAlaProSerGluGlnThrLeuValAlaPheGlnArgGlnLeuAsnAlaAlaLeuIleGlyTyr  160
          |||||||:::|||||||||||||||||||||||||
Db  504 CACCCGCCCTCCGGAGAGCTCACGGGCCTGATTGGCTAT  563

Qy  161 AspValThrAspValSerAsnValHisAspAspArgValHisHisProGluLeuGluPheThrArgArgLeu  180
          |||||||||||||||||||||||||||||||||||||||||
Db  564 GAGTCACTGACGTCAGCAACGTGCACGACGATGAGCTGGAGTTCACGCGCCGTGGCTTG  623

Qy  181 ValThrProArgMetAlaGluValAlaGlyArgAspGlyArgAspArgMetHisPro  200
          |||||||||||||||||||||||||||||||||||||
Db  624 GTGACCCCGCCGATGGCCGAGGTGGCCAGCCGCGACCCCAAGCTCTACGCACCCCG  683

Qy  201 TrpValThrSerLysProLeuProGluProGluTyrLeuLeuLysLysIleThrAsnAsnCysVal  220
          ||||||||||||||||||||||||||||||||||||:::
Db  684 TGGGTGACGTCCAAGCCCCTCCCGGAGTACCTGTGGAAGAAGATTGCCAACAACTGCATC  743

Qy  221 PheIleValIleHisArgSerThrThrSerGlnThrIleLysValSerAlaAspAspThr  240
          |||||||||||||||||||||||||||||||||||||||
Db  744 TTCATCGTCATTCACCGCAGCACCACCAGCCAGACCATTAAGGTCTCACCCGACGACACC  803

Qy  241 ProGlyThrIleLeuGlnSerPhePheThrIleLysMetAlaLysLysLysSerLeuMetAsp  260
          ||||||||||||||||||||||||||||||||||||||||
Db  804 CCCGGCGCCATCCTGCAGAGCTTCTTCACCAAGATGGCCAAGAAGAAGAGAATCTCTGATGAT  863

Qy  261 IleProGluSerGlnAsnGluArgAspPheValLeuArgArgValCysGlyValArgGluTyr  280
          ||||||||||||:::||||||||||||||||||||||||
Db  864 ATTCCCGAAAGCCAAAGCGAACAGATTTTGTGCTGCGTCGTGTGGCGGGATGAGTAC  923

Qy  281 LeuValGlyGluThrProIleLeuAsnPheGlnTrpValArgGlnCysLeuLysAsnGly  300
          ||||||||||||||||||||||||||||||||||||||
Db  924 CTGGTGGGAGAAACGCCCATCAAAAACTTCCAGTGGGTGAGGCAGTGCCTCAAGAACGGA  983

Qy  301 GluGluIleHisLeuValLeuAspThrProProAlaLeuAspGluGluAspValValArgLys  320
          ||||||||:::||||||||||||||||||||||||||||
Db  984 GAAGAGATTCACGTGGTACTGGACACGCCTCCAGACGAGGTGAGAAG  1043

Qy  321 GluGluTrpProLeuAspAspCysThrGlyValThrGlyTyrHisGluGlnLeuThr  340
          ||||||||||||||||||||||||||||||||||||||
Db 1044 GAAGAGTGGCCGCTGGTGGACACTGCACGGGAGTCACCGGCTACCAGCCTTACC  1103

Qy  341 IleHisGlyLysAspHisGluSerValPheThrValSerLeuTrpAspCysAspArgLys  360
          |||||||||||||||||||||||||||||||||||||||
Db 1104 ATCCACGGCAAGGACCACGAGAGTGTGTTCACCGTGTCCCTGTGGGACTGCGACCGCAAG  1163
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Db 3144 CGTCATCACAAACCTACTGATCATCCTGTTCCATGATGCTGATGACAGGAATGCCC  3203
          ||||||||||||||||||||||||||||||||||||
Qy 1041 GlnLeuThrSerLysGluIleGluTyrIleGluArgAspAlaLeuThrValGlyLysSer  1060
          |||||||||||||||||||||||||||:::
Db 3204 CAGTTAACAGCAAAGAAGAAGACATTGAATATATCCCGGATGCCCTCACAGTGGGGAAAAT  3263

Qy 1061 GluGluAspAlaLysTyrPheLeuAspGlnIleLeuAspValCysArgAspLysGlyTrp  1080
          |||||||||||||||||||||||||||||||||:::
Db 3264 GAGGAGGATGCGAAAATGTATTTTCTGATCAGATCGAAGTTGCAGAGGACAAAGGATGG  3323

Qy 1081 ThrValGlnPheAsnTrpPheLeuHisIleLeuValLeuGlyGlyIleLeuLysGlnGlnLysHis  1100
          |||||||||||||||||||||||||||||||||||
Db 3324 ACTGTGCAGTTTAATTGGTTTCTACATCTTGTTCTTGGCATCAAACAACAGGAGAGAAACAT  3383

Qy 1101 SerAla  1102
          ||||||
Db 3384 TCAGCC  3389
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RESULT 8
US-09-225-170-13
; Sequence 13, Application US/09225170
; Patent No. 6017763
; GENERAL INFORMATION:
;   APPLICANT: Stephens, Len
;   APPLICANT: Hawkins, Phillip Thomas
;   APPLICANT: Braselmann, Sylvia
;   TITLE OF INVENTION: G-BETA-GAMMA REGULATED
;   TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
;   NUMBER OF SEQUENCES: 14
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Pennie & Edmonds, LLP
;   STREET: 1155 Avenue of the Americas
;   CITY: New York
;   STATE: NY
;   COUNTRY: USA
;   ZIP: 10036-2811
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: Windows
;   SOFTWARE: FastSEQ for Windows Version 2.0b
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/225,170
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/916,917
;   FILING DATE: 15-AUG-1997
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Abrams, Samuel B
;   REGISTRATION NUMBER: 30,605
;   REFERENCE/DOCKET NUMBER: 8549-0006-999
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 650-493-4935
;   TELEFAX: 650-493-5556
;   TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 13:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 5162 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
US-09-225-170-13

Alignment Scores:

Pred. No.:	0	Length: 5162
Score:	5534.00	Matches: 1049
Percent Similarity:	97.10%	Conservative: 21
Best Local Similarity:	95.19%	Mismatches: 32
Query Match:	95.58%	Indels: 0
DB:	3	Gaps: 0

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Qy    721 LeuArgGlyCysGlyThrAlaMetLeuHisAspPheThrGlnValValGlnValIleAsp  740
          |||||||  |||  |||||||||||||||||||  ||  ||||||||||||||||  ::
Db   2244 CTGAGGGGCTGTGGCACAGCCATGCTGCACGACTTTACCAACAAGTCCAAGTAATCGAG 2303

Qy    741 MetLeuGlnLysValThrIleAspIleLysSerLeuSerAlaGluLysTyrAspValSer  760
          |||||||||||||  |::::|||||||||||||||  ||||||||||||||||||||||
Db   2304 ATGTTACAAAAGTCACCTATATCAAATCTGTCTGCTCTGGAAAAGATACGGTCAGT 2363

Qy    761 SerGlnValIleSerGlnLeuLysLysGlnLeuLeuGluAsnLeuGlnAsnLeuAsnLeuPro  780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2364 TCCCAAGTTATTTCACAACTTAAACAAAGTTGAAAACCTGCAGAATTCTCAACTCCCC 2423

Qy    781 GlnSerPheArgValProTyrAspTyrLeuLysAlaGlyAlaAlaLeuValIleGluLys  800
          :::||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2424 GAAAGCTTTAGAGTTCCATATGATTCCTGGACTGGCAGAAGGCCTGGCAATTGAAAAA 2483

Qy    801 CysLysValMetAlaSerLysLysLysProLeuTrpLeuLysPheLysGlyAspAspPro  820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2484 TGTAAAGTAATGGCCTCCAAGAAAAAACCACTATGGCTTAAATGGTTTAAATGTCCGGATCCT 2543

Qy    821 ThrAlaLeuSerAsnGluThrIleGlyIleLeuGluArgHisGlyGluTyr  840
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2544 ACAGCCCTATCAAATGAAACAATTGGAATTATCTTTAAACATGGTCAGTACTGTCGGCCAA 2603

Qy    841 AspMetLeuIleLeuArgIleMetGluSerIleTrpGluThrGluSerLeu  860
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2604 GACATGCTTATTTTACAGATTCTACGGAGTCTATTTGGGAGACTGAATCTTTG 2663

Qy    861 AspLeuCysLeuLysProTyrGlyCysIleSerSerThrGlyAspLysIleGlyMetIleGlu  880
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2664 GATCTATGCCTCCTGCCATATGGTTGCATTTCAACTGGTGACAAAATAGGAATGATCGAG 2723

Qy    881 IleValLysAspAlaThrArgThrLeuAlaLeuIleGlnSerAlaGlyValGlyAsnThrGly  900
          :::||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2724 ATTGTGAAAGACGCCACGAGAACAATTGCCAAATTCAGCAAGCACAGTGGGCAACACGGGA 2783

Qy    901 AlaPheLysAspGluValLeuSerHisTrpLeuLysSerCysProIleGluGluLys  920
          |||||||||||||||||||  :::|||||||||||||||||||||||||||||||||
Db   2784 GCATTTAAAGATGAAGTCCTGGCTCAAGCATCACTCCGGCTCAAAGAAAAATCCCCTACTGAGAAAAG 2843

Qy    921 PheGlnAlaAlaValGluArgPheValTyrSerCysValAlaGlyTyrCysValAlaThrPhe  940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2844 TTTCAGGCAGCAGTGGAGAGATTTGTTATTCCTGGTCAGGTCACTGTGTGGCAACCTTT 2903

Qy    941 ValLeuGlyIleGlyAspAlaArgHisAsnAspIleSerGluMetIleSerGluThrGlyAsnLeu  960
          ||||||||||||||:::||||||||||||||||||||||||||||||||||||||||||||
Db   2904 GTTCTTGGAATAGGCGACGCAGACAATATGACATATATGACACCGGACAGGAACCCTA 2963

Qy    961 PheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLys  980
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2964 TTTCATATTGACTTCGGGCACATTCTTGGGAATTACAAAAGTTTCCTGGGCATTAATAAA 3023

Qy    981 GluArgValProPheValLeuThrProAspPheLeuPheSerMetMetThrGlyMetPro  1000
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3024 GAGAGAGTTCCATTTGTTCTAACCCCTGACTTCCTCTTTTGTATGATGACAGGAATGCCC 3083

Qy   1001 LysThrSerLeuHisAspPheGlnLysPheGlnGluAlaIleLysThrAlaLeuAlaLeu  1020
          |||||||||||||||||||||||||:::||||||||||||||||||||||||||||||||
Db   3084 AAGACAAGCCCACACTTCCAGAAATTTCAGGAGGCTATCGTGTTAAGGCTTATCTAGCCTTT 3143

Qy   1021 ArgHisHisThrAsnLeuLeuIleIleLeuPheSerMetMetLeuMetThrGlyMetProLys  1040
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3144 CGTCATCACACAAACCTACTGATCATCCTGTTCTCCATGATGCTAATGACAGGAATGCCC 3203

Qy   1041 GlnLeuThrSerLysGluAspIleLysArgAspAlaLeuTyrArgLeuGlyLysSer  1060
          |||||||||||||||||||||||||:::||||||||||||||||||||||||||:::
Db   3204 CAGTTAACAAGCAAGGAAGACATTAAGATCGATGCCCTCACAGTTGGAAAAAAT 3263

Qy   1061 GluGlnAspAlaLysArgHisTyrArgGlnAsnIleLeuAspValCysArgAspPheGlyGlyTrp  1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3264 GAGGAGGATGCTAAAAGACATTATCGTCAGAACATCTTGGATGTTTGCAGAGATTTTGGGGGATGG 3323

Qy   1081 ThrValGlnPheAsnTrpPheHisValLeuLeuHisLeuLeuGluIleLeuLysGlyLeuLysGluLysHis  1100
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Qy    361 PheArgValLysIleArgGlyIleAspAlaIleProValLeuProArgThrAlaAspLeuThr  380
          |||||||  |||||||||||||||||||||||||||||||||||||  ||||||||||||
Db   1164 TTCAGGGTCAAGATCAGAGGCATTGATATCCCCGTCCTGCCTCGGACTGCAGACCTCACA 1223

Qy    381 ValPheGluValGlyAlaAlaAsnIleGlnTyrGlyGlnIlnValLeuCysGlnArgArgThrSer  400
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1224 GTTTTTGAGGAGGCAAACATCCAGTATGGGCAACAAGTCCTTTGCCAAGGAGAACCAGC 1283

Qy    401 ProLysProPheThrGluValLeuTrpAsnValTrpLeuGluPheIleLeuLysIle  420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1284 CCCAAACCCTTCACAGAGGAGGTGCTGTGGAATGTGTGGCTTGAGTTCAGTATCAAAATC 1343

Qy    421 LysAspLeuLysProLysGlyAlaLeuLeuAsnLeuIleTyrCysGlyLysAlaProAla  440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1344 AAAGACTTGCCCAAAGGGGCTCTACTGAACCTCGAATTACTCGCGTAAAGCTCCAGCA 1403

Qy    441 LeuSerGlyLysThrSerAlaGluMetProSerProGlySerLysGlyLysAlaGlnLeuLeu  460
          |||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||
Db   1404 CTGTCCAGCAAGGGCCTCTGCAGAGTCCCAGTTCTGAGTCCAAGGGCAAAGTTCGGCTT 1463

Qy    461 LeuTyrTyrTyrValAsnLeuLeuLeuIleAspAspHisArgPheLeuArgHisGlyGluTyr  480
          |||||||||||  |::::||||||||||||||||||||||||||||||||||||:::
Db   1464 CTCTATTATTATGTGAACCTGCTGCTGATAGACCACCGTTTCCTTCGCCGCGGTGAGAATAC 1523

Qy    481 ValLeuHisIleMetTrpGlnLeuSerGlyGlyGluAspGlnIleGlySerPheAsnAlaAsp  500
          |||||||||||||||||||:::|||||||||||||||||||||||||||||||||||||
Db   1524 GTCCTCCACATGTGGCAGATATCTGGGAGGAGAAGACCAAGAGCTTCAATGCTGAC 1583

Qy    501 LysLeuThrSerAlaThrAsnProAspLysAsnSerMetSerIleIleLeuLeu  520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1584 AAACTCACGTCTGCAACTAACCCAGACAAGAACAGGAGGAACTCAATGTCCATTCCATTCTCTG 1643

Qy    521 AspAsnTyrCysHisProIleAlaLeuProLysHisArgProAspThrProGluGly  540
          ||||||||||||||||||||||||||||||:::||||||||||||||||||||||||
Db   1644 GACAATTACTGCCACCCGATAGCCCTGCCTAAGCATCGACCCGACACCCCGGAAGGG 1703

Qy    541 AspArgValArgGlyAlaGluMetProAsnGlnLeuArgLysGlnLeuLeuGluAlaIleIleAla  560
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1704 GACCGGGTTCGAGGAGCAGAGAATGCCAACCAGCTTCGCAAGCAATTGGAGGCGATCATAGCC 1763

Qy    561 ThrAspProLeuAsnProLeuThrAlaGluLysAspLysLysGluLeuTrpHisProheArgTyr  580
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db   1764 ACTGATCCACTAAACCCTCTCACAGCAGAGAAAGGACAAGAAGGAGTTGCTGGCATTTTAGATAC 1823

Qy    581 GluSerLeuLysAspGluProLysProLysAlaTyrProLysPheSerSerValLysIleGly  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1824 GAAAGCCTTAAAGACGAGCCAAAAGCATAATCCTAAGCTATTAGTTCAGTGAAATGGGGACAC 1883

Qy    601 GlnIleIleValAlaLysThrTyrGlnLeuLeuAlaLysArgGluValArgTrpAspGlnSer  620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1884 CAAGAGAAATTGTGGCAAAACATACCAACATTGTTGGCCAGAAGGGAGTCTGGGGATCAAAGT 1943

Qy    621 AlaLeuAspValGlyLeuThrMetGlnLeuLeuAspCysAsnPheSerAspGluAsnVal  640
          |||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db   1944 GCTTTGGATGTGGGTCTGACCATGCAATTGCTTGACTGTAACTTCTCAGATGAAAAATGTA 2003

Qy    641 ArgAlaIleValAlaLysThrTyrGlnLeuLeuAlaLysArgGluValArgPhe  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2004 AGAACAAGCCCAGTTCAGGAGAGCTTCAGGAAAGGGAAGTCTGGGATCAAAGT 2063

Qy    661 LeuGlnLeuValGlnLeuAlaValGlyLeuThrMetGlnLeuLeuAspCysAsnPheSerAspGluAsnValArgAlaArgPhe  680
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2064 CTACAATTGGTCCAGCTGGCTGTGGGTTTAACAATGCGCCCTTGCCAGATTT 2123

Qy    681 LeuLeuLysLysArgGlyLeuAsnLysValTyrProAlaAlaValIleLeuGlnAlaTyr  700
          |||||||||||||||||||||||||||||||||||||||||||||||||:::
Db   2124 CTGCTGAAGAAGCGTGGTTTAAGAAACAAAGAGATTTGTTTTGGTTCTTGCAA 2183

Qy    701 SerGluIleAlaGlnLeuSerArgHisTyrGlnLeuArgPheAlaValIleIleLeuGlnAlaTyr  720
          ||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db   2184 AGTGAGGATAGCCCAGTTGAGACACTTATCAGCAGGCAGGAGGTTCGCTGTGATTCTGAAGCCTTAT 2243
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Db   3324  ||||||||||||||||||||||||||||||||||||||||||||
           ACTGTGCAGTTAATTGGTTTCTACATCTGTTCTGGCATCAAACAAGGAGAGAAACAT  3383

Qy   1101  SerAla  1102
           |||||
Db   3384  TCAGCC  3389


RESULT 9
US-08-817-090B-3
; Sequence 3, Application US/08817090B
; Patent No. 5885777
GENERAL INFORMATION:
;   APPLICANT: Stoyanov, Borislav
;   APPLICANT: Hanck, Theodor
;   APPLICANT: Wetzker, Reinhard
;   TITLE OF INVENTION: CLONING, EXPRESSION AND CHARACTERIZATION OF
;   TITLE OF INVENTION: A NEW FORM OF PHOSPHATIDYLINOSITOL-3-KINASE
;   NUMBER OF SEQUENCES: 7
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
;     STREET: 655 Fifteenth Street N.W. Suite 330
;     CITY: Washington
;     STATE: D.C.
;     COUNTRY: U.S.A.
;     ZIP: 20005-5701
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/817,090B
;     FILING DATE: 11-APR-1997
;     CLASSIFICATION: 514
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: DE P 44 36 696.5
;     FILING DATE: 13-OCT-1994
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: DE P 44 45 562.3
;     FILING DATE: 20-DEC-1994
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Berman, Richrd J.
;     REGISTRATION NUMBER: 39,107
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (202)638-5000
;     TELEFAX: (202)638-4810
;   INFORMATION FOR SEQ ID NO: 3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 4137 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: both
;       TOPOLOGY: linear
;     MOLECULE TYPE: cDNA
;     ORIGINAL SOURCE:
;       ORGANISM: Homo sapiens
;     FEATURE:
;       NAME/KEY: CDS
;       LOCATION: 423..3572
US-08-817-090B-3

Alignment Scores:
Pred. No.:                   0        Length:        4137
Score:                 5499.50        Matches:       1048
Percent Similarity:    96.92%         Conservative:    21
Best Local Similarity: 95.01%         Mismatches:      32
Query Match:           94.98%         Indels:           2
DB:                                   Gaps:             1

US-09-974-573-1 (1-1102) x US-08-817-090B-3 (1-4137)

Qy     1  MetGluLeuGlnAsnTyrGluGlnProValValLeuArgGluAsnArgAspAsnArgArgArgArg  20
          |||||||||||||||||||:|:|:||||||||||||||||||||||||     ||||||||||||||
Db   324  ATGGAGCTGGAGAACTATAAACAGCCCGTGGTCTGGTCTGAGAGAGAGAACAACTGCCGAAGCGC  383
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Qy    21  ArgArgMetLysProArgSerThrAlaAlaSerLeuSerMetGluLeuIleProIle  40
          ||||||||||||||||||||||||||||||||||||||        ||||||||||||
Db   384  CGGAGGATGAAGCCGCGCAGT---GCTGCCAGCTGTCCTCCATGGAGCTCATCCCCATC  440

Qy    41  GluPheValLeuProThrSerGlnAsnThrLysProGluThrAlaLeuLeuHis  60
          ||||||||||||||||||||||||||::::|||||||||||||||||||
Db   441  GAGTTCGTGCTGCCACCAGCCAAATGCAAATCAAGAGCCGAAACGGCGGCTGCGAC  500

Qy    61  ValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnValTrpLeuValArgAlaLeuGlu  80
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   501  GTGGCCGGCCACGGCAACGTGGAGCAGATGAAGGCCCAGGTGGTGTTGCGAGCGCTGGAG  560

Qy    81  ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTyr  100
          ||||||||||||::::|||||||||||||||||||||||||||||||||
Db   561  ACCAGCGTGGGCGGCGACTTCTACCACCGGCTGGGACCGCATCACTTCCTGCTCTCTTAT  620

Qy   101  GlnLysLysGlyGlnTrpTyrGluIleTyrGlnIleValValGlnThrLeuAsp  120
          |||||||||||||||||||||||:::||||||||||||||||||||||
Db   621  CAGAAGAAGGGCAGTGTACGAGATCTACAACAAGTACCAGTGGTGCAGACTCTGGAC  680

Qy   121  CysLeuArgTyrTrpLysValLeuHisArgSerProGlyGlnIleHisValValGlnArg  140
          |||||||||||||||||||||||||||||||||||:::||||||||||
Db   681  TGCCTGCGCTACTGGAAGGCCACGCACCCGGGCCAGATCCACGTGGTGCAGCGG  740

Qy   141  HisAlaProSerGluThrLeuAlaPheGlnArgGlnLeuAsnAlaLeuIleGlyTyr  160
          |||||||||||||||||::|:|||||||||||||||||||||||||||||
Db   741  CACGCGCCCTCCGAGACCCTGGGCAGCTCACGGGGCTGATTGGCTAT  800

Qy   161  AspValThrAspValSerAsnValHisAspAspGluLeuGluPheThrArgArgLeu  180
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   801  GACGTCACTGACGTCAGCAACGTGCACGACGATGAGCTGGAGTTCACGCGCCGTGGCTTG  860

Qy   181  ValThrProArgMetAlaGluValAlaGlyArgAspProLysProLeuTyrAlaMetHisPro  200
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   861  GTGACCCCGCGCATGGCGGAGGTGGCCAGCCGCGCGCCGCGAAGCTCTACGCCCATGCACCCCG  920

Qy   201  TrpValThrSerLysProLeuProGluTyrLeuLeuLysIleThrAsnAsnCysVal  220
          ||||||||||||||||||||||||||||||||||||:::||||||||||
Db   921  TGGGTGACGTCCAAGCCCCTCCCGAGTACCTGTGGAAGAAGATTGCCAACAACTGCATC  980

Qy   221  PheIleValHisArgSerGlnThrIleLysValSerAlaAspAspThr  240
          ||||||||||||||||||||||||||||||||||||||||
Db   981  TTCATCGTCATTCACCGCAGCCAGACCATTAAGGTCTCACCCGACGACACC  1040

Qy   241  ProGlyThrIleLeuGlnSerPhePheThrLysMetAlaLysLysLysSerLeuMetAsp  260
          |||||||||||||:|::|:||||||||||||||||||||||||||||||
Db  1041  CCCGGGCCCATCCTGCAGAGCTTCTTCACCAAGATGGCCAAGAAGAAATCTCTGATGGAT  1100

Qy   261  IleProGluSerGlnAsnGluArgAspPhePheValLeuArgValCysGlyArgGluTyr  280
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db  1101  ATTCCCGAAAGCCAAAGCGAACAGATTTTGTGCTGCGCCTGTGCGGCGGATGAGTAC  1160

Qy   281  LeuValGlyGluThrProIleLysGluAsnPheGlnTrpValArgGlnCysLeuLysAsnGly  300
          ||||||||||||||||||||||||||:::||||||||||||||||||||||||
Db  1161  CTGGTGGGCGAAACGCCCATCAAAAACTTCCAGTGGGTGGCACTGCCTCAAGAACGGA  1220

Qy   301  GluGluIleHisLeuValLeuAspThrProProAspProAlaLeuAspGluValArgLys  320
          ||||||||||||||:|:|||||||||||||||||||||||||||
Db  1221  GAAGAGATTCACGTGGTACTGGACACGCCCTCAGACCCGGCCCTAGAGGAGGTGAGGAAG  1280

Qy   321  GluGluTrpProLeuValAspAspCysThrGlyValThrGlyTyrHisGluLeuThr  340
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db  1281  GAAGAGTGGCCGCTGGTGGACGACTGCACGGGAGTTACCGGCTACCGGAGCAGTTACC  1340

Qy   341  IleHisGlyLysAspHisGluSerValPheThrValSerLeuTrpAspCysAspArgLys  360
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db  1341  ATCCACGGCAAGGACCACGAGAGTGTGTTCACCGTGTCCCTGTGGGACTGCGACCGCAAG  1400

Qy   361  PheArgValLysIleArgGlyTyrIleAspIleProValLeuProArgLeuProArgThrAlaAspLeuThr  380
          ||||||:||||||:::||||||||||||||||||||||||||||:||||:
Db  1401  TTCAGGGTCAAGATCAGAGGCATTGATATCCCCGTCCTGCCTCGGAACACCGACCTCACA  1460
```

```
Qy    381 ValPheValGluAlaAsnIleGlnTyrGlyGlnGlnValLeuCysGlnArgThrSer 400
          ||||| ::|::    |||||||| |||||||||||||||
Db   1461 GTTTTTGTAGAGGCAAACATCCAGCATGGGCAACAAGTCCTTTGCCAAAGGAGAACCAGC 1520

Qy    401 ProLysProThrGluPheGluValLeuTrpAsnValTrpLeuGluPheSerIleLysIle 420
          |||||||||||||| ::|||   |||||||||||||||||
Db   1521 CCCAAACCCTTCACAACTTAAACAAACTGGAATGTGTGGCTTGAGTTCAGTATCAAAATC 1580

Qy    421 LysAspLeuProLysGlyAlaLeuLeuLeuAsnLeuGlnIleTyrCysGlyLysAlaProAla 440
          ||    |||||||||||| ||||||||||||||||||
Db   1581 AAAGACTTTCCCAAAGGGGCTCTACTGAACCTCCAGATCTACTGCGGTAAAGCTCCAGCA 1640

Qy    441 LeuSerGlyLysThrSerAlaGluMetProSerProGluSerLysGlyLysAlaGlnLeu 460
          |||||||||||| :::||||
Db   1641 CTGTCCAGGAAGGCCTCTGCAGAGATGCCCCAGTCTCGAGTCCAAAGGGCAAAGTTCGGCTT 1700

Qy    461 LeuTyrTyrValAsnLeuLeuIleAspHisArgPheLeuArgHisGlyGluTyr 480
          |||||||| |||||||||||||||||||||||||
Db   1701 CTCTATTATGTGAACCTGCTGTCTGATAGACCACCGTTTCCTCCGCGGTGAGAATAC 1760

Qy    481 ValLeuHisMetTrpGlnLeuSerGlyLysGlyGluAspGlnGlySerPheAsnAlaAsp 500
          |||||||||||| :::||
Db   1761 GTCCTCCACATGTGGCAGAATCTGGCAGGAGGAGAAGATCAAGGAGAGCTTCAATGCTGAC 1820

Qy    501 LysLeuThrSerAlaThrAsnProAspLysGlyAlaAsnGlyGlySerMetSerIleLeuLeu 520
          ||||||||||||||||||
Db   1821 AAACTCACGTCTGCAACTAACCCTGACAAGGGAGCAAACGGAGGAAGCTTCCATCTCCATTCTG 1880

Qy    521 AspAsnTyrCysHisProIleAlaLeuProLysHisArgProThrProAspProGluGly 540
          ||||||||||||||||||
Db   1881 GACAATTACTGCCACCCGATAGCCCTGCCTAAGCATCAGCCCACCCCCGACCCGGAAGGG 1940

Qy    541 AspArgValArgAlaGlyMetProAsnGlnLeuArgLysGlnLeuGlnLeuAlaIleIleAla 560
          ||||||||||||||||||
Db   1941 GACCGGGTTCGAGCAGAAATGCCCAACCAGCTTCGCAAGCAATTGCAGCTGGCGATCATAGCC 2000

Qy    561 ThrAspProLeuAsnProLeuThrAlaGluLysIleAspLysLeuLeuTrpHisProAsnArgTyr 580
          ||||||||||||||||||
Db   2001 ACTGATCCACTTAACCCTCTCACAGCAGAGAAGATTGATAAGCTTCTGTGGCATTTAGATAC 2060

Qy    581 GluSerLeuLysAspProLysProLysGlyAlaTyrProLysProPheSerSerValLysTrpGlyGln 600
          ||||||||||||||||||
Db   2061 GAAAGCCTTAAGGACCCAAAGCCCAAAGGAGCATATCCTAAGCCATTCAGTAGTGAAATGGGGACAG 2120

Qy    601 GlnIleValAlaAlaLysThrTyrGlnLeuLeuAlaLysGluAlaArgGluValTrpAspGlnSer 620
          |||||||||||||| :::|||
Db   2121 CAAGAAATTGTGGCCAAAACATACCAAATTGTTGGCCAAGAGGAAGCTGGGGATCAAAGT 2180

Qy    621 AlaLeuAspValGlyLeuThrMetGlnLeuLeuAspCysAsnPheSerAspGluAsnVal 640
          ||||||||||||||||||
Db   2181 GCTTTGGATGTTGGGTTAACAATGCAGCTCCTGGACTGCAACTTCTCAGATGAAAATGTA 2240

Qy    641 ArgAlaIleAlaValGlnLysGlyLeuGluSerLeuGluAspAspValLeuHisTyrLeu 660
          ||||||||||||||||||
Db   2241 AGAGCCATTGCAGTTCAGAAAGGTCTTGAGAGCCTTGAGGACGATGTTCTGCATTACCTT 2300

Qy    661 LeuGlnLeuValGlnAlaValLysPheGluProTyrHisAspSerAlaLeuAlaArgPhe 680
          ||||||||||||||||||
Db   2301 CTACAATTGGTCCAGGCTGTGAAATTTGAACCATACCATGATAGCGCCCTTGCCAGATTT 2360

Qy    681 LeuLeuLysValGlnLysAsnLysArgAsnGlyLeuHisPheLeuHisPheAlaValIleLeuGluValAlaTyr 700
          ||||||||||||||||||
Db   2361 CTGCTGAAGGTGCAGAAGAACAAAAGAAATGGTCACTTTTTGTTTCATTTTGCTGTGATTCTGGAAGTCGCTTAT 2420

Qy    701 SerGluIleAlaGlnSerArgHisTyrArgLeuArgGlnArgPheAlaValIleLeuGlnAlaTyr 720
          |||||||||||| :::
Db   2421 AGTGAGATAGCCCAGTCCAGGCACTATCGGCTGCGGCAGAGGTTCGCTGTGATTCTGCAAGCCTAT 2480

Qy    721 LeuArgGlyCysGlyThrAlaMetLeuHisAspPheThrGlnGlnValGlnValIleAspSer 740
          |||||||||||| :::
Db   2481 CTGAGGGGCTGTGGCACAGCCATGCTGCACGACTTTACCCAACAAGTCCAAGTAATCGAC 2540

Qy    741 MetLeuGlnLysValThrIleAspIleIleGluAspLysSerSerLysSerAlaGluLysSerTyrAspValSer 760
          |||||||||||| :::
Db   2541 ATGTTACAAAAAGTCACCCTTGATATTATAGAAGATAAATCGTCTCTGAAAGTATGACGTCAGT 2600

Qy    761 SerGlnValIleSerGlnLeuLysGlnLeuLysAsnLeuGlnLysLysAsnLeuAsnLeuAsnLeuPro 780
          ||||||||||||||||||
Db   2601 TCCCAAGTTATTTCACAACTTAAACAAACTGAAACAACTGAAAACTGGAATTCTCAACTCCCC 2660

Qy    781 GlnSerPheArgValProTyrAspProValLeuLysProGlyLeuAlaGlyAlaValIleGluGluLys 800
          :::|||||||||||||| ::
Db   2661 GAAAGCTTAGAGTTCCATATGATCCATGGGTAAAGCTCCTGGCAATTGAAAAA 2720

Qy    801 CysLysValMetAlaSerLysLysLysProLeuProLeuPheLysCysAlaAspPro 820
          ||||||||||||||||||
Db   2721 TGTAAAGTAATGGCCTCCAAGAAAAAACCACTATGGCTTGAGTTTAAATGCCGATCCT 2780

Qy    821 ThrAlaLeuSerAsnGluLysThrIleGlyIleIleGlyLysHisGlyAspLeuArgGln 840
          ||||||||||||||||||
Db   2781 ACAGCCCTATCAAATGAAAACAATTGGAATATTCTTAAACATGGTGGGATATCTGGCCAA 2840

Qy    841 AspMetLeuIleLeuGlnIleLeuArgIleMetGluSerIleTrpGluThrGlySerLeu 860
          ||||||||||||||||||
Db   2841 GACATGTTAATTTTACAGATTCTACGAATCATGGAGTCTATTTGGGAGACTGAATCTTTG 2900

Qy    861 AspLeuCysLeuLeuProTyrGlyTyrCysIleSerGlyThrGlyLysProLysIleGlyMetIleGlu 880
          |||||||||||||| :::
Db   2901 GATCTATGCCTCCTGCCATATGGTTGCATTTCAACTGGTGACAAAATAGGAATGATCGAG 2960

Qy    881 IleValLysAspAlaThrThrIleAlaLysAlaIleGluGlnSerThrValGlyIleAsnThrGly 900
          ||||||||||||||||||
Db   2961 ATTGTGAAAGACGCACCGACAACAATTGCCAAATTCAGCAAGCACAGTGGGCAACACGGGA 3020

Qy    901 AlaPheLysAspGluValLeuSerHisTrpLeuLysTrpLeuLysCysProIleGluLeuLys 920
          ||||||||||||||||||
Db   3021 GCATTTAAAGATGAAGTCCTGAATCACTGGCTCAAAGAAAAATCCCTACTGAAGAAAAAG 3080

Qy    921 PheGlnAlaAlaValGluArgPheValTyrSerCysAlaGlyTyrCysValSerAlaThrPhe 940
          ||||||||||||||||||
Db   3081 TTTCAGGCAGCAGGTGGAGAGATTTGTTTATTCCTGTGGTGGCTACTGTGTCTCCGCAACCTTT 3140

Qy    941 ValLeuGlyLeuGlyAspArgHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeu 960
          |||||||||||| :::
Db   3141 GTTCTTGGAATAGGCGACAGACACAATGACAATATAATGATCAGCAAGCACAGGAAACCTA 3200

Qy    961 PheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysLysSerPheGlyIleIleAsnLys 980
          ||||||||||||||||||
Db   3201 TTTCATATTGACTTCGGGCACATTCTGGGAAATTACAAAAGTTTCCTGGGCATTAATAAA 3260

Qy    981 GluArgValProPheValLeuThrProAspPheLeuPheValMetGlyThrSerGlyLys 1000
          ||||||||||||||||||
Db   3261 GAGAGAGTGCCATTTGTTCTAACCCCTGACTTCCTCTTTGTGATGGGAACTTCTGGAAAG 3320

Qy   1001 LysThrSerLeuHisPheGlnAspValCysValLysAlaTyrLeuAlaLeu 1020
          |||||||||||| :::
Db   3321 AAGACAAGCCCACTCCACTTCCAGGATGTGTGTAAGGCTTATCTAGCCTT 3380

Qy   1021 ArgHisHisThrAsnLeuLeuIleLeuPheSerMetMetLeuMetThrGlyMetPro 1040
          ||||||||||||||||||
Db   3381 CGTCATCACACAAACCTCCTGATCATCTTCTCCATGATGCTGATGACAGGAATGCCC 3440

Qy   1041 GlnLeuThrSerLysGluGlnIleGluGluValAspAlaLeuThrLeuValGlyLysSer 1060
          ||||||||||||||| :::::
Db   3441 CAGTTAACAAGCAAAGAGCAAATAGAAGAAGTTGATGCATTGACTCTGGTTGGGAAAAAT 3500

Qy   1061 GlnLeuAspArgLysAsnLysGlyTyrProLeuLysHisArgIleGluGlnIleLysGluValGlnLysTyr 1080
          ||||||||||||||||||
Db   3501 GAGGAGGATGCTAAAAATGCTAAAAATGCTAAAAATGGGGAAAAAT 3560

Qy   1080 pThrValGlnPheAsnTrpPheLeuHisLeuValLeuGlyLysLysLysGlnGlyGluLysLysHis 1100
          |||||||||||| :::
Db   3561 GACTGTGCCAGTTTAATTGGTTTAATTGGTCCATCAACATCCAAGTAATGCAG 3620

Qy   1100 sSerAla 1102
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Db    3621 TTCAGCC 3627

RESULT 10
US-08-817-090B-1
; Sequence 1, Application US/08817090B
; Patent No. 5885777
; GENERAL INFORMATION:
;   APPLICANT: Stoyanov, Borislav
;   APPLICANT: Hanck, Theodor
;   APPLICANT: Wetzker, Reinhard
;   TITLE OF INVENTION: CLONING, EXPRESSION AND CHARACTERIZATION OF
;   TITLE OF INVENTION: A NEW FORM OF PHOSPHATIDYLINOSITOL-3-KINASE
;   NUMBER OF SEQUENCES: 7
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
;     STREET: 655 Fifteenth Street N.W. Suite 330
;     CITY: Washington
;     STATE: D.C.
;     COUNTRY: U.S.A.
;     ZIP: 20005-5701
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: Patentin Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/817,090B
;     FILING DATE: 11-APR-1997
;     CLASSIFICATION: 514
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: DE P 44 36 696.5
;     FILING DATE: 13-OCT-1994
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: DE P 44 45 562.3
;     FILING DATE: 20-DEC-1994
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Berman, Richrd J.
;     REGISTRATION NUMBER: 39,107
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (202)638-5000
;     TELEFAX: (202)638-4810
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 4134 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: both
;     TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   ORIGINAL SOURCE:
;     ORGANISM: Homo sapiens
;   FEATURE:
;     NAME/KEY: CDS
;     LOCATION: 423..3569
US-08-817-090B-1

Alignment Scores:
Pred. No.:                 0          Length:         4134
Score:               5440.00         Matches:        1046
Percent Similarity:  96.65%          Conservative:     20
Best Local Similarity: 94.83%        Mismatches:       35
Query Match:         93.96%          Indels:            4
DB:                        2         Gaps:              1

US-09-974-573-1 (1-1102) x US-08-817-090B-1 (1-4134)

Qy    1 MetGluLeuGlnAsnTyrGluGlnProValLeuArgGluAspAsnArgArgArgArg 20
          |||||||||||||| ||:::|||||||||||||||||||||||||||
Db  324 ATGGAGCTGGAGAACTATAAACAGCCCGTGGTGCTGAGAGAGGAGAGGGGC 383

Qy   21 ArgArgMetLysProArgSerThrAlaAlaSerLeuSerMetGluLeuIleProIle 40
          |||||||||||||||||||||||||||||||||||  ||:||
Db  384 CGGAGGATGAAGCCGCGCAGT---GCTGCCAGCCTGTCCTCCATGGAGCTCATCCCCATC 440

Qy   41 GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeuLeuHis 60
          ||||||||||||||||||||||||:::|||||||||||
Db  441 GAGTTCGTGCTGCCAACAAGCCAAATGCAAGAGCCCGAAACGGCGCTTGCTGCAC 500

Qy   61 ValAlaGlyHisGlyAsnValGlnMetLysLysAlaGlnValTrpLeuArgAlaLeuGlu 80
          ||||||||||||||||||||||||||||||||||||||||
Db  501 GTGGCCGGCCACGGCAACGTGCAGCAGAAGGCCCAGGTGTGGCTGCGAGCGCTGGAG 560

Qy   81 ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTyr 100
          |||||||||||||||||||||||||||||||||||
Db  561 ACCAGCT--GGGCGGGACTTCTACCACCGGCTGGGACCGCATCACTTCCTCCTGCTCTAT 618

Qy  101 GlnLysLysGlyGlnThrPheGlyIleTyrArgLeuIleTyrAspLysTyrGlnValValGlnThrLeuAsp 120
          |||||||||||||||||||||||||||||:::|||
Db  619 CAGAAGAA-GGGCAGTGGTACAGATCTACGACAAGTACCAGGTGGTGCAGACTCTGGAC 677

Qy  121 CysLeuArgTyrTrpLysValLeuHisArgSerProGlyGlnIleHisValValGlnArg 140
          ||||||||||||||||||||||||:::||
Db  678 TGCCTGCGCTACTGGAAGGTGCTGCACCGGAGCCCCGGCCAGATCCACGTGGTGCAGCGG 737

Qy  141 HisAlaProSerGluGlnThrLeuThrLeuAsnLeuAsnAlaAlaLeuLeuGlyTyr 160
          |||||||||||||||||||||||||||||||
Db  738 CACCCGCCCTCCGAGCAGACCCTGACCCTGAACCTCAACGCGGCTCACGCGCTGATTGGCTAT 797

Qy  161 AspValThrSerAsnValHisAspAspPheGlyLeuGlnPheThrArgArgLeu 180
          |||||||||||||||||||||||||||||||||
Db  798 GACGTCACTAGCAATGTGCACGATGACTTCGGCCTGCAGTTCACGCGCCGTGGCTTG 857

Qy  181 ValThrProArgMetAlaGlyGluValAlaAlaGlyArgArgAspProLysLysTyrAlaMetHisPro 200
          ||||||||||||||||||||||||||||:::||
Db  858 GTGACCCCGCGCATGGCCGGAGGTGGCCAGCGGCGGGACCCCAAGCTCTACGCCATGCACCCG 917

Qy  201 TrpValThrSerLysProLeuProGluLeuProGluLeuProLeuTyrLeuLeuLysLysLysIleThrAsnAsnCysVal 220
          |||||||||||||||||||||||:::
Db  918 TGGGTGACGTCAAGCCCCTCCGAGTACCTGTGTGAAGAAGATTGCCAACAACTGCATC 977

Qy  221 PheIleValIleHisArgSerThrSerGlnInThrIleLysValSerAlaAspAspThr 240
          |||||||||||||||||||||||||||||||
Db  978 TTCATCGTCATTCACCGCAGCACCAGCCAGACCATTAAGGTCTCACCCGACGACACC 1037

Qy  241 ProGlyThrIleLeuGlnSerPhePheThrLysMetAlaLysLysSerLeuMetAsp 260
          |||||||||||||||||||:::||
Db 1038 CCCGGCACCATCCTGCAGAGCTTCTTCACCAAGATGGCCAAGAAGAAATCTCTGATGGAT 1097

Qy  261 IleProGluSerGlnAsnGluArgAspPheValLeuArgAspValCysGlyValArgAspGluTyr 280
          ||||||||||:::|||||||||||||:::
Db 1098 ATTCCGGAAAGCCAAAGCGAACAGGATTTTGTGCTGCGCGACGTGTGTGGCGGATGAGTAC 1157

Qy  281 LeuValGlyGluThrProIleLysGluAsnPheGlnThrTrpValArgGlnCysLeuLysAsnGly 300
          |||||||||||||||||||||||||||||
Db 1158 CTGGTGGGCGAAACGCCCCATCAAAAACTTCCAGTGGGTGAGGCAGTGCCTCAAGAACGGA 1217

Qy  301 GluGluHisLeuValLeuAspThrProAspProAlaLeuValArgLys 320
          ||||:::||||||||||||
Db 1218 GAAGAGATTCACGTGGTACTGGACACGCCTCCAGACCCGGCCTAGACGAGGTGGAGAAG 1277

Qy  321 GluGluTrpProLeuValAspAspCysThrArgValThrGlyValThrHisGlyLeuLeuThr 340
          ||||||||||||||||||||||||||
Db 1278 GAAGAGTGGCCGCTGGTGGACGACTGCACGGGAGTCACCGGCTACCATGGACCAGCTTACC 1337

Qy  341 IleHisGlyLysValAspHisGluSerValPheThrValSerLeuTrpAspCysAspArgLys 360
          ||||||||||||||||||||||||||:::
Db 1338 ATCCACGGCAAGGACGACCACGAGAGTGTGTTCACCGTGTCCTTGTGGGACTGCGACCGCAAG 1397

Qy  361 PheArgValLysIleGluArgGlyTyrIleAspIleProArgValLeuProArgThrAlaAspLeuThr 380
          ||||||||||||||||||||||||:::||
Db 1398 TTCAGGGTCAAGATCAGAGGCATTGATATCCCCGTCCTCGGACACCGACCTCACA 1457

Qy  381 ValPheValGluAlaLeuAsnIleGlnTyrGlyInValLeuCysGlnAsnArgThrSer 400
          ||||||||||||||||:::
Db 1458 GTTTTTGTAGAGGCAAACATCCAGTGGCAACAAGTCCTTTGCCAAAGGAACCAGC 1517

Qy  401 ProLysProPheThrGluGluValLeuTrpAsnValTrpLeuGluPheLeuLysIle 420
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RESULT 11
US-08-162-081B-35
; Sequence 35, Application US/08162081B

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; Patent No. 5824492
; GENERAL INFORMATION:
; APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
; APPLICANT: Bala, Waterfield, Michael Derek; Parker, Peter
; APPLICANT: Joseph; Otsu, Maayuki; Panayotou, George; Volinia,
; APPLICANT: Stefano; Gout, Ivan Tarasovitch
; TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
; TITLE OF INVENTION: THEIR PREPARATION AND USE
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
;    ADDRESSEE: Felfe & Lynch
;    STREET: 805 Third Avenue
;    CITY: New York
;    STATE: New York
;    COUNTRY: USA
;    ZIP: 10022
; COMPUTER READABLE FORM:
;    MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
;    COMPUTER: IBM PS/2
;    OPERATING SYSTEM: PC-DOS
;    SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
;    APPLICATION NUMBER: US/08/162,081B
;    FILING DATE: February 7, 1994
;    CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
;    APPLICATION NUMBER: PCT/GB93/00761
;    FILING DATE: 13 April 1993
; ATTORNEY/AGENT INFORMATION:
;    NAME: Pasqualini, Patricia A.
;    REGISTRATION NUMBER: 34,894
;    REFERENCE/DOCKET NUMBER: LUD 5256
; TELECOMMUNICATION INFORMATION:
;    TELEPHONE: (212) 688-9200
;    TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 35:
;    SEQUENCE CHARACTERISTICS:
;       LENGTH: 3207 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
US-08-162-081B-35

Alignment Scores:
Pred. No.:              7.92e-160      Length:        3207
Score:                  1465.50        Matches:       382
Percent Similarity:     51.40%         Conservative:  204
Best Local Similarity:  33.51%         Mismatches:    405
Query Match:            25.31%         Indels:        149
DB:                     1              Gaps:          39

US-09-974-573-1 (1-1102) x US-08-162-081B-35 (1-3207)

Qy    23 MetLysProArgSerThrAlaAlaSerLeuSerSerMetGluIlePro---------- 39
            ::: ||:::|| ||    ||:|||
Db     1 ATGGCTCCAAGACCATCAGGTGAACTGTGGGCATCCACTTGATGCCCCCAAGAATC 60

Qy    40 ---IleGluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeu 58
            |||:::|| |||
Db    61 CTAGTAGAATGTTTACTACCAAATGGGATCGATAGTGACT------------------- 99

Qy    59 LeuHisValAlaGlyHisGlyAsnGluGluMetLysAlaGlnMetLysAlaGlyAlaArgAla 78
            |||  ::::::||||
Db   100 TTAGAATGCCTCCGTGAGGCTACGTTAATAACGATAAAGCATGAACTATTTAAAGAAGCA 159

Qy    79 LeuGluThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeu 98
            ::: ::: |||:::||
Db   160 AGAAAATACCCTCTC---------------CATCAACTTCTTCAAGATGAAATCTTCTTAC 204

Qy    99 LeuTyrGlnIleLysGlyGlnTrpTyrGluIleTyrArgLysTyrAspLysValValGlnThr 118
            ::: :::  |:||
Db   205 ATTTTCGTAAGTGTTACCCAAGAAGCAGAAGGAGAAGAATTTTTGATGAAACAAGACGA 264
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Qy   119 LeuAspCysLeuArgTyrTrpLysValLeuHisArgSerProGlyGlnIleHisValVal 138
            |||    ::: ||
Db   265 CTTTGTGACCTTCGGCTTTTCAACCCTTT---------------------TTAAAGTAATT 306

Qy   139 GlnArgHisAlaProSerGluGlnThrLeuAlaPheGlnArgLeuAsnAlaLeuIle 158
            ::: :::
Db   307 GAACCAGTAGGCAACCGTGAAGAAAAGATC---CTCAATCGAGAAATTGGTTTTGCTATC 363

Qy   159 GlyTyrAspValThrArgValSerAsnValHisAspAspGluLeuGluPheThrArgArg 178
            |||
Db   364 GGCATGCCAGTGTGTGAATTCGATATGGTTAAAGATCCAGAGTACAGGACTTCCGAAGA 423

Qy   179 ArgLeuValThrProArgMetAlaGluMetAlaGlyValAlaGlyArgAsp--------- 192
            :::::::
Db   424 AATATTCTCAATGTTGTAAGAAGCTGTGGATCTTAGCGGATCTTAATTCACCTCATAGT 483

Qy   193 ProLysLeuTyrAlaMetHisProTrpValThrSerLysPro---LeuProGluTyrLeu 211
            ::: ||| ||
Db   484 AGAGCAATGTATGTTTATCCTCCAAATGTAGAATCTTCACCCAAGAACTGCCAAGCACATA 543

Qy   212 LeuLysLysIleThrAsnAsnCysValPheIleValIle------------------His 225
            ::: :::
Db   544 TATAATAAATTGGATAAAGGGCAAATAATAGTGGTAATAGTTTCTCCAAAT 603

Qy   226 ArgSerThrThrSerGlnThrIleLysValSerAlaAspAspThrProGlyThrIleLeu 245
            |||:::
Db   604 AATGACAAACAGAGTATACTCTGAAAATCAACCATGACTGTGTGCCAGAACAAGTAATT 663

Qy   246 GlnSerPhePheThrLysMetAlaLysLysSerLeuMetAspIleProGluSer------- 264
            |||
Db   664 GCTGAAGGAATCAGGAAA------AAAACTCGAAGTATGTTGCTATCATCTGACCACTA 717

Qy   265 ----------GlnAsnGluArgAspPheValLeuArgValCysGlyValCysGlyArgAspGlu 279
            :::::: |||
Db   718 AACTCTGTGTTTTAGATATCAGGGCAAGTATATTTTAAAGTGTGGATGTGATGAA 777

Qy   280 TyrLeuValGlyValGluThrProIleLysAsnPheGlnTrpValArgGlnCysLeuLysAsn 299
            ::: |||
Db   778 TACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTATAATAGAGAGTGTATAATGCTT 837

Qy   300 GlyGluGluIleHisLeuValLeuAspThrProProAspProAlaLeuAspGluValArg 319
            |||
Db   838 GGGAGGATGCCCAATTTGATGCTG------------------ATGGCTAAAGAAAGCCTC 879

Qy   320 LysGluGluTrpProLeuValAspAspAspCysThrGlyValThrGlyTyrHisGluGlnLeu 339
            ::: :::
Db   880 TATTCTCAACTGCCAATG------GACTGTTTTACAATGCCATCATATTCCAGACCGCATC 933

Qy   340 Thr-----------IleHisGlyLysAspHisGluSerValPheThrValSerLeu 354
            :::
Db   934 TCCACAGTACGCCATATATGAATGGGAAG-------------ACATCTACAAAATCCTT 981

Qy   355 TrpAspCysAspArgLysPheArgValLys------------------- 364
            :::
Db   982 TGGGTTATAAATAGTGCACTCAGAATAAAAATTCTTTGTGCAACCATGTGATAATGAAAT 1041

Qy   365 IleArgGlyIleAspIleProValLeuProArgThrAlaAspLeuThrValGlu 384
            |||:::
Db  1042 ATTCGAAGACATTGAC-----------------------AAGATTTATGTTCGA 1071

Qy   385 AlaAsnIleGlnTyrGlyValGlnGlnValLeuCysGlnArgArgThrSerProLysProPhe 404
            :::::: |||:::
Db  1072 ACAGGTATCTACCATGGAGGAGAACCCTTATGTGATAATGTGAACACTCAAGAGTACCT 1131

Qy   405 ThrGluGluValLeuTrpLeuValTrpLeuGluProHisIleLysGluIleLysAspLeuPro 424
            :::
Db  1132 TGTTCCAATCCCAGGTGGAATGAATGGCTGGAATATACAATATATACATTCCTGATCTTCCT 1191

Qy   425 LysGlyValAlaLeuLeuAsnLeuGlnIleTyrCysGlyLysAlaProAlaLeuSerGlyLys 444
            ::: :::
Db  1192 CGTGTCGTCGACTTTGCCTTTCCATT---TGT--------TCTGTTAAAGGCCGA 1236

Qy   445 ThrSerAlaGluMetProSerProGluSerLysGlyLysAlaGlnLeuLeuTyrTyrVal 464
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Db 2248 GGCTTTCTGTCCTCTAAACCCTGCTCATCAGGCTGGAAATCCTCAGGCTTGAAGAGTGT 2307
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Db 1237 AAGGGTGCT---------------------AAAGAGGAACACTGTCCATTGGCCTGGGGA 1275

Qy   802 LysValMetAlaSerLysLysProLeuTrpLeuGluPheLysCysAlaAlaAspProThr 821
                                          ::: ||||| ||
Qy   465 AsnLeuLeuIleLeuHisArgPheLeuLeuArgHisGlyGluTyrValLeuHisMet 484

Db 2308 CGAATTATGTCTTCTGCAAAAGGCCACTGGTGAAATTGGGAG:-   -AACCCAGAC 2361
          ||||||||||||||||||||||||||::::::||||||||||
Db 1276 AATATAAAACTTGTTGTTGATTACACAGATACTCTAGTATCTGGAAAAATGGCTTTGAATCTT 1335

Qy   822 AlaLeuSer------------------AsnGluThrIleGlyIleIlePheLysHisGly 835
                                       ||||
Qy   485 TrpGlnLeuSerGlyLysGlyLysGluAspGlnGlySerPheAsnAlaAspLysThrSer 504

Db 2362 ATCATGTCAGAATTACTCTTCAGAACAATGAG------ATCATCTTTAAAAATGGG 2412
          :::
Db 1336 TGGCCAGTACCTCATGGACTAGAAGAT------TTGCTGAAACCCTATTGGTGTTACT--- 1386

Qy   836 AspAspLeuArgGlnAspMetLeuIleLeuGlnIleLeuArgIleMetGluSerIleTrp 855
                                         ||| ::::   ::
Qy   505 AlaThrArgAsnProAspLysGlyAsnSerMetSerIleSerIleLeuLeuAspAsnTyrCys 524

Db 2413 GATGATTTACCGCAAGATATGCTAACCCTTCAGATTATTCGCATTATGGAAAAATATCTGG 2472
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Db 1387 GGATCAAAATCAAAATAAAGAA--ACTCCATGTTTAGAGTTGGAGTTTGACTGTTCAGC 1443

Qy   856 GluThrGluSerLeuLysAspLeuCysLeuLeuProTyrGlyCysIleSerThrGlyLysAspLys 875
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Qy   525 HisProIleAlaLeuProLysHisArgProThrProAspProGluGlyProGluArgVal--- 543

Db 2473 CAAAATCAAGGTCTTGATCTTCGAAATGTTACCTTATGGATCGTCTGTCAATCGGTGACTGT 2532
          :::::
Db 1444 AGTGTGGTAAAGTTTCCAGATATGTCAGTGATTGAACAGAGCATGCCAATTGGTCTGATCC 1503

Qy   876 IleGlyMetIleGluIleLeuValLysAspAlaThrThrIleAlaLysIleGlnGlnSerThr 895
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Qy   544 ------------------------------------ArgAlaGluMetProAsn 549

Db 2533 GTGGGACTTATCGAGGTGGTGAGAAATTCTCCACACTATAATGCAGATT---CAGTGTAAA 2589
          |||
Db 1504 CGTGAAGCAGGATTAGTATTCCATGCAGGACTGAGTAACAGACTAGCTAGACGACAAT 1563

Qy   896 ValGlyAsnThrGlyAla------PheLysAspGluValLeuSerHisTrpLeuLysGlu 913
                                     :::
Qy   550 GlnLeuArg------------LysGlnLeuGluAlaIleAlaIleAlaThrAspProLeuAsn 565

Db 2590 GGGAGGCCTGAAAGGTGCACTGCAGTTTAACAGCCACACTCCATCAGTGGCTCAAAGAC 2649
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Db 1564 GAATTAAGAGAAAATGATAAAGAACAGCTCCGGACTGCAATTTGTACACGAGATCCTCTATCT 1623

Qy   914 LysCysProIleGluGluLysPheGlnAlaAlaAlaAlaValGluArgPheValTyrSerCysAla 933
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Qy   566 ProLeuThrAlaGluSerProLeuTyrProLysHisPheArgTyrGluSerLeuLysAsp 585

Db 2650 AAGAACAAG--GGGAAAATATGATGCGGCCANCGATTTGTTTACACGATCATGTGCT 2706
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Db 1624 GAAATCACTGAGCAAGAGAAAGATTTTCTGTGGAGCCACAGACACTATTGTGTAACTATC 1683

Qy   934 GlyTyrCysValAlaThrPheValLeuGlyTyrIleGluGlyAspArgHisAsnAspAsnIleMet 953
                         ||| :::
Qy   586 ProLysAlaTyrProLysLeuPheSerSerValLysTrpGlyGlnGlnIleValValAla 605

Db 2707 GGATATTGTGTTGCCACTTCATTTGGAGATGGAGAGATCGTCACAATAGTAATATCATG 2766
          :::::
Db 1684 CCCGAAATTCTACCCAAATTGCTTCTGTCTTGTTTAAATGAACGTTAGAGATGAAGTAGCT 1743

Qy   954 IleSerGluThrGlyAsnLeuPheHisIleAspPheGlyHisIleLeuGlyAsnTyrLys 973
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Qy   606 LysThrTyrGlnLeuLeuLeuAlaAlaLysArgGluValArgValArgValGlnSerAlaLeuAspValGly 625

Db 2767 GTTAAAGATGATGGACAACTGTTCATAGATTTTGGACACTTTTGGATCACAAGAAG 2826
                                        |||
Db 1744 CAGATGTACTGCTTG---------------GTAAAAGATTGGCCTCCAATCAAGCCTGAA 1788

Qy   974 SerPheLeuGlyIleAsnLysGluArgValProPheValLeuThrProPhePheLeuPhe 993
          :::::::|||||||| :::||||||||
Qy   626 LeuThrMetGlnLeuLeuAspCysAsnPheSerAspGluAsnValArgAlaIleAlaAlaVal 645

Db 2827 AAAAAATTTGGTTATAAAGCAGGAGAGGCCGGTGCCATCAAAGATTTCTTAATA 2886
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Db 1789 CAGGGTGAGCGGTTCTGGACTGCAATTACCCCAGATCCTATGCCGGAGGTTTTGCTGTT 1848

Qy   994 ValMetGlyThrSerGlyLysLys-------ThrSerLeuHisPheGlnLysPheGlnLnAsp 1011
          ||||| :::
Qy   646 GlnLysLeuGluSer---LeuGluGluAspAspValLeuHisTyrLeuLeuGlnLeuLeuVal 664

Db 2887 GTGATTAGTAAAGGAGCCCAAGAAATGCACAAAGACAAGAGAAATTTGAGAGGTTTCAGGAG 2946
          ::::::
Db 1849 CGGTGCTTAGAAAAAATATTTAACAGATGACAAAACTTTCTCAGTACCTAAATTCAGCTAGTA 1908

Qy 1012 ValCysValLysAlaTyrLeuAlaLeuArgHisHisThrAsnLeuLeuIleLeuIleGluLeuPhe 1031
          ||| :::
Qy   665 GlnAlaValLysPheGluHisProTyrHisAspAspLeuPheTrpLeuArgArgPheGluLysArg 684

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          ||| :::
Db 1909 CAGGTACTAAAAATATGAACAGATATTGGATAACCTGCTTGGATTTTTACTCAAAAAA 1968

Qy 1032 SerMetMetLeuMetThrGlyMetProGlnLeuThrSerGlyLysAspIleAlaThrIle 1051
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Qy   685 GlnLeuValAspAsnLysArgIleGlyHisPheAlaValIleLeuGlnValIleLeuAlaTyrLeuArg 704

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Db 1969 GCGTTAACTAATCAATCAAGGATCGGTCACTTTTTTGGCATTTTAAAATCTGAGATG-- 2025

Qy 1052 ArgAspAlaLeuThrArgLysAspIleGlyValLysSerGluGluAspAlaLysIleLysGln 1071
          ::: |||
Qy   705 GlnSerArgHisTyrGlnGlnArgPheGlnGlnValIleLeuGluAlaTyrLeuArgGlyGlyCys 724

Db 3067 CGAAAGACCCTAGCTTTAGATAAAACTGAGCAAGAGGCTTTGGAGTATTTCATGAAACAA 3126
          :::
Db 2026 CACAATAAAACAGTTAGTCAGAGTTTGGCCTGTTTGGAGTCCTATTGCCGTGCATGT-- 2085

Qy 1072 IleGluValCysArgAspLysGlyLysTrpThrValGlnPheAsnTrpThrLeuHisLeuVal 1091
          ::: :::
Qy   725 GlyThrAlaMetLeuHisAspPheThrGlnGlnLnValGlnLnValIleLeuAspMetLeuGlnLys 744

Db 3127 ATGAATGATGCACCATGGTGGCTGACAACAAAAATGATTGAATCTTCCACACATT 3186
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Db 2086 GGGATGTATCTGACGAC---CTTAATAGGCAAGTTGAGGCTATGAGGAAAAGCTCATTAAC 2142

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Qy 2143 TTGACT-----GACATT-----CTCAAACAGAGAAGGATGAAAACAAAAGGTA- 2190

Qy   765 SerGlnLysLysGlnLysLeuGlnAsnGlnAsn----------LeuAsnLeuProGln 781
          ::::::
Qy 2191 ---CAGATGAAGTTTTTTAGTTGAGCAAATGCGGCGACCAGATTCATGGATGCTCTCCAG 2247

Qy   782 SerPheArgValProTyrAspGlyProGlyLeuLysLysAlaGlyAlaLeuValIleGluLysCys 801
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Qy   801

RESULT 12
US-08-780-872-35
; Sequence 35, Application US/08780872
; Patent No. 5846824
; GENERAL INFORMATION:
;   APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
;   APPLICANT: Bala, Waterfield, Michael Derek; Parker, Peter
;   APPLICANT: Joseph; Otsu, Masayuki; Panayotou, George; Volinia,
;   APPLICANT: Stefano; Gout, Ivan Tarasovitch
;   TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
;   TITLE OF INVENTION: THEIR PREPARATION AND USE

```
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
  ADDRESSEE:  Felfe & Lynch
  STREET:  805 Third Avenue
  CITY:  New York
  STATE:  New York
  COUNTRY:  USA
  ZIP:  10022
COMPUTER READABLE FORM:
  MEDIUM TYPE:  Diskette, 5.25 inch, 360 kb storage
  COMPUTER:  IBM PS/2
  OPERATING SYSTEM:  PC-DOS
  SOFTWARE:  Wordperfect
CURRENT APPLICATION DATA:
  APPLICATION NUMBER:  US/08/780,872
  FILING DATE:  09-JAN-1997
  CLASSIFICATION:  435
PRIOR APPLICATION DATA:
  APPLICATION NUMBER:  08/162,081
  FILING DATE:  February 7, 1994
  APPLICATION NUMBER:  PCT/GB93/00761
  FILING DATE:  13 April 1993
ATTORNEY/AGENT INFORMATION:
  NAME:  Pasqualini, Patricia A.
  REGISTRATION NUMBER:  34,894
  REFERENCE/DOCKET NUMBER:  LUD 5256
TELECOMMUNICATION INFORMATION:
  TELEPHONE:  (212) 688-9200
  TELEFAX:  (212) 838-3884
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
  LENGTH:  3207 base pairs
  TYPE:  nucleic acid
  STRANDEDNESS:  single
  TOPOLOGY:  linear
US-08-780-872-35
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Alignment Scores:
Pred. No.:                          Length:       3207
Score:          7.92e-160           Matches:      382
Percent Similarity:  51.40%         Conservative: 204
Best Local Similarity: 33.51%       Mismatches:   405
Query Match:    25.31%              Indels:       149
DB:                                 Gaps:         39
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Qy 822 AlaLeuSer-------...-------AsnGluThrIleGlyIleIlePheLysHisGly 835
Db 2362 ATCATGTCAGAATTACTCTTCAGAACAATGAG-------ATCATCTTTAAAAATGGG 2412

Qy 836 AspAspLeuArgGlnAspMetLeuIleLeuGlnIleLeuArgIleMetGluSerIleTrp 855
Db 2413 GATGATTTACGGCAAGATATGCTAACCCTTCAGATTATTCGGATTATGGAAAGTATCTGG 2472

Qy 856 GluThrGluSerLeuAspLeuCysLeuLeuProTyrGlyCysIleSerThrGlyAspLys 875
Db 2473 CAAAATCAAGGTCTTGATCTTCGTGAGTTACCTTATGGATGTCTGCAATCGGTGACTGT 2532

Qy 876 IleGlyMetIleGluIleValLysAspAlaThrIleAlaLysIleGlnSerThr 895
Db 2533 GTGGGACTTATCGGAGGTGGTGAGAAATTCACACACTATAATGCAGATT---CAGTGTAA 2589

Qy 896 ValGlyAsnThrGlyAla------PheLysAspGluValLeuSerHisTrpLeuLysGlu 913
Db 2590 GGAGGCCTGAAAGGCCACTGCAGTTTAACAGGCCACCACACTCCATCAGTGGCTCAAGAC 2649

Qy 914 LysCysProIleGluGluLysPheGlnIleAlaAlaAlaValGluArgPheValTyrSerCysAla 933
Db 2650 AAGAACAAG---GGGAAATATATGATGCGGCCATCGAATTTGTTTACACGATCATGTGCT 2706

Qy 934 GlyTyrTyrCysValAlaThrPheValLeuGlyIleGlyAspArgHisAsnAspAsnIleMet 953
Db 2707 GGATATTGTGTTGCCACCTTCATTTTGGGAATTGGAGATCGTCACAATAGTAATCATG 2766

Qy 954 IleSerGluThrGlyAsnLeuPheHisIleAspPheGlyHisIleLeuGlyAsnTyrLys 973
Db 2767 GTTAAAGATGATGGACAACTGTTTCATATAGATTTTGGACACTTTTGGATCAACAAGAG 2826

Qy 974 SerPheLeuGlyIleAsnLysGluArgValProPheValLeuThrProAspPheLeuPhe 993
Db 2827 AAAAAATTTGGTTATAAACGAGCCCGGTTTGTTTTGACCACAGATTTCTTAATA 2886

Qy 994 ValMetGlyThrSerGlyLysLys------ThrSerLeuHisPheGlnLysPheGlnIleAsp 1011
Db 2887 GTGATTAGTAAGGAGCCCAAGAATGCACAAAGACAAGAGAATTTGAGAGGTTTCAGGAG 2946

Qy 1012 ValCysValLysAlaTyrLeuAlaLeuArgHisHisThrAsnLeuLeuIleIleLeuPhe 1031
Db 2947 ATGTGTTACAAGGCTTATCTTAGCTATTCGGCAGCATGCCAATCCTTCATAAATCTTTTC 3006

Qy 1032 SerMetMetLeuMetThrGlyMetProGlnLeuThrSerLysGluAspIleGluTyrIle 1051
Db 3007 TCAATGATGCTTGGCTCTGGAATGCCAGAACTGCAATCTTTTGATGATATTGCATACATT 3066

Qy 1052 ArgAspAlaLeuThrValGlyLysSerGluGluAspAlaLeuLysTyrPheLeuAspGln 1071
Db 3067 CGAAAGACCCTAGCTTTAGATAAAACTGACCAAGAGGCTTTGGAGTATTTCATGAAACAA 3126

Qy 1072 IleGluValCysArgAspLysGlyTrpThrValGlnAsnTrpPheLeuHisLeuVal 1091
Db 3127 ATGAATGATGCACACCATGTGGCTGGACAACAAAAATGGATTGGATCTTCCACACAATT 3186

Qy 485 TrpGlnLeuSerGlyLysSerGlyGluAspGlnGlySerPheAsnAlaAspLysThrSer 504
Db 1336 TGGCCAGTACCTACCTCATGGACTACGAAGAT------TTGCTGAACCCTATTGGTGTTACT-- 1386

Qy 505 AlaThrAsnProAspLysGluAsnSerMetSerIleLeuSerIleLeuAspAsnTyrCys 524
Db 1387 GGATCAAATCCAAATAAAGAA---ACTCCATGTTTAGAGTTGACTGGTCAGC 1443

Qy 525 HisProIleAlaLeuProLysHisArgProThrProGluGlyGluGlyArgVal- 543
Db 1444 AGTGTGTGTAAAGTTTCAGATAGTCAGTGATTGAAGAGCATGCCAATTGGTCTGTATCC 1503

Qy 544 ------------------ArgAlaGluMetProAsn 549
Db 1504 CGTGAAGCAGGATTAGTTATTCCCATGCCAGCAGCCTGAGTAACAGACTAGCTAGAGACAAT 1563

Qy 550 GlnLeuArg------------LysGlnLeuGluAlaIleAlaIleAlaThrAspProLeuAsn 565
Db 1564 GAATTAAGAGAGAAAATGATAAAGAACAGCTCCGAGCAATTGTACACGAGATCCTCTATCT 1623

Qy 566 ProLeuThrAlaGluAspAspLysGluLeuTrpHisTyrArgTyrGluSerLeuLysAsp 585
Db 1624 GAAATCACTGAGCAAGAGAAAGAGATTTTCTGTGTGGAGCCACAGACACTATTGTGTAACTATC 1683

Qy 586 ProLysAlaTyrProLysLeuPheSerSerValLysTrpGlyGlnGlnIleGluValAla 605
Db 1684 CCCGAAAATTCTACCCAAATTGCTTCTGTCTGTTAAAATGGAACTCTAGAGATGAAGTAGCT 1743

Qy 606 LysThrTyrGlnLeuLeuAlaLysSerArgGluValAlaTrpAspGlnSerAlaLeuAspValGly 625
Db 1744 CAGATGTACTGCTTG--------GTAAAGATTGGCCTCCAATCAAGCCTGAA 1788

Qy 626 LeuThrMetGlnLeuLeuAspCysAsnPheSerAspGluAsnValArgAlaIleAlaVal 645
Db 1789 CAGGCTATGGAGCTTAGAGCTGGACTTGCAATTACCCCAGATCCTATGGTTCGAGGTTTTGCTGTT 1848

Qy 646 GlnLysLeuGluSer---LeuGluValLeuHisTyrLeuLeuGlnLeuVal 664
Db 1849 CCGGTGCTTAGAGAAAATATTTAACAGATGACAAACTTTCTCAGTACCTAGTA 1908

Qy 665 GlnAlaValLysPheGluProTyrHisIleAspAspSerAlaGluAlaArgPheLeuLeuLysSerArg 684
Db 1909 CAGGTACTAAAAATATGACAGTATTTGGATAACCTGCTTGTGTGGGAGATTTTTACTCAAAAAA 1968

Qy 685 GlyLeuArgAsnAlaArgIleGlyHisPheLeuTrpPheSerLeuArgSerGluIleAla 704
Db 1969 GGGTTAACTAATCAAAAGGATCGGTCACTTTTCTTTTGGCATTTAAAATCTGAGAGTG-- 2025

Qy 705 GlnSerArgHisTyrGlnIleArgPheAlaValIleLeuGluAlaValLeuGlyArgGlyCys 724
Db 2026 CACAATAAAACAGTTAGTCAGAGGTTTGGCCTGCTTTGGGAGTCCTATTGCCGTGCATGT 2085

Qy 725 GlyThrAlaMetLeuHisAspPheThrGlnValGlnGlnValIleGluAspMetLeuGlnLys 744
Db 2086 GGGATGTATCTGAAGCAC---CTTAATAGGCAAGTCAAGTTGAGGCCATGAGGAAAGCTCATTAAC 2142

Qy 745 ValThrIleAspPheLysSerLeuSerLeuSerAlaGluLysTyrAspValSerGlnValIle 764
Db 2143 TTGACT---GACATT------CTCAAACAAGAGAAGAAGATGAAACACAAAAGGTA--- 2190

Qy 765 SerGlnLysGlnLysLysGluLeuGlnAsn------LeuAsnLeuProGln 781
Db 2191 ---CAGATGAAGTTTTAGTTGAGCAAATAGCCGGCGACCAGATTTCATGGATGCTCTCCAG 2247

Qy 782 SerPheArgValProTyrAspTyrLysProGlyLeuLysAlaLeuValIleGluLysLysCys 801
Db 2248 GGCTTTCTGTCTCTCCTCTAAACCCTGCTCATCAGCTGGGAAATCTCAGGCTTGCAAGAGTGT 2307

Qy 802 LysValMetAlaSerLysLysLysProLeuTrpLeuGluPheLysCysAlaAspProThr 821
Db 2308 CGAATTATGTCTTCTGCAAAAAGGCCACTGTGGTTGAATTGGGAG------AACCCAGAC 2361

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;   COUNTRY: USA
;   ZIP: 10022
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
;   COMPUTER: IBM PS/2
;   OPERATING SYSTEM: PC-DOS
;   SOFTWARE: Wordperfect
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/085,957
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/780,872
;   FILING DATE: 09-JAN-1997
;   APPLICATION NUMBER: 08/162,081
;   FILING DATE: February 7, 1994
;   APPLICATION NUMBER: PCT/GB93/00761
;   FILING DATE: 13 April 1993
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Pasqualini, Patricia A.
;   REGISTRATION NUMBER: 34,894
;   REFERENCE/DOCKET NUMBER: LUD 5256
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212) 688-9200
;   TELEFAX: (212) 838-3884
;   INFORMATION FOR SEQ ID NO: 35:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 3207 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
US-09-085-957-35
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Alignment Scores:

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Pred. No.:                          3207
Score:              7.92e-160       382
                    1465.50         204
Percent Similarity: 51.40%          405
Best Local Similarity: 33.51%       149
Query Match:        25.31%          39
DB:                 3
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Length: 3207
Matches: 382
Conservative: 204
Mismatches: 405
Indels: 149
Gaps: 39

US-09-974-573-1 (1-1102) x US-09-085-957-35 (1-3207)

RESULT 14
US-08-162-081B-34
; Sequence 34, Application US/08162081B
; Patent No. 5824492

GENERAL INFORMATION:
 APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
 APPLICANT: Bala; Waterfield, Michael Derek; Parker, Peter
 APPLICANT: Joseph; Otsu, Masayuki; Panayotou, George; Volinia,
 APPLICANT: Stefano; Gout, Ivan Tarasovitch
 TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
 TITLE OF INVENTION: THEIR PREPARATION AND USE
 NUMBER OF SEQUENCES: 50
 CORRESPONDENCE ADDRESS:
　ADDRESSEE: Pelfe & Lynch
　STREET: 805 Third Avenue
　CITY: New York
　STATE: New York
　COUNTRY: USA
　ZIP: 10022
 COMPUTER READABLE FORM:
　MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

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;     COMPUTER: IBM PS/2
;     OPERATING SYSTEM: PC-DOS
;     SOFTWARE: Wordperfect
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/162,081B
;     FILING DATE: February 7, 1994
;     CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: PCT/GB93/00761
;     FILING DATE: 13 April 1993
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Pasqualini, Patricia A.
;     REGISTRATION NUMBER: 34,894
;     REFERENCE/DOCKET NUMBER: LUD 5256
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (212) 688-9200
;     TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 34:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 3240 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
US-08-162-081B-34

Alignment Scores:
Pred. No.:              3.0e-159          Length:        3240
Score:                  1460.50           Matches:       385
Percent Similarity:     51.53%            Conservative:  206
Best Local Similarity:  33.57%            Mismatches:    394
Query Match:            25.22%            Indels:        163
DB:                     1                 Gaps:          40

US-09-974-573-1 (1-1102) x US-08-162-081B-34  (1-3240)
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Qy   23 MetLysProArgSerThrAlaAlaSerLeuSerSerMetGluSerIlePro-------- 39
              ||| |||||| ::::::: ||| ||| :::||
Db   1 ATGCCTCCAAGAACCATCAGGTGAACTGTGGGGCATCCACTGAGCCCCCAAGAATC 60

Qy   40 ---IleGluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeu 58
                  |||||::::|||||| |||:::|| ||||||||
Db   61 CTAGTGGAATGTTTACCAAATGGAATGAATGATAGTGACT------------------ 99

Qy   59 LeuHisValAlaAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnValTrpLeuArgAla 78
              :::|| ||||| |||||||||||||||| ||||||||||||||
Db   100 TTAGAATGCCTCCGTGAGGCTACATTAGTAACTATAAGCATGAACATATTAAAGAGCA 159

Qy   79 LeuGluThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeu 98
              ::: ||||||||| ||| |||||||||| ||||||||||||||
Db   160 AGAAAATACCCTC----------------CATCAACTTCTTCAAGATGAATCTTCTTAC 204

Qy   99 LeuTyrGlnLysGlyGlnTrpTyrTyrGluIleTyrArgLysTyrAspLysTyrGlnValValGlnThr 118
              ::: ||||||||||||| :::|| |||||||||| ||||||||||
Db   205 ATTTTCGTAAGTGTTACCCAAGAGCAGAAGGGAAGAATTTTTGATGAAACAAGACCA 264

Qy   119 LeuAspCysLeuArgTyrTrpLysValLeuValLeuHisArgSerProGlyGlnIleHisValVal 138
              ||||||||| ::: ||| ::: ||| |||||| |||
Db   265 CTTTGGATCTTCGGCTTTTCAACCATT-----------------TTAAAGTAATT 306

Qy   139 GlnArgHisAlaProSerGluThrLeuAlaPheGlnArgLeuAsnLeuAsnAlaLeuIle 158
              ||| ::: ||||||||||||| |||:::::::
Db   307 GAACCAGTAGGCAACGTGCAAGAAAAGATC---CTCAATGCAGAAGTTTGCTATC 363

Qy   159 GlyTyrAspValThrGlnLeuSerGlyValSerAsnValHisAspAspValGluPheThrArgArg 178
              ||| ||||||||||| ||| |||||||||||||||
Db   364 GGCATGCCAGTGCCGAATTTGAATATGGTTAAAGATGCCGAAGTACAGGACTTCCGAAGA 423

Qy   179 ArgLeuValThrProArgMetAlaGluValAlaGlyValArgAsp-------------- 192
              ::: ||| ||| ||||||||||||| ||||||
Db   424 AATATTCTTAATGTTGTAAAGAAGCTTGGGATCTTAGGAATCTTAATTCACCTCATAGT 483

Qy   193 ProLysLeuTyrAlaMetHisProTrpValThrSerLysPro---LeuProGluTyrLeu 211
              ::||| ||| ||| ||| ||| ||| |||||||||||:::
Db   484 AGAGCAATGTATGTCATCCGCCATGTAGAATCTTCACCGAGCTGCCAAAGCACATA 543

Qy   212 LeuLysLysIleThrAsnAsnCysValPheIleVal---------------------His 225
              :::|| :::   ::: ||||||| |||
Db   544 TATAATAAATTGGATAGAGGCCAAATATAGTGGTGATTGGTAATAGTTTCTCCAAAT 603

Qy   226 ArgSerThrThrSerGlnThrLeuGluArgAlaAspAspThrProGlyThrProIleLeu 245
              |||||| ||||||| ::::::::: |||||||||||||||
Db   604 AATGACAAGACAGAAGTAACTCTGAAATCAACCATGACTGTGTGCCAGAACAAGTAATT 663

Qy   246 GlnSerPhePheThrLysMetAlaLysLysLysSerLeuMetAspIleProGluSer---- 264
              ||| ::::::: ||| ::::::::::
Db   664 GCTGAAGCAATCAGGAAA-----AAAACTAGAAGTATGTTGCTATCATCTGAACAATTA 717

Qy   265 ----------------GlnAsnGluArgAspPheValLeuArgValCysGlyLysArgAspGlu 279
                            :::   ::::::   :::|||||||||||||| :::::::
Db   718 AAACTCTGTGTTTTAGAATATCCAGGGCAAGTACATTTTAAAGTGTGGATGTGATGAA 777

Qy   280 TyrLeuValGlyGluThrProIleLysAsnPheGlnTrpProValGlnCysLeuLysAsn 299
              :::   ::::::   ::: ||||||||||||| |||||||||:::::::
Db   778 TACTTCCTAGAAAATATCCTCGAGTCAGATAAGTATAAAGAAGCTGTATAATGCTT 837

Qy   300 GlyGluGluIleHisGluValLeuAspThrProProAspProAlaLeuAspGluValArg 319
                                                  :::
                                                  CCCAATTTGAAGATGATGGCT 867
Db   838 GGGAGGATG-   867

Qy   320 LysGlu---------------GluTrpProLeuValAspAspCysThrGlyValThrGlyIleTyr 335
              ||||| ::: |||||:::::: ||| ::: |||||||
Db   868 AAAGAAAGCCTTTATTCTCAACTGCCAATG------------GACTGTTTTACAATGCCATCTTAT 921

Qy   336 HisGluGlnLeuThr--------------------IleHisGlyLysAspHisGluSerValPhe 350
              ::::::::::   :::
Db   922 TCCAGACGCCATTTCCACGCTACACCATATATGAATGGAGA-   ACATCT 969

Qy   351 ThrValSerLeuTrpAspCysAspAspArgLysPheArgValLys-------------- 364
              :::   ::: ||||||||| :::::::   :::::::
Db   970 ACAAAATCCCTTGGGTTTATAAATAGAGCACTCAGAATAAAAATTCTTTGTGCAACCTAT 1029

Qy   365 --------------IleArgGlyIleLeuProValLeuProArgThrAlaAspLeuThrLeu 380
                            ||||||||| ||||||||| :::
Db 1030 GTGAATGTAAATATTCGAGACATTGAC-   --AAG 1059

Qy   381 ValPheValGluAlaAsnIleGlnTyrGlyGlnValLeuCysGlnAsnArgArgThrSer 400
              ||||||| :::|| ||||||| |||||||||||| :::   :::
Db 1060 ATTTATGTTCGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACT 1119

Qy   401 ProLysProPheThrGluGluValLeuTrpAsnValTrpAsnValTrpLeuGluPheSerIleLysIle 420
              ||||||||||||| ||| ||| ::: |||||||
Db 1120 CAAAGAGTACCTGTTCCAATCCCAGGTGGAATGGCTGAATTATGATAATATACATT 1179

Qy   421 LysAspLeuProLysGlyGlyAlaLeuAsnLeuAsnLeuIleTyrCysGlyLysAlaProAla 440
              ||||||| |||:::::: ||| |||||||
Db 1180 CCTGATCTTCCTCGTGCTGTCGGCCTTTGCCTTCATT---TGC   --TCT 1224

Qy   441 LeuSerGlyLysThrSerAlaGluMetProSerProGluSerLysGlyLysAlaGlnLeu 460
              ||| ||||||||||||||||||||||
Db 1225 GTTAAAGGCCGAAAGGGTGCT-   AAAGAGGAACACTGTCCA 1263

Qy   461 LeuTyrTyrValAlaAsnLeuLeuIleLeuIleLeuAsnAlaLeuIle 480
              ||||||| |||||| ::::::::: |||:::
Db 1264 TTGCATGGGGAAATTAAAACTGTTTGATATCAGACACTCTAGTATCTGGAAAAATG 1323

Qy   481 ValLeuHisMetTrpGlnLeuSerGlyIleLysGlyGlnLeuGlyGlySerPheAsnAlaAsp 500
              ||||||| ||| :::   :::
Db 1324 GCTTTGAATCTTTGGCCCTACCTCACTGGATTAGAGAT--   TTGCTGACCCCTATT 1377

Qy   501 LysLeuThrSerAlaThrArgAsnProAspLysGluAsn-------------- 512
              |||||||::::::   :::::::
Db 1378 GGTGTTACT---GGATCAAATCCAAATAAAGAAACTCCATGCTTAGAGTTGGAGTTTGAC 1434

Qy   513 -------------SerMetSerIleSerIleLeuLeuAspAsnTyr 523
                          ||||||:::::::
Db 1435 TGGTTCAGCAGTGTGGTAAAGTTCCAGATATGTCAGTG---------ATTGAAGAGCA- 1484

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;  APPLICATION NUMBER:   US/08/780,872
;  FILING DATE:   09-JAN-1997
;  CLASSIFICATION:   435
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER:   08/162,081
;  FILING DATE:   February 7, 1994
;  APPLICATION NUMBER:   PCT/GB93/00761
;  FILING DATE:   13 April 1993
;  ATTORNEY/AGENT INFORMATION:
;  NAME:  Pasqualini, Patricia A.
;  REGISTRATION NUMBER:   34,894
;  REFERENCE/DOCKET NUMBER:   LCD 5256
;  TELECOMMUNICATION INFORMATION:
;  TELEPHONE:   (212) 688-9200
;  TELEFAX:   (212) 838-3884
; INFORMATION FOR SEQ ID NO:  34:
;  SEQUENCE CHARACTERISTICS:
;  LENGTH:   3240 base pairs
;  TYPE:  nucleic acid
;  STRANDEDNESS:  single
;  TOPOLOGY:  linear
US-08-780-872-34

Alignment Scores:
Pred. No.:         3.0e-159          Length:           3240
Score:            1460.50           Matches:           385
Percent Similarity:  51.53%         Conservative:      206
Best Local Similarity:  33.57%      Mismatches:        394
Query Match:      25.22%            Indels:            163
DB:                                 Gaps:              40

US-09-974-573-1 (1-1102) x US-08-780-872-34   (1-3240)
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Qy      23 MetLysProArgSerThrAlaAlaSerLeuSerSerMetGluIlePro----------  39
           |||   |||||:||::|    ||         |||:::|||
Db       1 ATGCCCAAGACCACCATCAGGTGAACTGGGGGCATCCACTTGATGCCCCCAAGAATC  60

Qy      40 --IleGluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeu  58
             :::|||||          ||| ||      |||||:||
Db      61 CTAGTGGAATGTTTACTACCAAATGGAATGATAGTGACT--------------------  99

Qy      59 LeuHisValAlaGlyHisValGlyAsnValGluGlnMetLysAlaGlnValTrpLeuArgAla  78
           |||            ::|     :|:|||
Db     100 TTAGAATGCCCCGTGAGGCTACATTAGTAACTATTAAAGCATGAACTATTTAAAGAAGCA  159

Qy      79 LeuGluThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeu  98
                                 :||    |||:::||||
Db     160 AGAAAATAACCCTCTC----------CATCAACTTCTTCAAGATGAATCTTCTTAC  204

Qy      99 LeuTyrArgGlnLysLysGlyGlnTrpTyrGluIleTyrAspLysTyrGlnValValGlnThr  118
                 ||||            |:|         ::: |||
Db     205 ATTTTCGTAAGTGTACCCAAGAGGCAGAAAGGGAAGAATTTTTTGATGAAACAAGACCGA  264

Qy     119 LeuAspCysTyrLeuArgTyrTrpLysValHisArgSerProGlyGlnIleHisValVal  138
           ||:|:            ::::
Db     265 CTTTGTGATCTTCGGCTTTTTCAACCATTT----------------TTAAAAGTAATT  306

Qy     139 GlnArgHisAlaProSerGluGluThrLeuAlaPheGlnLeuArgGlnLeuAsnAlaLeuIle  158
              ::                 |||    |||||:|||::||:|
Db     307 GAACCAGTAGGCAACCGTGAAGAAGAAAGATC---CTCAATCGAGAAAATTCGTTTGCTATC  363

Qy     159 GlyTyrAspValThrAspValThrSerAsnValHisAspAspGlnGluGlyLeuGluPheThrArgArg  178
           |||                |||    |||||
Db     364 GGCATGCCAGTGCCGTGCGAATTTGAATATGGTAAAGATACAGGACTTCCGAAGA  423

Qy     179 ArgLeuValThrProArgMetAlaGlyValAlaValAlaGlyArgAsp----------  192
           ||::::      :|:|:||
Db     424 AATATTCTTAATGTTTGTAAAGAAGCTGTGCATTAGGGATCTTAGGTCTTAATTCACCTCATAGT  483

Qy     193 ProLysLeuTyrAlaMetHisProTrpValThrSerLysPro---LeuProGluTyrLeu  211
           ||::      :|           ||||:|:
Db     484 AGAGCAATGTATGTCATCCGCCACACATGAGAATCTTCACCAGAGCTGCCAAAGCACATA  543
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Qy     212 LeuLysLysIleThrAsnAsnCysValPheValIle----------His  225
                 :|:||       ::
Db     544 TATAATAAATTGGATAGAGGCCCAAATATATAGTCGTGTAATATAGTTTCTCCAAAT  603

Qy     226 ArgSerThrSerGlnThrIleLysValSerAlaAspAspThrProGlyThrIleLeu  245
           |||           ||||||     ||
Db     604 AATCAACAAGAGAAGTATCTCTGAAATCAACCATGACTGTGTGCCAGAACAAGTAATT  663

Qy     246 GlnSerPhePheThrLysMetAlaLysLysSerLeuMetAspIleProGluSer----  264
               ::||              :|:|
Db     664 GCTGAAGCAATCAGGAAA------AAAACTAGAGTATGTTGTCTATCATCTGACAATTA  717

Qy     265 ----------GlnAsnGluArgAspPheValLeuArgValCysGlyArgAspGlu  279
                     :::||      ||:|||||::||:||
Db     718 AAACTCGTGTTTTAGATATCAGGGCAGTACATTTTAAAAGTGTGGGATGTGATGAA  777

Qy     280 TyrLeuValGlyValGluThrProIleLysAsnPheGlnTrpValArgGlnCysLeuLysAsn  299
                  ||    :::    |||:::|||:|||
Db     778 TACTTCCTAGAAAAAATATCCTCTGAGTCAGTAGAGTATATAAGAAGCTGTATAATGCTT  837

Qy     300 GlyGluGluIleHisLeuValLeuAspThrProProAspProAlaLeuAspGluValArg  319
                 |||           |||
Db     838 GGGAGGATG---------------------------------CCCAATTTGAAGATGATGGCT  867

Qy     320 LysGlu----------GluTrpProLeuValAspAspCysThrGlyValThrGlyTyr  335
           ||||           :::|||    :|
Db     868 AAAGAAAGCCTTTATTCTCAACTGCCAATG------GACTGTTTACAATGCCATCTTAT  921

Qy     336 HisGluGlnLeuThr---------------IleHisGlyLysAspHisGluSerValPhe  350
           |||                   :::
Db     922 TCCACACGGCATTTCCACAGCTACACCATATATGAATGGAGAA----------ACATCT  969

Qy     351 ThrValSerLeuTrpAspCysAspSerArgLysPheArgValLys-----  364
           ||                   ::
Db     970 ACAAAATCCCTTGGGTTATAATAGAGCACTCAGAATAAAAATTCTTTGTGCAACCTAT  1029

Qy     365 -----------IleArgGlyIleAspIleProValLeuProArgThrAlaAspLeuThr  380
                    |||||     |||
Db    1030 GTGAATGTAAATTCGAGACATTGAC-----------------------AAG  1059

Qy     381 ValPheValGluAlaAsnIleGlnTyrGlnValGlnGlnValCysSerArgArgThrSer  400
           |||||              ::|       ||||
Db    1060 ATTTATGTTCGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAAATGGAACACT  1119

Qy     401 ProLysProPheThrGluGlyValLeuValTrpAspAsnValThrProLeuGluPheSerIle  420
               |||    |||              ||||
Db    1120 CAAAGGGTACCTTGTTCCAATCCAGGTGGAATGATGAATGGCTGAATTATGATATATACATT  1179

Qy     421 LysAspLeuProLysGlyValAlaLeuAsnLeuGlnIleTyrCysGlyLysAlaProAla  440
           :::                  |||              :::
Db    1180 CCTGATCTTCCTCGTGCTGCTGACTTTGCCTTTCCATT--TGC-----------TCT  1224

Qy     441 LeuSerGlyLysThrSerAlaGluMetProSerProLysGlyLysLysAlaGlnLeu  460
           |:                           :::
Db    1225 GTTAAAGGCCGAAAGGGTGCT------------AAAGAGGAACACTGTCCA  1263

Qy     461 LeuTyrTyrValAsnLeuLeuIleLeuAspHisArgPheLeuLeuGluArgHisGlyGluTyr  480
                                ||||:::|||||
Db    1264 TTGGCATGGGAAATAAAAACTTGTTGATTACAGACACACTCCTAGTATCTGGAAAAATG  1323

Qy     481 ValLeuHisMetTrpGlnLeuSerGlyGlyLysGlyGluAspGlnGlyLeuSerPheAsnAlaAsp  500
                    |||::      :||||||
Db    1324 GCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGAT----------TTGCTGAACCCCTATT  1377

Qy     501 LysLeuThrSerAlaThrAsnProAspLysGluAsn----------  512
           |:::|||
Db    1378 GGTGTTACT---GGATCAAATCCAAATAAAGAACTCCATGCTTAGAGTTGGAGTTTGAC  1434

Qy     513 ----------SerMetSerIleSerIleLeuLeuAspAsnTyr  523
                         ::::|||
Db    1435 TGGTTCAGCAGTGTGGTAAAGTTCCCAGATATGTCAGTG------ATTGAAGAGCA  1484

Qy     524 CysHisProIleAlaLeuProLysHisArgProThrProAspProGlu-GlyAspAlaArgVa  543
              :::|
Db    ...
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Db  1485  TGCCAATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCACGCAGGACTGAGTAA  1544
          |||  :::||||||||            |||
Qy   543  lArgAlaGluMetProAsnGlnLeuArg----------LysGlnLeuGluAlaIleIl   559

Db  1545  CAGACTAGCTAGAGACAATGAATTAAGGGAAAATGACAAGAACAGCTCAAAGCAATTTC  1604
          ::::||||                    |||:::
Qy   559  eAlaThrAspProLeuAsnProLeuThrAlaGluAsnProLeuLeuTrpHisPheAr   579

Db  1605  TACACGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTCTATGGAGTCACAG  1664
          |||||||||||          :::|||::::         |||
Qy   579  gTyrGluSerLeuLysAspProLysAlaTyrProLysLeuPheSerSerValLysTrpGl  599

Db  1665  ACACTATTGTGTAACTATCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAA  1724
          |||||||||||
Qy   599  yGlnGlnGluIleValAlaAlaLysThrTyrGlnLeuLeuAlaLysArgGluValTrpAspGl  619

Db  1725  TTCTAGAGATGAAGTAGCCCAGATGTATTGCTTG---------------GTAAAAGATTG  1769
          |||||||||              :::
Qy   619  nSerAlaLeuAspValGlyLeuThrMetGlnLeuLeuAspCysAsnPheSerAspGluAs  639

Db  1770  GCCCTCCAATCAAACCTGAACAGGCTATGCATGGAACTTCTCGGACTGTAATTACCCAGATCCTAT  1829
          :::
Qy   639  nValArgAlaIleAlaValGlnLysGlnLeuGluSer----LeuGluAspAspAspValLeuHi  658

Db  1830  GGTTCGAGGTTTTGCTGTTCGGTGCTTGAAAAATATTTAACAGGATGACAAACTTTCTCA  1889
          |||||||||||||||||             :::
Qy   658  sTyrLeuLeuGlnLeuValGlnAlaValLysPheGluProTyrHisAspSerAlaLeuAl  678

Db  1890  GTATTTAATTCAGCTAGTACAGGTCCTAAAATATGAACAATATTTGGATAACTTGCTTGT  1949
          |||                    |||
Qy   678  aArgPheLeuLeuLysArgGlyLeuArgAsnLysIleGlyHisPheLeuPheTrpPh  698

Db  1950  GAGATTTTTACTGAAGAAACATTGACTAATCAAAGGATTGGGCACTTTTCTTTTGGCA  2009
          |||
Qy   698  eLeuArgSerGluIleAlaGlnSerArgHisTyrGlnLeuArgPheAlaValIleLeuGl  718

Db  2010  TTTAAAATCGAGATG----CACAATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTGGA  2066
          |||:::||||||              :::
Qy   718  uAlaTyrLeuArgGlyCysGlyThrAlaMetLeuHisAspPheThrGlnIleValGlnVa  738

Db  2067  GTCCTATTGTCGTGCATGTGGATGTATTGAAGCAC---CTGAATAGGCAAGTCGAGGC  2123
          ::::|||||::::
Qy   738  lIleAspMetLeuGlnLysValThrIleAspIleLysSerLeuSerAlaGluTyrAs  758

Db  2124  CTCAAACAGGAGGAGGAAGGA  2174
          |||
Qy   758  pValSerSerGlnValIleSerArgGlnLeuLysGlnLysLeuAsnLeuGlnAsn-----  776

Db  2175  TGAAACACAAAGGTA------CAGATGAAGTTTTTAGTTGAGCAAATGAGGCGGACCAGA  2228
          ::::|||:::
Qy   777  ---LeuAsnLeuProGlnSerPheArgValProTyrAspProGlyLeuGlyAlaGlyAl  795

Db  2229  TTTCATGGATGCCCTACAGGGCTTGCTGTCCTCCTAAACCCTGCTCATCAACTAGGAAA  2288
          |||
Qy   795  aLeuValIleGluLysCysLysLysValMetAlaSerLysLysLysProLeuTrpLeuGluHi  815

Db  2289  CCTCAGGCTTAAAGATGTCAAATATGTCTTCTGCAAAAGGCCACTGTGGTTGAATTG  2348
          |||::::
Qy   815  eLysCysAlaAspProThrAlaLeuSer----------AsnGluThrIleGl  829

Db  2349  GGAG-----AACCCCAGACATCATGTCAAGATCAGAGTTACTGTTTCAGACAATGAG----  2394
          ||| :::|||
Qy   829  YIleIlePheLysHisGlyAspAspLeuArgGlnAspMetLeuIleLeuGlnIleLeuLeuAr  849

Db  2395  -ATCATCTTTAAAAATGGGGATGATTTACGGCAAGATAATGCTAACACTTCAAATTATTCG  2453
          |||::::
Qy   849  gIleMetGluSerIleTrpGluThrGluSerLeuAspLeuCysLeuLeuProTyrGlyCy  869

Db  2454  TATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAATGTTAACCTATATGGTTG  2513
          ||||||
Qy   869  sIleSerThrGlyAspLysIleGlyMetIleGluIleValLysAspAlaThrIleAl  889
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Db  2514  TCTGTCAATCGGTGACTGTGTGGACTTATTGAGGTGGTGCGAAATTCTCACACTATTAT  2573
          |||
Qy   889  aLysIleGlnSerThrValGlyAsnThrGlyAla------PheLysAspGluValLe  907

Db  2574  GCAAATT---CAGTGCAAAGCGGCTTGAAAGGTGCACTGCAGTTCAACAGCCACACACT  2630
          |||||||            |||
Qy   907  uSerHisTrpLeuLysGluLysCysProIleGluGluLysCysProGlnAlaAlaValGluAr  927

Db  2631  ACATCAGTGGCTCAAAGACAAGAACAAA---GGAGAAATATATGATGCAGCCATTGACCT  2687
          :::             ||||||||
Qy   927  gPheValTyrSerCysValAlaGlyTyrCysValAlaThrPheValGlyTyrIleGlyAspAr  947

Db  2688  GTTTACACGTTCATGTGCTGGATACGTGTAGCTACCTTCATTTTGGGAATTGGGAGATCG  2747
          |||:::|||
Qy   947  gHisAsnAspAsnIleMetIleSerGluGluThrGlyAsnLeuPheHisIleIleAspPheGlyHi  967

Db  2748  TCACAATAGTAACATCATGGTGAAAGACGATGGACAACTGTTTCATATAGATTTTGGACA  2807
          |||
Qy   967  sIleLeuGlyAsnTyrLysSerPheLeuGlyIleLysGluArgValProPheValLe  987

Db  2808  CTTTTTGGATCACAAGAAGAAGAAAAATTTGGTTATAAACGACGAAGCGGTGCGTCATTTGTTTT  2867
          |||:::
Qy   987  uThrProAspPheValMetGlyThrSerGlyLyaLys------ThrSerLeuHi  1005

Db  2868  GACACAGGATTTCTTTTATAGTGATTAGTAGTTAGTAAAGGAGCCCAAGAATGCACAAGACAAGAGA  2927
          |||||||||:::::
Qy  1005  sPheGlnLysPheGlnSerAspValCysValLysAlaTyrLeuLeuAlaLysArgHisHisThrAs  1025

Db  2928  ATTTGAGAGTTTCAGGAGATGTGTTACAACAGCCATTCGACAGCATGCCAA  2987
          |||||||||
Qy  1025  nLeuLeuIleLeuPheSerMetMetLeuMetProGlnLeuThrSerLy  1045

Db  2988  TCTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCTGGAATGCCCAGAACTACAAATCTTT  3047
          |||||||:::||||||
Qy  1045  sGluAspIleGluTyrIleArgAspAspAlaLeuThrValGlyLyaSerGluGluAspAlaLaLy  1065

Db  3048  TGATGACATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTT  3107
          |||||||||||
Qy  1065  sLysTyrPheLeuAspGlnIleGluGluValCysArgAspAspLysGlyTrpValGlnPheAs  1085

Db  3108  GGAGTATTTCATGAAACAAATGAATGACACATCATCGGTGGCTGCTGGACAACAAAAATGGA  3167
          |||||||             :::
Qy  1085  nTrpPheLeuHisLeuVal  1091

Db  3168  TTGGATCTTCCACACAATT  3186
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Search completed: February 15, 2004, 06:44:12
Job time : 486 secs

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                GenCore version 5.1.6
        Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on:    February 15, 2004, 05:14:49 ; Search time 889 Seconds
                                           (without alignments)
                                     4566.213 Million cell updates/sec

Title:          US-09-974-573-1
Perfect score:  5790
Sequence:       1 MELENYEQPVVLREDNRRRR.........QFNWFLHLVLGIKQGEKHSA 1102

Scoring table:  BLOSUM62
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                Ygapop  10.0 , Ygapext  0.5
                Fgapop   6.0 , Fgapext  7.0
                Delop    6.0 , Delext   7.0

Searched:       249703 seqs, 184181637 residues

Total number of hits satisfying chosen parameters:    4899406

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters: -DEV=xlh
-MODEL=frame+_p2n.model
-Q=/cgn2_1/USPTO_spool/US0997457573/runat_11022004_180018_18255/app_query.fasta_1.1287
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
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-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :  Published_Applications_NA:*
 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
 3: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
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 7: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
 8: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB ID		Description
1	5538	95.6	5309	US-10-334-143-120	12	Sequence 120, App
2	5523.5	95.4	3342	US-10-101-235A-3	13	Sequence 3, Appli
3	5309	91.7	3237	US-10-101-235A-5	13	Sequence 5, Appli
4	1460.5	25.2	3213	US-10-101-235A-7	13	Sequence 7, App
5	1354.5	23.4	5220	US-10-440-464-145	12	Sequence 145, App
6	1352.5	23.4	5220	US-10-337-192-1	13	Sequence 1, Appli
7	1352.5	23.3	3387	US-10-027-591-1	14	Sequence 1, Appli
8	1349.5	23.1	3777	US-10-162-160-2	15	Sequence 2, Appli
9	1337.5	18.5	5061	US-09-814-353-19587	13	Sequence 19587, A
10	1074	17.9	3504	US-10-092-219-1	14	Sequence 1, Appl
11	1034	17.9	3504	US-09-205-658-47	9	Sequence 47, Appl
12	1034	17.9	3504	US-09-844-353A-47	9	Sequence 47, Appl
13	1034	16.3	627	US-09-963-693-47	9	Sequence 47, Appl
14	944	15.9	5990	US-10-101-235A-1	13	Sequence 1, Appli
15	922	15.9	5990	US-09-917-800A-477	10	Sequence 477, App
16	922	12.4	3473	US-10-388-934-72	12	Sequence 72, App
17	719.5	12.4	3063	US-10-252-157-370	13	Sequence 370, App
18	709.5	12.3	3063	US-10-117-722-474	13	Sequence 474, App
19	709.5	12.1	441	US-10-037-270-474	15	Sequence 474, App
20	699	11.9	3252	US-09-867-701-5505	10	Sequence 5505, Ap
21	690.5	11.9	3252	US-09-921-232-1	10	Sequence 1, Appli
22	690.5	11.7	3252	US-09-921-330-1	10	Sequence 1, Appli
23	690.5	11.0	2784	US-09-921-329-1	12	Sequence 1, Appli
24	678.5	11.0	2462	US-10-369-493-26898	12	Sequence 26898, A
25	638.5	9.7	2418	US-10-369-493-25482	12	Sequence 25482, A
26	561.5	6.6	473	US-09-771-161A-10	9	Sequence 10, Appl
27	384.5	6.6	5703	US-09-864-761-16057	10	Sequence 16057, A
28	380	6.0	2620	US-09-801-368-389	13	Sequence 389, App
29	356.5	6.0	3205	US-09-925-302-205	13	Sequence 205, App
30	345.5	5.7	7864	US-09-834-975-805	10	Sequence 805, Appl
31	330	5.6	2451	US-09-976-165-29	13	Sequence 29, Appl
32	322.5	5.6	2451	US-10-342-276-29	10	Sequence 29, Appl
33	322.5	5.6	2487	US-09-976-165-32	13	Sequence 32, Appl
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37	322.5	5.6	3324	US-10-342-276-33	13	Sequence 33, Appl
38	322.5	5.6	3602	US-09-976-165-30	13	Sequence 30, Appl
39	322.5	5.6	3602	US-10-342-276-30	10	Sequence 30, Ap
40c	322.5	5.6	339	US-09-796-692-7359	12	Sequence 7359, Ap
41c	294	5.1	339	US-10-057-475B-7359	12	Sequence 7359, Ap
42c	294	5.1	339	US-10-154-884B-7359	15	Sequence 7359, Ap
43c	294	5.1	339	US-10-040-862-7359	10	Sequence 7359, Ap
44	281	4.9	1894	US-09-771-161A-11	10	Sequence 11, Appl
45c	278	4.8	326	US-09-796-692-7451	10	Sequence 7451, Ap

ALIGNMENTS

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US-10-334-143-120
; Sequence 120, Application US/10334143
; Publication No US20040009549A1
; GENERAL INFORMATION:
; APPLICANT: GRIGORIEV, IGOR VYACHESLAVOVICH
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: METHOD FOR DETECTING REMOTE HOMOLOGUES AND NOVEL
; TITLE OF INVENTION: KINASES IDENTIFIED WITH THE METHOD
; FILE REFERENCE: 038602/1543
; CURRENT APPLICATION NUMBER: US/10/334,143
; CURRENT FILING DATE: 2002-12-31
; PRIOR APPLICATION NUMBER: 60/343,169
; PRIOR FILING DATE: 2001-12-31
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 120
; LENGTH: 5309
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-334-143-120
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Alignment Scores:
Pred. No.:   0   Length: 5309

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Percent Similarity:        97.10%        Conservative:       20
Best Local Similarity:     95.28%        Mismatches:         32
Query Match:               95.65%        Indels:              0
DB:                                      Gaps:                0

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Qy 121 CysLeuArgArgTyrThrProLysValLeuHis...ArgSerProGlyGlnIleHisVal ValGlnArg 140
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Qy 161 AspValThrAspValSerArgAsnValHisAspAspProLysLysGluPheThrArgArgArgLeu 180
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Qy 201 TrpValThrSerLysProGluLeuProGluTyrLeuLysLysLysIleThrLysAsnAsnCysValVal 220
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Db 911 ...

Qy 221 PheIleValIleHisArgSerThrThrSerGlnThrIleLeuLysValSerAlaAspAspThr 240
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Qy 241 ProGlyThrIleLeuGlnInSerPhePheThrLysSerLysLysSerLeuSerLeuMetAsp 260
        CCCGGCACCATCCTGCAGAGCTTCTTCACCAAGAGCAAGAAGTCCCTGTCGCTCATGGAT
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Qy 341 IleHisGlyLysLysAspHisGluSerValPheThrValSerLeuTrpAspCysAspArgGlyLys 360
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Db 1331 ...

Qy 361 PheArgValLysIleArgGlyIleLeuAspIleProValLeuProValThrAlaAspLeuThr 380
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Qy 381 ValPheValGluAlaAsnIleGlnInTyrGlyValGlnInValLeuCysValArgArgThrSer 400
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Qy 401 ProLysProPheThrGluGluValTrpLeuValLeuGluTrpLeuGluSerIleLysIleIle 420
        CCCAAACCCTTCACAGAGGAGGTGTGTGGAATGTGTGTGAATGTGTCAGTATCAAAATC
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Qy 441 LeuSerGlyLysThrSerAlaGluMetProSerProGluSerLysSerGlyLysAlaGlnInLeu 460
        CTGTCCAGCAAGGACCTCTGCGAGTCCCCAGTTCTGAGTCGAGTCTCCAAGGGCAAAGTTCAGCTT
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Qy 461 LeuTyrTyrValAsnLeuLeuLeuIleLeuAspHisArgPheLeuLeuArgHisGlyGluTyr 480
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Qy 481 ValLeuHisMetTrpGlnInLeuSerGlyLysGlyGluGlyInGlySerPheAsnAlaAsp 500
        GTCCTCCACATGTGGCAGATCTGGAGATCTGGGAGAGGGAGAAGGACCAAGGAGCTTCAATGCTGAC
        ||||||||||||||||||:::||||||||||||||||||||||||||||||||||||||
Db 1751 ...

Qy 501 LysLeuThrSerAlaThrAsnProAspLysGluAsnSerMetSerIleSerIleLeuLeuLeu 520
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Qy 541 AspArgValArgValAlaAlaGlyMetProAsnGlnInLeuArgLysGlnInLeuIleIleAla 560
        GACCGGGTTCGAGAGTAGTGGCGGCAATTGCCAAACCAGCTTCGCAAGCAATTGGAGCGGATCATAGCC
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Qy 561 ThrAspProLeuAsnProLeuThrAlaGluLeuLysGluLeuLeuTrpHisPheArgTyr 580
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Qy 581 GluSerLeuLysAspProLysLeuProPheSerSerValLysTrpProGlyGln 600
        GAAAGCCTTAAGCACCCAAAAAGCATATCCTAAGCTATTTAGTTCAGTGAAATGGGGACAG
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Db 2171 ...

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Qy   701 SerGluIleAlaGlnSerArgHisTyrGlnArgPheAlaValIleLeuGluAlaTyr  720
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Qy   721 LeuArgGlyCysGlyThrAlaMetLeuHisAspPheThrGlnIleValGlnHisValIleAsp  740
Db  2471 CTGAGGGGCTGTGGCACAGCCATGCTGCACGACTTTACCCAACAAGTCCAAGTAATCGAG 2530

Qy   741 MetLeuGlnLysValThrIleAspIleLysSerLeuSerAlaGluLysTyrAspValSer  760
Db  2531 ATGTTACAAAAGTCACCCTGATATTAAATCGCTCTCTGCTGAAAAGATGACGTCAGT 2590

Qy   761 SerGlnValIleSerGlnLeuLysGluAsnLeuGlnAsnLeuGlnAsnLeuAsnLeuPro  780
Db  2591 TCCCAAGTTATTTCAACAACTTAAACAAAAGCTTGAAAACCTGCAGAATTCTCAACTCCCC 2650

Qy   781 GlnSerPheArgValProTyrAspProGlyLeuLysAlaGlyAlaLeuValIleGluLys  800
Db  2651 GAAAGCTTTAGAGTTCCAATATGATCCTGGACTGAAAGCAGGAGCGCTGGCAATTGAAAA 2710

Qy   801 CysLysValMetAlaSerLysLysProLeuPheLysGluPheLysCysAlaAspPro  820
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Qy   821 ThrAlaLeuSerAsnGluThrIleGlyIleIleGlnPheLysHisGlyAspAspLeuArgGln  840
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Qy   841 AspMetLeuIleLeuGlnIleLeuArgIleMetGluSerIleTrpGluThrGluSerLeu  860
Db  2831 GACATGCTTATTTTACAGATTCTACGAATCATGGAGTCTATTTGGGAGACTGAATCTTTG 2890

Qy   861 AspLeuCysLeuLeuProTyrGlyCysIleSerThrGlyCysIleSerThrGlyValSerThrGlyLysIleGlyMetIleGlyGlu  880
Db  2891 GATCTATGCCTCCTCGCACCATGGTTGCATTTCAACTGGTTGCACTTATTTGGACAAAATGATGATCGAG 2950

Qy   881 IleLeuGlyIleValAspAlaThrThrIleAlaLysThrLysGlnGlnSerThrValGlnAsnThrGly  900
Db  2951 ATTGTGAAAGACGGCCACGACAATTGCCAAAATTCAGCAAGCACAGTGGGCACACCGGA 3010

Qy   901 AlaPheLysAspGluValLeuSerHisTrpLeuLysGluHisIleTrpLeuLysSerProIleGluGluLys  920
Db  3011 GCATTTAAAGATGAAGTCCTGAGTCACTGGCTCAAAGAAAATCCCCACTGAAGAAAAG 3070

Qy   921 PheGlnAlaAlaValAlaValGluArgPheValThrSerCysAlaGlyTyrSerCysValAlaThrPhe  940
Db  3071 TTTCAGGCAGCAGTGGCAGAGATTTGTTTATTCCTGCAGGCTACTGTGTGCCAACCTTT 3130

Qy   941 ValLeuGlyValIleGlyAspArgHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeu  960
Db  3131 GTTCTTGGAGTAATAGGGACACAGACCGCGCAGT--GTTGCCAGCCCGTCCTCCATGGAGCTCATCCCATC 3190

Qy   961 PheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLys  980
Db  3191 TTTCATATTGACTTCGGGCACATTCTTGGGAATTACAAAGTTTCCTGGGCATTAATAAA 3250

Qy   981 GluArgValProPheValLeuThrProAspPheLeuPheValMetGlyThrSerGlyLys 1000
Db  3251 GAGAGAGTGCCATTTGTGCTAACCCCTGACTTCCTTTTGTGATGGGAACTTCTGGAAAG 3310

Qy  1001 LysThrLeuHisPheGlnLysPheGlnAspValCysValLysAlaTyrLeuAlaLeu 1020
Db  3311 AAGACAAGCCCACACTTCCAGAAATTTCAGGACACATCTGTTAAGGCTTATCTAGCCCTT 3370

Qy  1021 ArgHisHisThrAsnLeuLeuIleIleLeuPheSerMetMetLeuMetThrGlyMetPro 1040
Db  3371 CGTCATCACCACAAACCTACTGAATCATCCTGTTCCCATGATGCTGATGACAGGAATGCCC 3430

Qy  1041 GlnLeuThrSerLysGluAspIleGluTyrIleArgAspAlaLeuThrValGlyLysSer 1060
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Qy  1061 GluGluAspAlaAlaLysTyrPheLeuAspGlnIleGluValCysArgAspLysGlyTrp 1080
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Qy  1101 SerAla 1102
Db  3611 TCAGCC 3616

RESULT 2
US-10-101-235A-3
; Sequence 3, Application US/10101235A
; Publication No. US20030182669A1
; GENERAL INFORMATION:
;  APPLICANT: Rockman, Howard A.
;  APPLICANT: Naga Prasad, Sathyamangla V.
;  APPLICANT: Laporte, Stephane A.
;  APPLICANT: Barak, Larry S.
;  APPLICANT: Caron, Marc G.
;  TITLE OF INVENTION: Phosphoinositide 3-Kinase Mediated Inhibition of GPCRs
;  FILE REFERENCE: 033072-064
;  CURRENT APPLICATION NUMBER: US/10/101,235A
;  CURRENT FILING DATE: 2002-03-19
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;  LENGTH: 3342
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-10-101-235A-3

Alignment Scores:
Pred. No.:                              Length:           3342
Score:               0                  Matches:          1049
Percent Similarity:  5523.50            Conservative:       21
Best Local Similarity: 97.10%           Mismatches:         31
Query Match:         95.19%             Indels:              1
DB:                  95.40%             Gaps:                1
                     13

US-09-974-573-1 (1-1102)  x  US-10-101-235A-3  (1-3342)

Qy     1 MetGluLeuGluAsnTyrGlyGluGlnProValValLeuArgGluAsnArgArgArgArg   20
Db     1 ATGGAGCTGGAGAACTATAAACAGCCCGTGGTGCTGAGAGAGGACAACTGCGAAGGCGC   60

Qy    21 ArgArgMetLysProArgSerThrAlaAlaSerLeuSerSerMetGluLeuIleProIle   40
Db    61 CGGAGGATGAAGCCGCGCAGT--GTTGCCAGCCCGTCCTCCATGGAGCTCATCCCATC  117

Qy    41 GluPheValLeuProThrSerGlnAsnArgThrLysProGluThrAlaLeuLeuHis   60
Db   118 GAGTTCGTGCTGCCCACCAGCCAGAATAGCAAGACCCCGAAACGGGCCTGCTGCAC  177

Qy    61 ValAlaGlyHisGlyAsnValGluArgGlnLysMetLysAlaGlnValTrpLeuArgLeuGlu   80
Db   178 GTGGCCGGCCACGGCAACGTGGAGCAGATGAAGGCCCAGTGTGGCTGGCGCTGGAG  237

Qy    81 ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTyr  100
Db   238 ACCAGCGTGTCCGCGGGGGACTTCTACCACCGGCTGGGACCCGATCACTTCCTCCTGTCTTAT  297

Qy   101 GlnLysLysGlyGlnTrpTyrGluLluTyrAspLysTyrGlnValValGlnThrLeuAsp  120
Db   298 CAGAAGAAGGGGCAGTGGTACGAGCTGTACGACAAGTACCAGGTGGTGCAGACTCTGGAC  357

Qy   121 CysLeuArgTyrTrpLysTrpGluValLeuHisSerArgSerProGlyGlnIleIleSerValValGlnAsnArg  140
Db   358 TGCCTGCGCTACTGGAAGCCGAAGGGCCACCGACCCGGAGCCCGGCCAGATCCACCTGGTGCAGCGCGG  417

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Qy  141  HisAlaProSerGluGluThrLeuAlaPheGlnArgGlnLeuAsnAlaLeuIleGlyTyr  160
              ||||||||||||||||||||||||||||||||||||||||||||||| :::
Db  418  CACCCGCCCTCCGAGGAGACTCCAAGCTTCCAGCGGCAGCTGAATGCGCTGATTGGCTAT  477

Qy  161  AspValThrAspValSerAsnValHisAspAspGluProPheThrArgArgArgLeu  180
              ||||||||||||||||||||||||||||||||||||||||||||||
Db  478  GACGTCACTGACGTCAGCAACGTGCACGACGATGAGCCGTTCACGCGCCGTGGCTTG  537

Qy  181  ValThrProArgMetAlaGluValAlaAlaGlyAlaArgAspAspProLysLeuTyrAlaMetHisPro  200
              ||||||||||||||||||||||||||||||||||||||||||||||
Db  538  GTGACCCCGCGCATGGCGGAGGTGGCCGCAGCCCGCGACGACCCCAAGCTCTACGCCATGCACCCCG  597

Qy  201  TrpValThrSerLysProLeuProGluTyrLeuLeuLysLysLysIleThrAsnAsnCysVal  220
              |||||||||||||||||||||||||||||||||||||||||||||     :::
Db  598  TGGGTGACAAGTCCAAGCCCCTCCCGGAGTACCTGTTGAAGAAGAAGATTACCAACAACTGCATC  657

Qy  221  PheLeuValIleHisArgSerThrSerGlnThrIleLysValSerAlaAspAspAspThr  240
              ||||||||||||||||||||||||||||||||||||||||||||||
Db  658  TTCATCGTCATTCACCGCAGCACCAGCCAGACCATTAAGGTCTCAGCCGACGACGACACC  717

Qy  241  ProGlyThrIleLeuGlnSerPheProPheThrLeuThrLysLysLysSerLeuMetAsp  260
              ||||||||||||||||||||||||||||||||||||||||||||||
Db  718  CCCGGCGCCATCCTGCAGAGCTTCCTTCACCAAGTGGCCAAGAAGAAGAAATCTCTGATGGAT  777

Qy  261  IleProGluSerGlnAsnGluArgAspPheLysAsnGlyGlnCysLeuLysArgGluTyr  280
              ||||||||||||||||::::|||||||||||||||||||||
Db  778  ATTCCGGAAAGCCAAAGCCAAGAGGATTTTGTGTCTCGGCCGTCGTCAAGGACGTAC  837

Qy  281  LeuValGlyGluHisProIleLysArgGlnAsnPheGlnIleTrpValArgGlnCysLeuLysAsnGly  300
              |||||||||||||||||||||||||||||||||||||||||||||
Db  838  CTGGTGGGCGAAACGCCCATCAAAAACTTCCAGTGGTGGTGAGGCCACTGCCTCAAGAACGGA  897

Qy  301  GluGluIleHisLeuValLeuAspAspCysHisValThrGlyTyrHisGluLeuThr  320
              ||||||||||||||||||||||||||||||||||||||||||::::
Db  898  GAAGAGATTCACGTGGTACTGGACGACTGCCACGTGACGGGTACCACGAGTGAGGAAG  957

Qy  321  GluGluTrpProLeuProValAspAspCysHisThrGlyTyrValThrGlyLeuAsnLeuThr  340
              |||||||||||||||||||||||||||||||||||||||||||||
Db  958  GAAGAGTGGCCGCTGCCCGTGGTGGACGACTGCCACACGGGCTACCGGACCAGCTTACC  1017

Qy  341  IleHisGlyLysLysAspHisGluSerValPheThrValSerLeuTrpAspCysAspArgArgLys  360
              ||||||||||||||||||||||||||||||||||||||||||||||
Db  1018 ATCCACGGCAAGGACACAGAGAGTGTCTTCACCGTGTCCCTGTGGGACTGCGACCGCCGCAAG  1077

Qy  361  PheArgValLysIleAsnIleProValLeuProAspGlnThrAlaAspLeuThr  380
              :::|||||||||||||||||||||||||||||||||||||||:::
Db  1078 TTCAGGGTCAAGATCAACATCCCCGTGCCTCCGGACCAGACCGCCGACCTCACA  1137

Qy  381  ValPheValGluValGlyAsnIleGlnTyrGlyGlnGlnValLeuCysGlnIleArgArgThrSer  400
              :::|||||||||||||||||||||||||||||||||||||||
Db  1138 GTTTTTGTAGAGGCCAACATCCAGTACGGGCAACAAGTCCTTTGCCAAGGAGAACCAGC  1197

Qy  401  ProLysProPheThrGluLeuTrpLeuValLeuValGlyLeuGlyLysLeuLeuValGlyAlaProAla  420
              |||||||||||||||||||||||||||||||||||||||||||||
Db  1198 CCCAAACCCTTCACAGAGCTGTGGCTGGTGCTTGTGGGCTTGGGCAAGCTGCTTGTCGGGGCTCCAGCA  1257

Qy  421  LysLysAspHisLysLeuLeuAsnLeuAsnLeuGlnLeuAsnLeuGlnLeuAlaLeuAlaGlnLeuLeu  440
              |||||||||||||||||||||||||||||||||::::
Db  1258 AAAGACTTGCCCAAAGGGGCTCAACTACTGCGGTAAAGCTCCAGCA  1317

Qy  441  LeuSerGlyLysThrSerArgAlaGluMetProSerProGluSerLysGlyLysValAlaGlnLeu  460
              ||||||||||||||||||||||||||||||||||||||||||||||
Db  1318 CTGTCCAGCAAGGGCTCTGCAGAGATGCCCAGTCCTGAGTCCAAAGGGCAAAGTTCGGCTT  1377

Qy  461  LeuTyrTyrValAsnLeuLeuIleLeuAspHisArgPheLeuArgHisGlyGluTyr  480
              ||||||||||||||||||||||||||||||||||||||||||
Db  1378 CTCTATTATGTGAACCTGCTGATAGACCACCGTTTCCTCGCGGTGGAGAATAC  1437

Qy  481  ValLeuHisMetTrpGlnLeuSerGlyLysLysGlyGlnGlyLysSerPheAsnAlaAsp  500
              ||:::|||||||||||||||||||||||||||||||||||||
Db  1438 GTCCTCCACATGTGGCAGATATCTGGGAAGAAGGGAGAAGACCAAGGAAGCTTCAATGCTGAC  1497

Qy  501  LysLeuThrSerAlaThrAsnProLysGluAsnSerMetSerIleSerIleLeuLeuLeu  520
              ||||||||||||||||||||||||||||||||||||||||||||||
Db  1498 AAACCACGTCGCAACTAACCCAGACAAGAGAACTCAATGTCCATCTCATTCCTCTG  1557


Qy  521  AspAsnTyrCysHisProIleAlaLeuProLysHisArgProThrProAspProGluGly  540
              ||||||||||||||||||||||||||||||||||||||||||||:::
Db  1558 GACAATTACTGCCACCCGATAGCCCTGCCTCAAGCATCAGCCCACCCTGACCCCGAAGGG  1617

Qy  541  AspArgArgValArgAlaGlyMetProAsnGlnLeuArgLysGlnLeuGluAlaIleIleAla  560
              ||||||||||||||||||||||||||||||||||||||||||||||
Db  1618 GACCGGGTTCGAGCAGAGAATGCCCAACCAGCTTCGCAAGCAGTTGGAGGCGATCATAGCC  1677

Qy  561  ThrAspProLeuAsnProLeuThrAlaGluAspLysGluLeuLeuTrpHisPheArgTyr  580
              ||||||||||||||||||||||||||||||||||||||||||||||
Db  1678 ACTGATCCACTTAACCCTCTCACAGCAGAGGACAAAGAATTGCTCTGGCATTTTAGATAC  1737

Qy  581  GluSerLeuLysAspProLysAlaTyrProLysLeuPheSerSerValLysTrpGlyGln  600
              ||||||||||||||||||||||||||||||||||||||||||||||
Db  1738 GAAAGCCTTAAGGACCCCAAAAGCATATCCTAAGCTATTTAGTTCAGTGAAGTGGGGACAG  1797

Qy  601  GlnGluIleValAlaLysThrTyrGlnLeuLeuAlaLysArgGluValTrpAspGlnSer  620
              ||||||||||||||||||||||||||||||||||||||||||||||
Db  1798 CAAGAAAATTGTGGCCAAACATACCCAATTGTTGGCCAGAAGGGAAGTCTCGGATCAAAGT  1857

Qy  621  AlaLeuAspValGlyLeuThrMetGlnLeuLeuAspCysAsnPheSerAspGluAsnVal  640
              ||||||||||||||||||||||||||||||||||||||||||||||
Db  1858 GCTTTGGATGTTGGGTTAACAATGCAGCTCCTGGACTGCAACTTCTCAGATGAAAATGTA  1917

Qy  641  ArgAlaAlaLeuAlaValGlnLysLeuGluSerLeuGluAspProValLeuHisTyrLeu  660
              ||||||||||||||||||||||||||||||||||||||||||||||
Db  1918 AGAGCCGCCTTGGCTGTTCAGAAGCTTGAGAGCCTGGAGGACCCTGTTCTGCATTACCTT  1977

Qy  661  LeuGlnLeuValGlnAlaValGlnLysLeuAspPheGluGluProTyrHisAspGluProTyrHisAspGluProPheLeu  680
              ||||||||||||||||||||||||||||||||||||||||||||||
Db  1978 CTACAATTGGTCCAGGCTGTGAAATTTGAACCAACCATGATAGCGCCCTTGCCAGATTT  2037

Qy  681  LeuLeuLysArgGlyLeuValGluArgAsnLysArgIleGluGlyTyrHisPheLeuPheTrpPheLeuArg  700
              ||||||||||||||||||||||||||||||||||||||||||||::::
Db  2038 CTGCTGAAGCGTGGTTTAAGGAACAAAAGAATTGGTCACTTTTGTTTGTTTCTTGAGA  2097

Qy  701  SerGluIleAlaGlnSerArgHisTyrGlnIleArgPheAlaValIleLeuLeuAlaTyr  720
              ||||||||||||||||||||||||||||||||||||||||||||||
Db  2098 AGTGAGATAGCCCAGTCCAGACACTATCAGCAGAGGTTCGCTGTGATTCTGGAAGCCTAT  2157

Qy  721  LeuArgGlyCysGlyThrAlaMetGluHisProProPheTyrAspLeuThr  740
              ||||||||||||||||||||||||||||||||||||::::
Db  2158 CTGAGGGGCTGTGGCACAGCCATGGTGCACACTGAGCCCCACAGTAATGAGTAATCGAG  2217

Qy  741  MetLeuGlnLysValThrThrLeuAspAsnIleLysSerLeuSerLeuLysTyrAspValSer  760
              :::|||||||||||||||||||||||||||||||||
Db  2218 ATGTTACAAAAGTCACCCTTGATATTAAATCGCTTCTGTCTGAAAGTATGACGTCAGT  2277

Qy  761  SerGlnValIleSerGlnLysLeuGlnLysLeuGlnLysLeuGlnLysAsnLeuAsnLeuProPro  780
              ||||||||||||||||||||||||||||||||||||||||||||||
Db  2278 TCCCAAGTTATTTCACAACTTAAACAAAAGCTTGAAAACCTGCAGAATTCCAACTCCCC  2337

Qy  781  GlnSerPheArgValProTyrLeuTrpProGlyLeuLysGluLeuLysLys  800
              ||||||||||||||||||||||||||||||||||||||||||||||
Db  2338 GAAAGCTTTAGGGTTCCATATGGTTAAACAAAAGGGCTGGCAATTGAAAAA  2397

Qy  801  CysLysValMetAlaSerLysLysProLeuTrpLeuGluPheLysLysCysAlaAspPro  820
              ||||||||||||||||||||||||||||||||||||||||||||||
Db  2398 TGTAAAGTAATGGCCTCCAAGAAAAAACCACTATGGCTTGAGTTTAAATGTGCCGATCCT  2457

Qy  821  ThrAlaLeuSerAsnGluThrIleLysIleIlePheLysHisGlyValAspLeuArgGln  840
              ||||||||||||||||||||||||||||||||||||||||||||||
Db  2458 ACAGCCCTATCAAATGAAACAATTAAAATTATCTTTAAACATGGTGATGAATGCCGCCAA  2517

Qy  841  AspMetLeuIleLeuGlnIleLeuArgIleMetGluThrGluTrpSerLeu  860
              ||||||||||||||||||||||||||||||||||||||||||||||
Db  2518 GACATGTTAATTTTACAGATTCTACGAATCATGGAGACTGAGTGGAGTCTTTG  2577

Qy  861  AspLeuCysLeuLeuProTyrGlyTyrCysIleSerSerThrGlyMetIleGlyMetGlu  880
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Pred. No.:   0
Score: 5309.00
Percent Similarity: 93.92%
Best Local Similarity: 92.11%
Query Match: 91.69%
DB: 13

Length: 3237
Matches: 1015
Conservative: 20
Mismatches: 31
Indels: 36
Gaps: 2

US-09-974-573-1 (1-1102) x US-10-101-235A-5 (1-3237)

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Qy    1 MetGluLeuGluAsnTyrGluGlnProValValLeuArgGluAspAsnArgArgArgArg   20
          ||||||||||||||||||||||:::||||||||||||||||||||||||||||||||||
Db    1 ATGGAGCTGGAGAACTATGAACAGCCCGTGGTGCTGAGAGAGGACAACTGCCGAAGGCGC   60

Qy   21 ArgArgMetLysProArgSerThrAlaAlaSerLeuSerMetGluSerMetGluIleProIle   40
          ||||||||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db   61 CGGAGGATGAAGCCGCGCCAGT---GCTGCCAGCCTGTCCATGGAGTCCATCCCCATC  117

Qy   41 GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeuLeuHis   60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  118 GAGTTCGTGCTGCCCACCAGCCAGCGCAATACCAAGACCCCGGAAACGGCGCTGCTGCAC  177

Qy   61 ValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnIleValTrpLeuArgAlaLeuGlu   80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  178 GTGGCCGGCCACGGCAACGTGGAGCAGATGAAGGCCCAGATCGTGTGGCTGCGAGCGCTGGAG  237

Qy   81 ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTyr  100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  238 ACCAGCGTGGGCGGGACTTCTACCACCGGCTGGGACCCGATCACTTCCTCCTGCTCTAT  297

Qy  101 GlnLysGlyGlyValGlnTrpTyrGluIleTyrGlnValValValGlnThrLeuAspLeuAsp  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  298 CAGAAGAAGGGCAGTGGTGTACGAGATCTACCAGACAGTACCAGGTGGTGCGACTCTTGGAC  357

Qy  121 CysLeuArgTyrTrpLysValLeuHisArgSerProGlyGlnIleHisValValGlnArg  140
          ||||||||||||||||:::::||||||||||||||||||||||||||||||||||||||
Db  358 TGCCTGCGCTACTGGAAGGTCCTGGAAGGCCCGGGCCAGATCCACCTGGTGCAGCGCGG  417

Qy  141 HisAlaProSerGluGluThrLeuAlaPheGlnArgGlnLeuAsnAlaLeuLeuGlyTyr  160
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  418 CACCCCGCCTCCGAGGAGTCCCAAGCCTTCAGCGGCAGCCTCACGGCGCTGATTGGCTAT  477

Qy  161 AspValThrArgAspValSerAsnValHisAspAspHisHisLeuGluPheThrArgArgLeu  180
          |||:||||||||:|||||||||||||||||||||||||||||||||||||||||||||||
Db  478 GACGTCACTGACGTCAGCAACGTGCACGACGATGACCAGTGAGTTCACGCGCCGTGGCTTG  537

Qy  181 ValThrProArgMetAlaGlyValAlaGlyArgGlyArgAspProLysLeuTyrAlaMetHisPro  200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  538 GTGACCCCGCGCATGGCGGGAGTGGCCGGCCGCGGCGACCCGAAGCTCTACGCCATGCACCCG  597

Qy  201 TrpValThrSerLysProLeuProGluProLeuLeuLysLysIleThrAsnAsnCysVal  220
          |||||||||||||||||||||||||||||||||:|||||||:::||||||||||||||||
Db  598 TGGGTGACGTCCAAGCCCCTCCCGGAGTACCTGTTGAAGAAGATTGCCAACAACTGCATC  657

Qy  221 PheIleValHisArgSerThrThrSerGlnThrThrSerGlnThrIleLysValSerAlaAlaAspAspThr  240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  658 TTCATCGTGCATTCACCGCAGACCACCAGCCAGACCATTAAGGTCTCACCCGAGACACACC  717

Qy  241 ProGlyThrIleLeuGlnSerPhePheThrLeuMetAlaLeuLysLysLysSerLeuMetAsp  260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  718 CCCGGGCCCATCCTGCAGAGCTTCTTCACCAAGATGGCCAAGAAGAAATCTCTGATGGAT  777

Qy  261 IleProGluSerGlnAsnGluArgAspPheValLeuArgValCysGlyValArgAspGluTyr  280
          |||||||||:::|||||||:::||||||||||||||||||||||||||||||||||||||
Db  778 ATTCCCGAAAGCCAAAGCGAACAGGATTTTGTGCTGCGCGTGTGCGGTGTGGCGGATGAGTAC  837

Qy  281 LeuValGlyGluThrProIleLeuLysAsnPheGlnTrpValArgGlnCysLeuLysAsnGly  300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  838 CTGGTGGGCGAACGCCCCATCAAAAACTTCCAGTGGGTGAGGCAGTGCCTGAAGAACGGA  897

Qy  301 GluGluIleHisLeuValLeuAspThrProProAlaLeuAspThrProAlaLeuAspThrProLeuValArgLys  320
          |||||||||:::||||||||||||||||||||||||||||||||||||||||||||||||
Db  898 GAAGAGATTCACGTGGTACTGGACACGCCCCCAGCACCCGGCCCTAGACAAGGTGAGGAAG  957
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Db 2578 GATCCATGCCTCCTGCCCATATGGTTGCATTCAACTGGTGACAAAATAGGAATGATCGAG 2637

Qy  881 IleValLysAspAlaThrArgIleAlaLysSerIleGlnInSerThrValGlyAsnThrGly  900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2638 ATTGTGAAAGACGCCACGACAATTCCAAAATTCAGCAAAGCACAGTGGGCACACGGGA 2697

Qy  901 AlaPheLysAspGluValLeuSerHisTrpLeuLysGluLysSerProIleGluGluLys  920
          ||||||||||||||||||||||:::|||||||||||||||||||||||||||||||||||
Db 2698 GCATTTAAAGATGAAGATGAGTCCTGAATCACTGGCTCAAAGAAAAATCCCTACTGAAGAAAAG 2757

Qy  921 PheGlnInAlaAlaValGluArgPheValTyrSerCysAlaGlyTyrCysValAlaThrPhe  940
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2758 TTTCAGGCAGCAGTGGAGAGATTTGTTTATTCCTGCGCAGGCTACTGTGTGGCAACCTTT 2817

Qy  941 ValLeuGlyValIleGluIleGlyAspHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeu  960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2818 GTTCTTGGAATAGCCGACAGAACATGACAAATTATGATCACCGAGACACAGAAACCTA 2877

Qy  961 PheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleLeuAsnLys  980
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2878 TTTCATATTGACTTCGGGCACATTCTTGGGAATTACAAAAGTTTCCTGGGCATTAATAAA 2937

Qy  981 GluArgValProPheValLeuProAspPheLeuProValMetGlyThrSerGlyLysLys 1000
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2938 GAGAGAGTGCCATTTGTGCTAACCCCTGACTTCCTCCTTTGTGATGGGAACTTCTGGAAAG 2997

Qy 1001 LysThrSerLeuHisPheGlnLysAspPheGlnLysLysPheGlyProValCysLysGluValCysValLysAlaTyrLeuAlaLeu 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2998 AAGACAAGCCCACACTTCCAGAAAATTCAGGACATCTGTGTTAAGGCTTATCTGGCCCTT 3057

Qy 1021 ArgHisHisThrAsnLeuLeuIleIleLeuPheSerMetMetLeuMetThrGlyMetPro 1040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3058 CGTCATCACACAAACCTACTGATCATCCTGTTCTCCATGATGTCGATGACAGGAATGCCC 3117

Qy 1041 GlnLeuThrSerLysGluAspProIleGluLeuTyrIleArgAspAlaLeuTyrIleLysGlyTyrLysSer 1060
          ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db 3118 CAGTTAACAAGCAAAGAAGACCATTGAATATATCCGGGATGCCCTCAGTGGGGAAAAT 3177

Qy 1061 GluGluAspAlaLeuLysLysTyrPheLeuLysTyrPheLeuLysTyrTrpLysAspProGlnIleGluGlyValCysArgAspLysLysSerGlyTrp 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3178 GAGGAGGATGCTAAAAAGTATTTTTCTTGATCAGATCGAAGTTTGCAGAGACAAAGGATGG 3237

Qy 1081 ThrValGlnInPheAsnTrpPheAsnLeuHisLeuValLeuGluLeuGlyIleLysGlnGluGlyGlnLeuGlyLysLysHis 1100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3238 ACTGTGCGAGTTTTAATTGGTTTCTTACATCTTGTTCTTGGCATCAAACAAGGAGGAGAAACAT 3297

Qy 1101 SerArgAla 1102
          ||||||||
Db 3298 TCAGCC 3303
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Qy   321 GluGluTrpProLeuValAspAspCysThrGlyValThrGlyTyrHisGluGlnLeuThr 340
             |||||||||||||||||||||||||||||| ||||||||||| |||||||||||||||||
Db   958 GAAGAGTGGCCGCTGGACGACTGCACGGGAGTCACCGGCTACCATGAGCAGCTTACC 1017

Qy   341 IleHisGlyLysAspHisGluSerValPheThrValSerLeuTrpAspCysAspArgLys 360
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1018 ATCCACGGCAAGGACCACGAGAGTGTGTTCACCGTGTCCCTGTGGGACTGCGACCGAAAG 1077

Qy   361 PheArgValLysIleArgGlyIleAspIleProValLeuProValAlaAspLeuThr 380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1078 TTCAGGGTCAAGATCAGAGGCATTGATATCCCCGTCCTGCCTGGAACACCGACCTCACA 1137

Qy   381 ValPheValGluAlaAsnIleGlnTyrGlyGlnValLeuCysGlnArgArgThrSer 400
             |||||||||||| ||||||||||||  :::||||||||||||||||||||||||
Db  1138 GTTTTTGTAGAGGCAAACATCCAGTATGGGCAACAAGTCCTTTGTCCAAAGGAGAACCAGC 1197

Qy   401 ProLysProPheGluGluLeuTrpAsnValTrpLeuGluPheSerIleLysIle 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1198 CCCAAACCCTTCAGAGAGGGTCTGTGGAATGTGTGGCTTGAGTTCAGTATCAAAATC 1257

Qy   421 LysAspLeuProLysGlyAlaLeuLeuAsnLeuGlnIleTyrCysGlyLysLysAlaProAla 440
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1258 AAAGACTTGCCCAAAGGGGCTCTACTGAACCTCCAGATCTACTGCGGTAAAGCTCCAGCA 1317

Qy   441 LeuSerGlyLysThrSerAlaGluMetProSerProGluSerLysLysLysGlnLeu 460
             ||||||||||||||||||||||||||||||||||||||| :::||||||||||
Db  1318 CTGTCCAGCAAGGCCTCTGCAGAGTTCTGAGTCCAAGGGCAAAGTCGGCTT 1377

Qy   461 LeuTyrTyrValAsnLeuLeuIleLeuAspArgPheLeuLeuArgHisGlyTyr 480
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1378 CTCTATTATGTGAACCTGCTGCTGATAGACCGGTTTCTCCTCCGCCGTGGAAATAC 1437

Qy   481 ValLeuHisMetTrpGlnLeuSerGlyLysGlyGlnGlySerPheAsnAlaAsp 500
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1438 GTCCTCCCAATGTGGCAGATATCTGGCAGGGAAGGACAAGGAAGCTTCAATGCTGAC 1497

Qy   501 LysLeuThrSerAlaThrAsnProLysAspLysAsnSerMetSerIleSerLeuLeu 520
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1498 AAACTCACGTCTGCAACTAACCCAGACAGGACACTCAATGTCCATCTCCATTCTTCTG 1557

Qy   521 AspAsnTyrCysHisProIleAlaLeuProLysHisArgProThrProAspProGluGly 540
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1558 GACAATTACTGCCACCCGATAGCCCTGCCTAAGCATCGACCCACCCCTGACCCGGAGGGG 1617

Qy   541 AspArgValArgAlaGluMetProAsnGlnLysGlnLeuGlnLeuGluAlaIleIleAla 560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1618 GACCGGGTTCGAGCAGAAATGCCCAACCAGCTTCGGCTGGAGGCGATCATAGCC 1677

Qy   561 ThrAspProLeuAsnProLeuTrpThrAlaAspLysProLysGluLeuLeuLeuTrpHisSerPheArgTyr 580
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1678 ACTGATCCACTTAACCCTCTCACAGCAGAGAAACCCAAAGAATTGCTCTGCATTTTAGATAC 1737

Qy   581 GluSerLeuLysAspProLysProLysLeuPheSerSerValLysTrpProGln 600
             ||||||||||||||||||| :::||||||||||||||||||||||||||||||
Db  1738 GAAAGCCTTAAGGACCCCAAGCCCAAAACATATCCTAAGCTATTTAGTTCAGTGAAATGGGGACAG 1797

Qy   601 GlnGluIleGluValAlaLysThrTyrGlnLeuIleLeuAlaLysArgGluValTrpAspGlnSer 620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1798 CAAGAAATTGTGGCCAAAACATACCAATTGTTGGCCAAAGGGAAGTCGGGATCAAAGT 1857

Qy   621 AlaLeuAspValGlyLeuThrMetGlyMetAspLysCysAsnPheSerAspGluAsnVal 640
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1858 GCTTTGGATGTTGGGTTAACAATGGCAGCTCTGACTGCAACTTCAGATGAAAATGTA 1917

Qy   641 ArgAlaIleAlaValGlnLysGlnSerLeuGluLeuAspAspAspValHisTyrLeu 660
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1918 AGAGCCATTGCAGTTCAGAAACAGAGCCTTGAGAGACTGGAGACGATGATGTTCTGCATTACCTT 1977

Qy   661 LeuGlnLeuValGlnAlaLysValLysPheGluProTyrHisAspSerArgAlaLeuAlaArgPhe 680
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1978 CTACAATTGGTCCAGGCTGTGAAATTTGAACCATACCATGATAGCGCCCTTGCCCAGATTT 2037

Qy   681 LeuLeuLysLysArgGlyLeuArgAsnLysArgIleGlyIleHisPheLeuPheLeuArg 700
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Qy   701 SerGluIleGlnSerArgHisTyrGlnGlnArgPheAlaValIleLeuGluLeuAlaTyr 720
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2098 AGTGAGATAGCCAGTCCAGACACTCATCAGCAGAGGTTCGCTGTGATTCTGGAGCCTAT 2157

Qy   721 LeuArgGlyCysGlyThrAlaMetLeuHisAspPheThrGlnGlnValIleValAsp 740
             |||||||||||||||||||||||||||||||||||||||||||||||: :::
Db  2158 CTGAGGGGCTGTGGCAGCACAATGCTGCACGACTTTACCCAACAGTCCAAGTAATCGAG 2217

Qy   741 MetLeuGlnLysValThrLeuIleAspIleLysSerLeuLysSerAlaGluLysTyrAspValSer 760
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2218 ATGTTACAAAAAGTCACCCTGATATTAAATCGCTCTGCTGAAAAGTACGTCAGT 2277

Qy   761 SerGlnValIleSerGlnLeuLysGlnLysLeuGluGlnAsnLeuGlnAsnLeuAsnLeuPro 780
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2278 TCCCAAGTATTTCAACAACTTAAACAAAAGCTTGAAAATCTGCAGAATTCAACTCCCC 2337

Qy   781 GlnSerPheArgValProTyrAspProGlyLeuLysGlyAlaGlyAlaLeuValIleGluLeuLys 800
             :::|||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2338 GAAAGCTTAGATGTTCCATATGATCCTGGACTGAAAGGCAGGAGCGCTGGCAATTGAAAA 2397

Qy   801 CysLysValMetAlaSerLysLysProLeuTrpLeuGluPheLysCysAlaAspPro 820
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2398 TGTAAAGTAATGGCCTCCAAGAAAAAACCCACTATGGCTTGAGTTTAAATGTGCCGATCCT 2457

Qy   821 ThrAlaLeuSerAsnGluThrIleGlyIleIleLeuGluPheLysHisGlyAspArgLeuArgGln 840
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2458 ACAGCCCTATCAAATGAAACAATTGGAATTATCTTAAAACATGGTGATGATCTGCGGCCAA 2517

Qy   841 AspMetLeuLeuLeuGlnIleAsnIleLeuLeuArgIleMetGluSerIleThrGluSerLeu 860
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2518 GACATGTTATTTTTACAGATCAACATCCTACTCAGAGTCATTGGAGACTGAATTCTTTG 2577

Qy   861 AspLeuCysLeuLeuProTyrTyrGlyCysIleSerTyrThrGlyAspLysLysMetIleGlu 880
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2578 GATCTATGCTGCCTCTGCCATATGGTTGCATTTCAACTGGTGACAAAATAGGAATGATGGAG 2637

Qy   881 IleValLysAspAlaThrIleAlaLysIleGlnInSerThrValGlyAsnThrGly 900
             ||||||||||||||||||||||||||||||||: :::|||||||||||||
Db  2638 ATTGTGAAAGACGCCACGACATTGCCAAAATTCAGCAAGACACGTGGGCAACACGGGA 2697

Qy   901 AlaPheLysAspGluValLeuSerHisTrpLeuLysSerProIleGluGluLys 920
             ||||||| :::||||||||||||||||||||||||||||||||||||||||
Db  2698 GCAATTTAAAGATGAAGTCCTGAATCACTGGCTCAAAGAAAAATCCCTACTGAAGAAAAG 2757

Qy   921 PheGlnAlaAlaValGluArgPheValTyrSerCysSerAlaGlyTyrTyrCysValAlaThrPhe 940
             |||||||||||||||||||||||||||||||||||||||||||||||||
Db  2758 TTTCAGGCAGCAGTGGAGAGGTTTGTTTATTCCTGCTCAGCTGGTTGTGTGGCAACCTTT 2817

Qy   941 ValLeuGlyIleGlyAspTyrAspArgHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeu 960
             ----------------------------------------------
Db  2818 GTTCTTGGAATAGGCGAC------------ 2835

Qy   961 PheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLys 980
             --------------------------------------------
Db  2835 ----------------------------------------

Qy   981 GluArgValProPheValLeuThrProAspPheLeuPheValMetGlyThrSerGlyLys 1000
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2836 ---AGAGTGCCATTTGTGCTAACCCCTGACTTCCTCTTTGTGATGGGAACTTCTGGAAAG 2892

Qy  1001 LysThrSerLeuHisPheGlnLysValCysValAspIleAlaValTyrLeuAlaLeu 1020
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2893 AAGACAAGCCACACTTCCAGAAATTTCAGGACAATTCTGTGTTAAGGCTTATCAGCCCTT 2952

Qy  1021 ArgHisHisThrAsnLeuLeuIleLeuPheSerMetMetLeuMetThrGlyMetPro 1040
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2953 CGTCATCACACAAACCTACTGACATCATCCGTGTTCTCCATGATGCTCATGACAGGAATGCCC 3012

Qy  1041 GlnLeuThrSerLysGluAspIleGluTyrIleLeuArgAspAlaLeuThrValGlyLysSer 1060
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Db   3013  CAGTAACAAGCAAGAAGACATTGAATATATCCGGGATGCCCTTCACAGTGGGGAAAAAT  3072

Qy   1061  GluGluAspAlaLysTyrPheLeuAspGlnIleGluValCysArgAspLysGlyTrp   1080
                 |||  ||||      |  |||    |  ||  ||  |||||| ||  |
Db   3073  GAGGAGGATGCCAAAGTATTTCTTGATCAGATCGAAGTTTGCAGAGACAAAGGATGG   3132

Qy   1081  ThrValGlnPheAsnTrpPheLeuHisLeuValLeuGlyIleLysGlnGluLysHis  1100
                 ||| ||||    |||   ||||  ||| |   ||||||  |||   ||  ||
Db   3133  ACTGTGCAGTTTAATTGGTTTCTACACATCTGTTCTTGGCATCAAACAAGGAGAAACAT  3192

Qy   1101  SerAla  1102
           ||||||
Db   3193  TCAGCC  3198
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RESULT 4
US-10-101-235A-7
; Sequence 7, Application US/10101235A
; Publication No. US20030182669A1
GENERAL INFORMATION:
; APPLICANT: Rockman, Howard A.
; APPLICANT: Naga Prasad, Sathyamangla V.
; APPLICANT: Laporte, Stephane A.
; APPLICANT: Barak, Larry S.
; APPLICANT: Caron, Marc G.
; TITLE OF INVENTION: Phosphoinositide 3-Kinase Mediated Inhibition of GPCRs
; FILE REFERENCE: 033072-064
; CURRENT APPLICATION NUMBER: US/10/101,235A
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 3207
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-101-235A-7

Alignment Scores:
Pred. No.:   Length: 3207
Score: 5.34e-160   Matches: 385
Percent Similarity: 1460.50   Conservative: 206
Best Local Similarity: 51.53%   Mismatches: 394
Query Match: 33.57%   Indels: 163
                     25.22%   Gaps: 40
                     13

US-09-974-573-1 (1-1102) x US-10-101-235A-7 (1-3207)

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Qy     23  MetLysProArgSerThrAlaAlaSerLeuSerSerMetGluLeuIlePro          39
               |||      |||  ||   |||    :::  |||
Db      1  ATGCCCCAAGACCATCATCAGGTGAACGTGGGGCATCCACCTGAATGCCCCCCAAGAATC  60

Qy     40  ---IleGluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeu  58
                 :::      ||||||  ::||||          |||
Db     61  CTAGTGGGAATGTTTACTACCAAATGGAATGATAGTGACT---                   99

Qy     59  LeuHisValAlaLeuyHisGlyAsnValGluGlnMetGluValGlnMetTrpLeuArgAla  78
               :::          |:| |||   |||    ||    ::
Db    100  TTAGAATGCCTCCGTGAACGTGGGGCATCCACCTGAACATGAACATGAAAGACATTAAAGAAGCA  159

Qy     79  LeuGluThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeu  98
               :::                      ||
Db    160  AGAAAATACCCTCTC---               CATCAACTTCTTCAAGATGAATCTTCTTAC  204

Qy     99  LeuTyrGlnIleLysGlyGlnInTrpTyrGluIleTyrArgLysTyrAspInValGlnThr  118
               |||    ||    |||          ::    |||
Db    205  ATTTTCGTAAGTGTTACCCAAGAGACAGAAAAGGAGAAGATTTTTGATGAAACAAGACGA  264

Qy    119  LeuAspCysLeuArgTyrTrpLysValLeuHisArgSerProGlyGlnIleHisValVal  138
               :::          ||||          ||   :::
Db    265  CTTTGTGTGATCTTCGGCTTTTCAACCATTT---               TTAAAAGTAATT  306

Qy    139  GlnArgHisAlaProSerGluGluThrLeuAlaPheGlnArgGlnLeuAsnAlaLeuIle  158
               :::          |||||        |||
Db    307  GAACCAGTAGGCAACCGTGAAGAAAAAGATC---CTCAATCGAGAAATTGGTTTGCTATC  363
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Qy    159  GlyTyrAspValThrAspValSerAsnValHisAspAspGluGluPheThrArgArg  178
                     |||        :::          ||  ||  ||||||||
Db    364  GGCATGCCAGTGTGCGAATTGATATGTTAAGATCCTGAAGTACAGGACGTTCCGAAGA  423

Qy    179  ArgLeuValThrProArgMetAlaGluValAlaGlyAlaGlyAspAsp---          192
               :::                |||||
Db    424  AATATTCTTAATGTTGTAAAGAGACGTGGGATCTTAGGGATCTTAATTCACCTCATAGT  483

Qy    193  ProLysLeuTyrAlaMetHisProTrpValThrSerLysPro---LeuProGluTyrLeu  211
               ||||||                ||              |||
Db    484  AGAGCAATGTATGTCATCCGCCACATGTAGAATCTTCACCAGAGCTGCCAAAGCACATA  543

Qy    212  LeuLysLysIleThrAsnAsnCysValPheIleVal---          His          225
               ||    |||               :::         ||||||   :::
Db    544  TATAATAAATTGGATAGAGGCCAAATAATAGTGGTTGGGTAATAAGTTCTCCAAAT  603

Qy    226  ArgSerThrSerGlnThrThrIleLysValSerAlaAspAspThrProGlyThrIleLeu  245
               :::                |||                      |||||
Db    604  AATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTGCCAGAACAAGTAATT  663

Qy    246  GlnSerPhePheThrLysMetAlaLysLysLysSerLeuMetAspIleProGluSer---  264
               |||                ||  :::           :::
Db    664  GCTGAAGCAAATCAGGAA---AAAACTAGAAGTATGTTGCTATCATCTGAACAATTA  717

Qy    265  ---                GlnAsnGluArgAspPheValLeuArgValCysGlyArgAspGlu  279
                                   :::    :::          ||||||||
Db    718  AAACTCTGTGTTTAGATATCAGGGCAAGTACATTTTAAAGTGTGTGGATGTGATGAA  777

Qy    280  TyrLeuValGlyValGluThrProIleLeuLysAsnPheGlnTrpValArgGlnCysLeuLysAsn  299
               |||                :::||||                   |||||
Db    778  TACTTCCTAGAAAAAATATCCTCTGAGTCAGATAAGTAATAAAGAAGCTGTATAATGCTT  837

Qy    300  GlyGluGluIleHisLeuValLeuAspThrProProAspProAlaLeuAspGluValArg  319
               :::                                       :::
Db    838  GGGAGGATG---               CCCAATTTGAAGATGATGGCT  867

Qy    320  LysGlu---               GluTrpProLeuValAspAspCysThrGlyValThrGlyTyr  335
               |||                :::
Db    868  AAAGAAAGCCTTTATTCTCAACTGCCATG---GACTGTTTACAATGCCATCTTAT  921

Qy    336  HisGluGlnLeuThr---          IleHisGlyLysAspHisGluSerValPhe  350
               :::                :::
Db    922  TCCAGACAGCCATTCCCAGCTACCACCATATGAATGGAGAA---               ACATCT  969

Qy    351  ThrValSerLeuTrpAspCysAspArgLysPheArgValLys---               364
               |||                |||::
Db    970  ACAAAATCCCTTTGGGTTATAATAGAGCACTCAGAATAAAAATTCTTGTGCAACCTAC  1029

Qy    365  ---               IleArgGlyIleAspIleProValLeuProArgThrAlaAspLeuThr  380
                                   :::
Db   1030  GTGAATCTAAATATTCGAGACATTGAC---               AAG  1059

Qy    381  ValPheValGluAlaAsnIleGlnInTyrGlyValLeuGlnValLeuArgThrSer  400
               :::                ||||||
Db   1060  ATTTATGTTGGAACAGGTATCTACCATGGAGGAGAACCCTTATGTGACAATGTGAACACT  1119

Qy    401  ProLysProPheThrGluValLeuTrpAsnValTrpLeuGluProSerIleLysIle  420
               :::                |||||
Db   1120  CAAAGAGTACCTTGTTCCAATCCAGTGGAATGGCTGAATTATGATATATACATT  1179

Qy    421  LysAspLeuProLysGlyAlaLeuLeuAsnLeuGlnIleTyrCysGlyLysAlaProAla  440
               :::                ||||||
Db   1180  CCTGATCTTCCTCGTGCTGTCGACTTTGCCTTTCCATT---               TGC  1224

Qy    441  LeuSerGlyLysThrSerAlaGluMetProSerProGluSerLysLysGlyGlnLeu  460
               :::                :::
Db   1225  GTTAAAGGCCGAAAGGGTGCT---               AAAGAGGAACACTGTCCA  1263

Qy    461  LeuTyrTyrValAsnLeuLeuLeuIleAspHisArgPheLeuArgHisGlyGluTyr  480
               :::                ||||||
Db   1264  TTGGCATGGGGAAATAAACTTGTTTGATTACACAGACACTCTAGTATCTGGAAAAATG  1323
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Qy   481  ValLeuHisMetTrpGlnLeuSerGlyLysGlyGluAspGlnGlySerPheAsnAlaAsp 500
          |||||||::|||::||                                    |||||
Db  1324  GCTTTGAATCTTTGGCCAGTACCTCATGGATTAGAAGAT-----TTGCTGAACCCTATT 1377

Qy   501  LysLeuThrSerAlaThrAsnProAspLysGluAsn 512
          :::|||        |::::|::|||:::|||||
Db  1378  GGTGTTACT---GGATCAAATCCAAATAAAGAAACTCCATGTTAGAGTTGGAGTTGAC 1434

Qy   513  ------------SerMetSerIleSerIleLeuLeuAspAsnTyr 523
                      ||:::|:|:::||:::::::|
Db  1435  TGGTTCAGCAGTGTGGTAAAGTTCCCAGATATCAGTG-------ATTGAAGAGCA- 1484

Qy   524  CysHisProIleAlaLeuProLysHisArgProThrProAspProGlu-GlyAspArgVa 543
          :::|       |:::::|||                 :::|||  :::::||||
Db  1485  TGCCAATGGTCGTATCCCGAGAAGCAGAGATTAGCTATCCCACGAGGACTGAGTAA 1544

Qy   543  lArgAlaGluMetProAsnGlnLeuArg------------LysGlnLeuGluAlaIleIl 559
          |||||                         :::|||::|:||  ||:|||
Db  1545  CAGACTAGCTAGAGACATAGAATTAAGGGAGAAAATGACAAGAACACTCAAAGCAATTTC 1604

Qy   559  eAlaThrAspProLeuAsnProLeuThrAlaAspLysGluGluProGlyGluAlaGlyPheAr 579
          |||:|:|        :::||||:::|||||||||||||
Db  1605  TACACGAGATCCCTCTCTGAAATCACTGAGCGAGAAAGATTTTCTATGGAGTCACAG 1664

Qy   579  gTyrGluSerLeuLysAspProLysAlaTyrProLysPheSerSerValLysTrpGl 599
          |:::          ::::||::||||||||||||
Db  1665  ACACTATTGTGTAACTATCCCGAAATTCTACCCCAAATTGCTTCTGTCTGTTAAATGGAA 1724

Qy   599  yGlnGlnGluIleValAlaLysThrTyrGlnLeuLeuAlaTyrArgGluValTrpAspGl 619
          ||:::|:::|||:||                        |||||||||||
Db  1725  TTCTAGAGATGAACGAGCCCAGATGATTGCTTG----------GTAAAAGATTG 1769

Qy   619  nSerAlaLeuAspValGlyLeuThrMetGlnLeuLeuAspCysAsnPheSerAspGluAs 639
          |||                |||||:::||:::|:||:||
Db  1770  GCCTCCAATCAAACCTGACACAGGCTATGGAACTTCTCGACTGTAATTACCCAGATCCTAT 1829

Qy   639  nValArgAlaAlaValAlaValGlnLeuGluSer---LeuGluAspAspAspValLeuHi 658
          ||:::                 |||||||||::    :||
Db  1830  GGTTCGAGTTTTGCTGTTCGGTGCTTGGAAAAATATTTAACAGACAAACTTTCTCA 1889

Qy   658  sPheGlnLysPheGlnAspValCysValLysPheSerAlaLeuAl 678
          |||||||||||                    :||::::|
Db  1890  GTATTTAATTCAGCTAGTACAGTCCAAAAATGACCAATATTTGGATAACTTGCTTGT 1949

Qy   678  aArgPheLeuLeuLeuValArgLeuArgAsnLysArgIleGlyHisPheLeuPheTrpPh 698
          ||:::||:::|||||||||||                    |||||||||
Db  1950  GAGATTTTTACTGGAAGAAAAGCATTGACTAATCAAAGAGGATTGGGCACTTTTTCTTTTGGCA 2009

Qy   698  eLeuArgSerGluIleAlaGlnSerArgHisTyrGlnGlnArgPheAlaValIleLeuGl 718
          :::|                --CACAATAAAAACAGTTAGTTTTGCCTGCTTTTGGA
Db  2010  TTTTAAAATCTGAGATG---CACAATAAAAACAGTTAGTTTTGCCTGCTTTTGGA 2066

Qy   718  uAlaTyrLeuArgGlyCysGlyThrAlaMetLeuHisAspPheThrGlnGlnValGlnVa 738
          |||                   |||:::|
Db  2067  GTCCTATTGTCGTGCATGTGGGATGTATTGAAGCAC---CTGAATAGGCAAGTCGAGGC 2123

Qy   738  lIleAspPheMetLeuGlnLysValThrLeuAspThrIleLeuSerLeuSerAlaGluLysTyrAs 758
          :::|:::          ::||||:::|||
Db  2124  AATGAAAAGCTCATTAACTTAACT--GACATT-----CTCAAACAGCAGGAGGAGGAGGA 2174

Qy   758  pValSerSerGlnValIleSerGlnLeuLeuSerGlnLysLeuGluAsnLeuGlnAsn------ 776
          :::|        ||:::|
Db  2175  TGAAACACAAAAGTA-----CAGATGAAGTTTTTAGTTGAGCAAATGAGGCGACCAGA 2228

Qy   777  ---LeuAsnLeuProGlnSerPheArgValProTyrAspProLyrLeuLysAlaGlyAl 795
          :::::                   ::::|
Db  2229  TTTCATGGATGCCCTACAGGGCTTGGTCGTCTCCCTCAAACCCTGCTCATCAACTAGGAAA 2288

Qy   795  aLeuValIleGluLysCysGlyLysValMetAlaSerLeuLysLysProLeuTrpLeuGluPh 815
          ||:::||||::|:::|||:::         :::
Db  2289  CCTCAGGCTAAAGAGTCGAATTAATGTCTTCTGCAAAAAGGCCACTGTGGTTGAATTG 2348

Qy   815  eLysCysAlaAspProThrAlaLeuSer------------AsnGluThrIleGl 829
          :::|                     ------AACCCAGACACATCATGTCAGAGTTACTG
Db  2349  GGAG------
```

```
Qy  2349  GGAG------AACCCAGACACATCATGTCAGAGTTACTGTTCAGAACAATGAG---------- 2394
          :::|
Db   829  yIleIlePheLysHisGlyAspAspLeuArgGlnAspMetLeuIleLeuGlnIleLeuArg 849
          ||||||||||||||||
     2395  -ATCATCTTTAAAATGGGATGATTTACGGCAAGATATGCTAACACTTCAAATTATTCG 2453

Qy   849  gIleMetGluSerIleLeuTrpGluThrGluSerLeuAspLeuCysLeuLeuProTyrGlyCy 869
          ||||||||::|||             :::::  :::||:
Db  2454  TATTATGGAAAATATCTGGCAAAAATCAAGGTCTTGATCTTCGAATGTTACCTTATGGTTG 2513

Qy   869  sIleSerThrGlyAspLysLeuGlyMetIleGluValLysAspAlaThrThrIleAl 889
          |:::|||:||||||                   :::|||||
Db  2514  TCTGTCAATCCGTGACGTGTGTGGACTTATTGAGGTGGTCGAAATTCTCACACTATTAT 2573

Qy   889  aLysIleGlnIleSerThrValGlyAsnThrGlyAla-----PheLysAspGluValLe 907
          ||:::||||               :::||        |||
Db  2574  GCAAATT--CAGTGCAAAGGCGGTTGAAAGGTGCACTGCAGTCCACAGCCACACACT 2630

Qy   907  uSerHisTrpLeuLysGlyCysProIleGluGluLysGlnAlaAlaValGluAr 927
          ||||||||:::||||:::           :::
Db  2631  ACATCAGTGGTCAAAGACAAGAACAAA--GGAGAAATATGATGCAGCCATTGACCT 2687

Qy   927  gPheValTyrSerCysAlaGlyTyrCysValAlaThrPheValLeuGlyIleGlyAspAr 947
          |||||||:::           :::
Db  2688  GTTTACACGTTCATGTGCTGGATACTGTGTAGCTACCTTCATTTGGAATTGGAGATCG 2747

Qy   947  gHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeuPheHisIleAspPheGlyHi 967
          |||||||:::          :::
Db  2748  TCACAATAGTAACATCATGATTAGTGAAAGACAGATGGACAACTGTTTCATATAGATTTTGGACA 2807

Qy   967  sIleLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLysGluArgValProPheValLe 987
          |:::|                    :::
Db  2808  CTTTTTGGATCACAAGAAGAAAAAATTGGTTATAAACGAGAACCGTGTGCCATTGTTTT 2867

Qy   987  uThrProAspPheLeuPheValMetGlyThrSerGlyLysLys-----ThrSerLeuHi 1005
          |||                 :::
Db  2868  GACAACAGATTTCTTAATAGTGATTAGTAGAAGGAGCCCAGAATGCCAAAGACAAGAGA 2927

Qy  1005  sPheGlnLysPheGlnAsnValCysValLysAlaTyrLeuAlaLeuArgHisHisThrAs 1025
          ||||||||||               :::
Db  2928  ATTTGAGAGGTTCCAGGAGAGTGTGTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAA 2987

Qy  1025  nLeuLeuIleLeuLeuPheSerMetMetLeuMetThrGlyMetProGlnLeuThrSerLy 1045
          :::||||||              :::
Db  2988  TCTCTTCCATAAATCTTTCTCAATGATGCTTGGCCTGGAATGCCAGAACTACAATCTTT 3047

Qy  1045  sGluAspIleLeuTyrIleArgAspAlaLeuThrValGlyLysSerGluGluAspAlaLy 1065
          :::                  :::
Db  3048  TGATGACAATTGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTT 3107

Qy  1065  sLysTyrPheLeuAspGlnIleLeuValCysArgAspLysLysGlyTrpValGlnPheAs 1085
          :::                  :::
Db  3108  GGAGTATTTCATGAAACAAACAAATGAAGTCGAGCTCGAGGC 3167

Qy  1085  nTrpPheLeuHisLeuVal 1091
          :::||
Db  3168  TTGGATCTTCACACAATT 3186
```

RESULT 5
US-10-440-464-145
; Sequence 145, Application US/10440464
; Publication No. US20040018528A1
GENERAL INFORMATION:
; APPLICANT: DEPRIMO, SAMUEL
; APPLICANT: O'FARRELL, ANNE-MARIE
; APPLICANT: MORIMOTO, ALYSSA
; APPLICANT: SMOLICH, BEVERLY
; APPLICANT: MANNING, WILLIAM
; APPLICANT: WALTER, SARAH
; APPLICANT: CHERRINGTON, JULIE
; APPLICANT: SCHILLING, JIM
; TITLE OF INVENTION: NOVEL BIOMARKERS OF TYROSINE KINASE INHIBITOR EXPOSURE

```
;  TITLE OF INVENTION:  AND ACTIVITY IN MAMMALS
;  FILE REFERENCE: 038602/1592
;  CURRENT APPLICATION NUMBER: US/10/440,464
;  CURRENT FILING DATE:  2003-05-19
;  PRIOR APPLICATION NUMBER: 60/380,872
;  PRIOR FILING DATE:  2002-05-17
;  PRIOR APPLICATION NUMBER: 60/448,922
;  PRIOR FILING DATE:  2003-02-24
;  PRIOR APPLICATION NUMBER: 60/448,874
;  PRIOR FILING DATE:  2003-02-24
;  NUMBER OF SEQ ID NOS: 185
;  SEQ ID NO 145
;   LENGTH: 3213
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-440-464-145

Alignment Scores:
Pred. No.:               1.52e-147      Length:         3213
Score:                   1354.50        Matches:        361
Percent Similarity:      49.60%         Conservative:   202
Best Local Similarity:   31.81%         Mismatches:     407
Query Match:             23.39%         Indels:         165
DB:                      12             Gaps:           37

US-09-974-573-1 (1-1102) x US-10-440-464-145  (1-3213)
```

Qy   30 AlaSerLeuSerMetGluLeuIleProIleGluPheValLeuProThrSerGlnArg 49
              :::::::||| :::::|||:::|||::|||||:::|||||||
Db   64 TCACGATAGCATCTGATGGCTCCATACCTGTGGATTTCCTTTGCCCACTGG------ 117

Qy   50 AsnThrLysThrProGluThrAlaAlaLeuHisValAlaGlyHisValAlaGlyGln 69
              || :::|||| ::::||||||||:::|||||
Db   118 -------------ATTTATATCCAGTTGGAGGTACCTCGGGAAGCTACCATTTCTTAT 162

Qy   70 MetLysAlaGlnValTrpLeuArgAlaLeuGluThrSerValSerAlaAspPheTyrHis 89
              ::   :::|||
Db   163 ATTAAGCAGAGATGTTATGGGAAGCCAAGTTCACAATTACCCAATG-------------- 204

Qy   90 ArgLeuGlyProAspHisPheLeuLeuLeuTyrGlnLysLysGlyGlnInTrpTyrGluIle 109
              |||||| :::||| ||||||:::
Db   205 ------------------TTCAACCTCCTTATGATATTGACTCCTATATGTTGCATGT 246

Qy   110 TyrAspLysTyrGlnValValGlnInThrLeuAsp--------------------Cys----- 121
              :::::||| ||| |||:::
Db   247 GTGAATCAGACTGCTGTATGAGGAGCTTGAAGACGAAACACGAAGAGCTCTGTGATGTC 306

Qy   122 -------------LeuArgTyrTrpLysValLeuHisArgSer------ProGlyGlnIleHis 136
              ||||||::: |||||
Db   307 AGACCTTTTCTTCCAGTTCTCAAATTAGTGACAAGAAGTGTGACCCAGGGGAA------ 360

Qy   137 ValValGlnInArgHisAlaProSerGluGluThrLeuAlaPheGlnLeuArgGlnLeuAsnAla 156
                                          :::::
Db   361 --AAATTAGACTCAAAAATTGGAGTC 384

Qy   157 LeuIleGlyTyrAspValThrAspValSerArgAsnValHisAspAspGluLeu---GluPhe 175
              :::::::||| :::::||| |||:::
Db   385 CTTTATAGGGAAAAGGTCTGCATGAAAGTTCCTGAAGGATCCTGAAGTAAATGAATTT 444

Qy   176 ThrArg-------ArgArgLeuValThrProArgMetAlaGluValAlaGlyValArgAsp--- 192
              ||| |||||| |||:::
Db   445 CGAAGAAAAATGCGCAAATTCAGCGAGAAAAAATCCTGTCACTTGTGGGATTGTCTTGG 504

Qy   193 ---ProLysLeuTyrAlaMetHisProValThrSerLysProGluTyrLeu 211
              :::::|||
Db   505 ATGGACTGCTAAAACAAACATATCCACCAGAGCCATCCATCCCTGAAAACTTA 564

Qy   212 LeuLysLysIleThrAsnAsnCysValPheIleValIleHisArgSerThrSerGln 231
              ::: |||||||:::
Db   565 GAAGATAAACTTTATGGGGAAAGCCTCATCGTAGCTGTTCATTTGAAAACTGCCAGGAC 624

Qy   232 -----ThrIleLysValSerAlaAspAspThrProGlyThrIleLeuGlnSerPhePhe 249
              :::||:::
```

Db   625 GTGTTTAGTTTCAAGTGTCTCCTAATATGAATCCTATCAAAGTAAATGAA--------- 675
              ::: |||||

Qy   250 ThrLysMetAlaLysLysLysSerLeuMetAspIleProGluSerGlnAsnGluArgAsp 269
              ||||| :::||
Db   676 TTGGCAATCCAAAACGTTGACTATTCATGGGAAGGAAGATGAAGTTAGCCCCTATGAT 735

Qy   270 PheValLeuArgValCysGlyArgAspGlyTyrLeuValGlyValGlyThrProIleLeuLysAsn 289
              :::::||:::||| :::|||:::
Db   736 TATGTGTTGCAAGTCAGCGGCGGAGTAGAATATGTTTTTGGGATCATCCACTAATTCAG 795

Qy   290 PheGlnInTrpValArgGlnInCysLeuLysAsnGlyLysGluGluIleHisLeuValLeuAspThr 309
              |||||| :::|||::::
Db   796 TTCCAGTATATCCGGAACTGTGTGATGAACAGAGCCCTGCCCCATTTTATACTT------ 849

Qy   310 ProProAspProLeuAspProValArgLysGluGluTrpProLeuValAspAspCys 329
              :::::
Db   850 ---GTGGAATGC 858

Qy   330 ThrGlyValThrGlyTyrHisGluGln------LeuThrIleHisGlyLysLysAspHisGlu 347
              :::||| ||||||
Db   859 TGCAAGATCAAGAAAATGTATGAACAAGAAAATGATTGCCATAGAGGCTGCCATAAATCGA 918

Qy   348 SerValPheThrValSerLeu-------------------------------- 354
              :::
Db   919 AATTCATCTAATCTTCCTTCTCCATTACCACCACAAAGAAAACACGAATTATTCTCATGTT 978

Qy   355 TrpAspCysAspArgLysPheArg---ValLysIleArgGlyIleAspIleProValLeu 373
              |||||| :::   :::   :::::
Db   979 TGGGAAAATAACAACCCTTCCAAATGTCTTGGTTAAGGGA-----------AATAAACTT 1029

Qy   374 ProArgThrAlaAspLeuThrValPheValGluAlaAsnIleGlnTyrGlyValGlnInVal 393
              :::::|||
Db 1030 AACACAGAGGAGAACTGTAAAAGTTCATGTCAGGGTCGTCTTTTCATGGTACTGAGCTC 1089

Qy   394 LeuCysGlnArgArgAspThrSerProLys---ProPheThrGluValValTrpAsnVal 412
              |||||| :::   :::
Db 1090 CTGTGTAAAACCATCGTAAGCTCAGGAGGTATCAGGGAAAAATGATCATATTGGAATGAA 1149

Qy   413 TrpLeuGluPheSerIleLysIleLeuAspLeuProLysGlyAlaLeuAsnLeuGln 432
              :::::|| :::::
Db 1150 CCACTGGAATTTGATATTAATATTTGACTTACCAAGAATGGCTCGATTATGTTTTTGCT 1209

Qy   433 IleTyrCysGlyLysGlyAlaProAlaLeuSerGlyLysThrSerAlaGluMetProSerPro 452
              :::::||| :::::
Db 1210 GTTTAT---GCAGTTTGGATAAAGTAAAAACGAAGAAATCAACGAAAACTATTAATCCC 1266

Qy   453 --------GluSerGlyLysAlaGlnInLeuLeuTyrTyr--------------ValAsn 465
              :::::
Db 1267 TCTAAAATATCAGAACCATCAGGAAAGTGGAAAAAGTGCATTATCCGTAGCGTGGGTAAAT 1326

Qy   466 LeuLeuLeuIleAspHisArgPheLeuLeuArgHisGlyGluTyrValLeuHisMetTrp 485
              |||||| ::::::
Db 1327 ACGATGGTTTTGACTTTAAAGACAATTGGAGACATAATATTACACAGCTGG 1386

Qy   486 GlnLeuSerGlyLysGlyGluAspGlnGlySerPheAsnAlaAspLysLeu----- 502
              :::::||| |||||
Db 1387 --------------TCTTCATTT----CCTGATGAACTCGAAGAAAATG 1416

Qy   503 --------ThrSerAlaThrAsnProAspLysGluAsnSerMetSerSer 517
              :::::|||
Db 1417 TTGAATCCAATGGAACTGTTCAAACAAATCCATAATACTGAAAATGCAACAGCTTTGCAT 1476

Qy   518 IleLeuLeu---AspAsnTyrCysHisProIleAlaLeuPro----- 530
              :::   :::
Db 1477 GTTAAATTTCCAGAGAATAAAAAACAACCTTATTATTACCCTCCCTTCGATAAGATTATT 1536

Qy   531 ---LysHisArgProThrProAspProGluGlyAspArgValArgAlaGluMetProAsn 549
              :::::||| :::
Db 1537 GAAAAGCAGCTGAGTTGCAAGCAGTAGTGTCAAGTCGAGTCGAGGTGGAAAA 1596

Qy   550 GlnLeuArgLysGlnInLeuGluAlaIleIleAlaThrAspProLeuAsnProLeuThrAla 569
              ::: ||||||:::::
Db 1569

```
Qy    917 IleGluGluLysPheGlnAlaAlaAlaValGluArgPheValTyrSerCysAlaGlyTyrCys  936
          :::|:::  ||||||||||||||| :::||||||   :|||| |||| ||
Db   2671 GGGGATGAC---CTGGACCGAGCCATGAGGAATTACACGTGCTCGTGCTGGCTACTGT 2727

Qy    937 ValAlaThrPheValLeuGlyIleGlyAspArgHisAsnAspAsnIleMetIleSerGlu  956
          ||||||||| ||  ::||||||||||||||||||| ::::|||||:::  :: ::
Db   2728 GTAGCTCTTATGTCCTTGGGATTGGTGACAGACATAGTGACAACATCATGGTCAAAAAA 2787

Qy    957 ThrGlyAsnLeuPheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeu  976
          |||||||| |||| :|||||||||||||||||||||||:::|||||||||||:||||||
Db   2788 ACTGGACCAGCTCCTTCCACATTGACTTTGGACATATTCTTGGAAATTCAAATCTAAGTTT 2847

Qy    977 GlyIleAlaAsnLysGluArgValProPheLeuThrProAspPheLeuProMetValMetGly  996
          :::||||||||   |||||||||||| |||||||||||:::|||||| ||||
Db   2848 GGCATTAAAAGGGAGGTGCCTTTTATTCTTACCTATGATTTCATCCATGTCATTCAA 2907

Qy    997 ThrSerGlyLysThrSerLeuHisPheGlnLysPheValCysValValLysAla 1016
          ||||||||||||||||||| ||||||||:::|||||:::|||||||:|||
Db   2908 CAAGGAAAAACAGGAAATACAGAAAAGTTGGCCGGTTCCGCCAGTGTGTGAGGATGCA 2967

Qy   1017 TyrLeuAlaLeuArgHisHisThrAsnLeuLeuIleLeuPheSerMetMetLeuMet 1036
          :::||:::||||||||| ||||||||:::::||||||:::|:::||||
Db   2968 TATCTGATTTTACGACGGCATGGGAATCCTTCATCAACTCTTGCGCTGATGTTGACT 3027

Qy   1037 ThrGlyMetProGlnLeuThrSerLysGlnAspIleTyrIleArgAspAlaLeuThr 1056
          |||||||:::|||||||||||||||:::|:::||||||||:::||||||
Db   3028 GCAGGGCGTTCCTGAACTCACATCAGTCAAAGATATACAGTATCTTAAGGACTCCTTGCA 3087

Qy   1057 ValGlyLysSerGluGluAspAlaLysLysLysTyrPheLeuAspGlnIleGluValCysArg 1076
          :::|||||||||:::  ||||||||||||||||||||:::
Db   3088 TTAGGGAAGAGTGAAGAAGAAGCACTCAAACAGTTTGAAGCAAAAATTTGATGAGGCGCTC 3147

Qy   1077 AspLysGlyTrpThrValGlnPheAsnTrpPheLeuHisLeuVal 1091
          |||||||
Db   3148 AGGGAAAGCTGGACTACTAAAGTGAACTGGATGGCCCACACAGTT 3192
```

RESULT 6
US-10-337-192-1
; Sequence 1, Application US/10337192
; Publication No. US20030195211A1
; GENERAL INFORMATION:
;   APPLICANT: SADHU, Chanchal et al.
;   TITLE OF INVENTION: INHIBITORS OF HUMAN PHOSPHATIDYLINOSITOL 3-KINASE DELTA
;   FILE REFERENCE: 27866/39033
;   CURRENT APPLICATION NUMBER: US/10/337,192
;   CURRENT FILING DATE: 2003-01-06
;   PRIOR APPLICATION NUMBER: 60/199,655
;   PRIOR APPLICATION FILING DATE: 2000-04-25
;   PRIOR APPLICATION NUMBER: 60/238,057
;   PRIOR FILING DATE: 2000-10-25
;   NUMBER OF SEQ ID NOS: 6
;   SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 5220
;   TYPE: DNA
;   ORGANISM: Human p110delta complete cDNA
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (196)..(3327)
US-10-337-192-1

Alignment Scores:
Pred. No.:   Length: 5220
Score: 6.05e-147   Matches: 365
Percent Similarity: 1352.50   Conservative: 200
Best Local Similarity: 49.87%   Mismatches: 415
Query Match: 32.22%   Indels: 153
DB: 23.36%   Gaps: 40
                      13

US-09-974-573-1 (1-1102) x US-10-337-192-1 (1-5220)

```
Qy     20 ArgArgArgMetLysProArgSerThrAlaAla----------SerLeuSerSerMet  35
          ||||||||||||||||||||||||||| |||||||
Db   2611 GCTCGTCGCAGCAGCCTTCAACAAAGATGCCCTTCGAACTGGCTAAAGAAATACAACTCT 2670
```

```
Db   1597 AAGTTTCCTCGTATTGAAAGAAATCTTGGACAGGGATCCCTTGTCTCAACTGTGTGAA 1656

Qy    570 GluAspLysGluLeuTrpHisHisPheArgTyrGluSerLeuLys---AspProLysAla  588
          :::|||||:::|||  |||||||:: ||::|||||||:::::  :::|||:::||
Db   1657 AATGAAAATGGATCTTATTTGACTTGCCACAAGACGTGCCGAGAGATTTTCCCACAATCA 1716

Qy    589 TyrProLysPheSerSerValLysTrpGlyGlnGlnGluValLeuAlaLysThrThr  608
          |||||||   ||||||||||:::|| ::|||  |:::::||
Db   1717 CTGCCAAAATTACTGCTGTCAATCAGTGAATAAACTTGAGGATGTTGCT------ 1767

Qy    609 GlnLeuLeuAlaLysArgGluValTrpAspGlnSerAlaLeuAspValGlyLeuThrMet  628
          |||||||:: ||||||  :::  ||
Db   1768 CAGCTTCAGGCGCTGCTCAGATTGGCCTAAA------CTGCCCCCCGGGAGGCCCTA 1821

Qy    629 GlnLeuLeuAspCysAsnPheSerAspGluSerArgAlaLeuAlaValAlaGlnLysLysLeu  648
          :::|||||||:::||||||||||:: |||||| |||  :::|:::  ::||||||
Db   1822 GAGCTTCTGGATTTCAACTATCCAGACCAGTACGTTGAGAATATGCTGTAGGCTGCCTG 1881

Qy    649 GluSerLeuGluAspAspAspValHisLeuHisTyrLeuLeuValGlnLnLeuAlaValLys  668
          ::: |||||||::::|||||||||||| |::||||||||||| :::||
Db   1882 CGACAGAGTGATGAAGAACTTTCTCAATATCTTTACAACTGGTGCAAGTGTTAAAA 1941

Qy    669 PheGluProTyrHisAspSerArgAlaLeuAlaArgPheLeuLeuLysArgGlyLeuArgAsn  688
          ||||| ||||||  :::|:::|||||||::: |::||||||
Db   1942 TATGAGCCTTTCTTTGATTGCGCCCCTCCATTAGAAAAGACCACTTGGTAAT 2001

Qy    689 LysArgIleIleGlyHisLeuProPhePheLeuArgSerGluIleAlaGlnSerArgHis  708
          |:::::|||||||| ::|||| ::||||||||||
Db   2002 CGGAGGATAGGGCAGTTTCTATTTTGGCATCTAAGTCAGAAGTG--------CAC 2049

Qy    709 --------TyrGlnArgPheAlaValIleLeuLeuLysAlaTyrLeuArgLeuGlyCysGly  725
                  :::|||  ||||||||||||::::::|||||||  :::
Db   2050 ATTCCTGCTGTCTCAGTACAATTTGGTGTCATCCTGAAGCATACTGCCGGGGA--AGT 2106

Qy    726 ThrAlaMetLeuHisAspPheThrGlnGlnValGlnIleAspMetLeuGlnLysVal  745
          :::  |||||||| ||||| :::|:::::||
Db   2107 GTGGGGCCACATGAAAGTGCTTCTCAAGCAGGTTGAAGCACTCAATAAGTTAAAAACTTTA 2166

Qy    746 Thr-------IleAspIleLysSerLeuSerAlaGluLysTyrAspValSerSerGlnVal  763
          :::                :::  :::|||| ::|
Db   2167 AATAGTTTAATCAAACTGATGCCTGAAGTGAAGTAAACAGAGCCAGAGGAAGAGCAGGCCATG 2226

Qy    764 IleSerGlnLeuLysGlnLys----------LeuGluAsnLeuGlnAsnLeuAsn  778
          :::::: |||||||                 |||||||||||:::|||
Db   2227 CATACCTGTTTAAAACAGAGTGCTTACCGGGAGCCCTTCTGACCTGCAGTCA------ 2280

Qy    779 LeuProGlnSerPheArgValTyrAspProGlyLeuLysAlaGlyAlaLeuValIle  798
          ||||||||||| :::  |||||||||:::
Db   2281 --------CCCTGACCCATGTGTATCCTCCAGAACTCTATGTT 2319

Qy    799 GluLysCysLysValMetAlaSerLysLysLysProLeuTrpLeuGluPheLysCysAla  818
          |||||||||  |||  |||:::||||||:: :::
Db   2320 GAAAAGTGCAAATACAATGGATTCCAAAATGAAGCCTTTGTGGCTGTATAC------ 2370

Qy    819 AspProThrAlaLeuSerAsnGluThrIleGlyIleIlePheLysHisGlyAspAspLeu  838
          :::  |||||||  ||::|||||||:: |||||||
Db   2371 AATAACAAAGGTATTGGTGAGATTCAGTGAGTGATTTTTAAAAATGTGATGATTTA 2430

Qy    839 ArgGlnAspMetLeuLeuGlnIleLeuGluArgIleMetGluSerIleTrpGluThrGlu  858
          ||||||||||||| |||||||||:::  :::  :::|||:::
Db   2431 CGACAGGATATGTTGACACTCAAATGTTGCGCTTGATTTACTCTGGAAAGAAGCT 2490

Qy    859 SerLeuAspCysLeuLeuLeuProTyrGlyCysIleSerThrGlyAspLysIleGlyMet  878
          ||||||  :::|||| ||| :::||:::|||||:::|||:::||||
Db   2491 GGTTTGGATCTTCGGAGTGCCTTATGGCTGTTTAGCAACAGGAGATCGCTCTGGCCCTC 2550

Qy    879 IleGluIleValLysAspAlaThrThrIleAlaLysIleGln-----GlnSerThrVal  896
          ||||||||||||| ||||||:::  |||  :::::|||
Db   2551 ATTGAAGTTGTGAGCGATGCCACCTCTGAAACAATTGCTGACAATTCAGCTGAACAGTAGCAAATGTG 2610

Qy    897 GlyAsnThrGlyAlaPheLysAspGluValLeuSerHisTrpLeuLysGluLysCysPro  916
          :::  ||| |||||||::: |:: :::||||||
Db   2611 GCTCGTCGCAGCAGCCTTCAACAAAGATGCCCTTCGAACTGGCTAAAGAAATACAACTCT 2670
```

```
Db   1123 AAGCTTCCTCT--------GTGTCCCTGTGTCCCTGGAGCAGCCGTTCCGCATGAG 1173
          :::|||||||||            |||
Qy    187 CAACCAGGATGCCCCTGGGGTGACCCTGGGGTGACCCCATGGAATTCTGACCAAGGAGGAGAAT 246

Qy    365 ---IleArgGlyIleAspIlePheProValLeuProArgThrAlaAspLeuThrProGlu 383
          ::|                  ||       |||
Db   1174 CTCATCCAGGGCAGCAAAGTGAACGCCGACAGACGG--------ATGAAGTGGTGGTG 1224

Qy     36 GluLeuIleProIleGluPheLeuLeuProThrSerGlnArgArgAsnThrLysThrProGlu 55
          ::|      |||||       ||||         
Db    247 CAGAGCGGTTGGGTTGGTTGACTTCCTGCTGCCCACAGGG--- 282

Db   1225 CAGGCCGGGCTTTTCCACGCCAACGAGATGCTGTCCAAGACGGTGTCCAGCTGGGAGGTG 1284
          ::|||||            |||||||
Qy     56 ThrAlaLeuLeuHis------ValAlaGlyHisGlyAsnValGluGlnMetLysAlaGln 73

Qy     74 ValTrpLeuArgAlaLeuGluThrSerValSerAlaAspPheTyrHisArgLeu---Gly 92
          :::|||||            :::
Db    283 --GTCTACCTGAACTTCCCTGTCCCGCAATGCCAACCTCAGCACCATCAAGCAGCTG 339

Db   1285 AGGGTGGTCCGGAGCCCGTGGTGGAAGCAGCGGCTGGAGTTCGACATCAACATCTGCGAC 1344
          ::|||      |||       |||
Qy     74 CTGTGGCACCGGCGCCAGTATGAGCCGCTC------TTCCACATGCTCCAGTGC 387

Qy     93 ProAspHisPheLeuLeu--LeuTyrGlnLysLysGlyGlnTrpTyrGlnIleTyrAsp 111
          ::|||||           |||||
Db   1345 CTGCCCCCATGGCCCGTCCTGCTTCGTTTGCGTGTACGCC---GTGATGGAG 1392

Qy    112 LysTyrGlnValValGlnThrLeuAspCysLeuArgTyrTrpLysValLeuHisArgSer 131
          :::|                :::|||
Db    388 CCCGAGGGCCTATGTGTTCACCTGACCAGGGAGCAGCAGAGCTGGAGGAC 447

Db   1393 AAAGCCAAGAAGCTCGCTCCACCAAGAGAGTCCAAGAAGCGGACTGCCCCATTGCC 1452
          :::|||      |||||
Qy    112 GAGCAACGG------CGTCTGTGTGACGTGCAGCCCTTCCTGCCCGTCCTG--- 492

Db   1453 TGGGCCACCTCATGCTGTTTGACTACAAGGACCAGCTTAAGACCGTGAACCGCTGCCTC 1512
          ::|||            |||||||
Qy    132 ProGlyGlnIleHisValValGlnArgHisAlaProSerGluGlyThrLeuAlaPheGln 151

Qy    132 ---------CGCCTGGTGGCCCGTGAGGGCGACCGCGGCTGAGGAGGTC---ATCAAC 537
          :::||               ||||
Db    493 HisMetTrpGlnLeuSerGlyGlyAspGlnGlySerPheAsnAlaAspLysLeu 502

Db   1513 TACATGTG--------CCCTCCGTCCCAGATGAAGGGCGAGCCTGCTGAACCCACGGGC 1566
          ::||||||
Qy    152 ArgGlnLeuAsnAlaLeuIleGlyTyrArgAspValThrArgValSerAsnValHisAspAsp 171

Qy    152 TCACAGATCACAGCCCTCTCATCGGCAAAGGCCTCCACGAGTTTGACTCCTTGTCGCACCCA 597
          :::|||||||            |||
Db    538 ThrSerAlaThrAsnProAspLysGluAsnSerMetSerIleSerIleLeuLeuAspAsn 522

Db   1567 ACTGTGTGGCAGTAACCCAACACGGATAGCGCCCGCTGCCCTGCTCTCTGCCTGCCCGAG 1626
          ::|||      |||||
Qy    172 GluLeuGluPheThrArgArgMetAlaGluValThrProArgGlyLysAlaGlyArg 191

Qy    172 GAAGTGAACGACTTTCGCGCCAAGATGTG------CAATTCTGCAGGAGGGCGGGCGCC 651
          |||||||            |||
Db    598 LysHis 532

Db   1627 GTGCCCCCCGTGTACTACCCCGGCTGGAGAGATCTTGGGGGGGACCAC 1686
          :::|||            |||
Qy    192 AspProLysGluTyrAlaMetHisProValTrpThr---SerLysProLeu--- 207

Qy    192 CGCGGCCAGCTGGGCTGGGAGGCCGTGGCTGCGAGTACCAGTTTCCCCTGCGAGCTGGAG 652
          :::|||
Db    533 ArgProThrProAspProGluGlyAspGlyAspArgValArgAlaGluMetProAsnGlnLeuArg 552

Db   1687 --------------------AGCGAGTGTGTGCATGTCACCGAGGAGGAGCAGAGCTG--- 1722
          :::
Qy    208 --------------ProGluTyrLeuLeuLysLysIleLeuThrAsnAsnCysVal 220

Qy    208 CCCTGCGCTCAAACCTGGGGGTCTGGTACCCTG-----CGGCTCCCGGACCGGGGCCCTT 765
          |||      |||||
Db    712 LysGlnLeuGluAlaIleLeuIleAlaThrAspProLeuAsnProLeuThrAlaGluAspLys 572

Db   1723 ---CAGTTGCGGGAAATCCTGGAGCGGCGGGCATGGAAGTTCAGGAGCACGAGAAG 1779
          :::|||||||
Qy    221 PheIleValIle-----HisArgSerThrSerGlnThrArgIleLysValSerValAlaAsp 238

Qy    221 CTGGTCAACGTTAAGTTGAGGGCAGCGAGGAGAGCTTCACCTGTGTCCACCAAG 825
          :::|||
Db    573 GlyLeuLeuTrpHisTyrPheGluTyrGluSerLeuLysAsp---ProLysAlaTyrProLys 591

Db   1780 GACCTGGTGTGGAAGTGCGGCGATGAAGTCCAGGAGCACTTCCCGAGGGCCTAGCCGG 1839
          ::||||||            |||
Qy    239 AspThrProGlyThrIleLeuGluIleSerPhePheThrLysMetAlaLys----LysLys 256

Qy    239 GACGTGGAGCTGGGCCTGGTCGGCTGATGGGCCTGTGCCCTGCGGAGAAGGCCACAGTGTTCCGGCAG 885
          ||||||||||      |||||
Db    826 LeuPheSerSerValLysTrpThrHisAspAlaArgTrpTyrGlnLeuLeu 611

Db   1840 CTGCTGCTGGTCACCAGTGGAACAAGCATGAGGATGTGGCCCAGATGCTCTACCTGCTG 1899
          :::|||      |||||
Qy    257 SerLeuMetAspIleProGluSerGlnAsnGluArgGlnPheValLeuArgValCysGly 276

Qy    257 CCGCTGGCTGGAGCAGCCGGAA------GACTACACGGTGCAGGTGAACCAG 930
          :::|||
Db    612 AlaLysArgGluValGlyValTrpAspArgGlnSerAlaLeuAsnAspAlaValGlyLeuThrMetGlnLeuLeu 631

Db   1900 TGCTCC--------CTGCCCGGAG--------CTGCCCGTCCTGGAGCCTGAGCTGCTA 1944
          ::::
Qy    277 ArgAspGluTyrLeuValGlyLeuThrProIleLysProValArgGlnCys 296

Qy    277 AGGGATGAGTACCTGTATGGCAACTACCCGTCTCGACTGCAGCTCTGCAGCTGC 931
          :::|||      |||
Db    632 AspCysAsnPheSerAspGluAlaAsnValArgAlaIleLysLysLeuGluSerLeu 651

Db   1945 GACTTCAGCTTCCCCGATTGCCACGTAGGCTCCTTCCTGCTCAAGTCGCTGCGGAAACTG 2004
          ||||||||
Qy    297 LeuLysAsnGlyGluGlnIleHisLeuValLeu-----------ProGlutyrLeuLeu 307

Qy    297 CTGCACAGTGGGTTGACCCCTCACCTGACCATGGTCCATTCCTCCTCATCCTCCATCCTGCCCATG 1050
          :::|||||||
Db    652 GluAspAspCysAspValLeuAsnLeuAlaValLysPheGluPro 671

Db   2005 ACGGACCATGAGCTGTTCCAGTAGCTGTTCCAGTGGTGCTCAAGTACGAGTCC 2064
          :::|||
Qy    308 --------AspThrProGlyProAspProAlaLeuAspLysLysGluLysTrpProPro 324

Qy    308 CGGGATGAGCAGAGCAACCCTGCCCCCCAGGTCCAGGAAACCGCGTGCCAAACCACCTCC 1110
          :::|||||
Db    672 TyrHisAspSerAlaLeuAlaArgPheLeuLysLeuValArgGlyLeuArgAsnLysArgIle 691

Db   2065 TACCTGGACTGCGAGCTGACCAAATTCGTGCTGCACCGGACCGGGCCCTGCCAACCGCAAGATC 2124
          :::||||||
Qy    325 LeuValAspAspCysThrGlyValThrGlyTyrHisGluGlnLeuThrIleHisGlyLys 344

Qy    325 ATTCCTGCCCAAG 1122
          :::|||
Db    691 GlyHisGluLeuTrpPheTyrArgSerArgGluIleAlaGlnSerArgHisTyrGlnGln 711

Db   2125 GGCCACTTCCTTTTCTGCACCTCCGCTCCCGAGATG--------CACGTGCCGTCG 2172
          ::::::
Qy    345 AspHisGluSerValPheThrValSerLeuTrpAspCysAspArgLysPheArgValLys 364
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Qy 1059 LysSerGluGluAspAlaLysTyrPheLeuAspGlnIleGluValCysArgAspLys 1078
              ::: ||||||||:||:|||| :||||
Db 3211 AAAACAGAGGAGGAGGCACTGAAGCACTTCGAGTGAAGTTAACGAAGCCCTCCGTGAG 3270

Qy 1079 GlyTrpThrValGlnPheAsnTrpPheLeuHisLeuVal 1091
Db 3271 AGCTGGAAAACCAAAGTGAACTGGTTCCTGCACCACACGTG 3309

RESULT 7
US-10-027-591-1
; Sequence 1, Application US/10027591
; Publication No. US20020161014A1
; GENERAL INFORMATION:
;   APPLICANT: SADHU, Chanchal et al.
;   TITLE OF INVENTION: INHIBITORS OF HUMAN PHOSPHATIDYLINOSITOL 3-KINASE DELTA
;   FILE REFERENCE: 27866/36170C
;   CURRENT APPLICATION NUMBER: US/10/027,591
;   CURRENT FILING DATE: 2001-10-19
;   PRIOR APPLICATION NUMBER: 09/841,341
;   PRIOR FILING DATE: 2001-04-24
;   PRIOR APPLICATION NUMBER: 60/199,655
;   PRIOR FILING DATE: 2000-04-25
;   PRIOR APPLICATION NUMBER: 60/238,057
;   PRIOR FILING DATE: 2000-10-25
;   NUMBER OF SEQ ID NOS: 6
;   SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 5220
;   TYPE: DNA
;   ORGANISM: Human p110delta complete cDNA
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (196)..(3327)
US-10-027-591-1

Alignment Scores:
Pred. No.:
Score: 6.05e-147   Length: 5220
                          1352.50   Matches: 365
Percent Similarity: 49.87%   Conservative: 200
Best Local Similarity: 32.22%   Mismatches: 415
Query Match: Indels: 153
DB: Gaps: 40

US-09-974-573-1 (1-1102) x US-10-027-591-1 (1-5220)

Qy   20 ArgArgMetLysProArgSerThrAlaAla----------SerLeuSerSerMet 35
             :::||||| :::
Db   187 CAACGGAGGATGCCCCGGGTGGACTGCCCCATGGAATTCTGGACCAAGGAGGAGAAT 246

Qy   36 GluLeuIleProIleGluProValLeuProThrSerGlnArgAsnThrLysThrProGlu 55
             |||| |||
Db   247 CAGAGCGGTTGTGGTTGACTTCCTGCTCCCCACAGGG---------------------- 282

Qy   56 ThrAlaLeuLeuHis------------ValAlaGlyHisGlyAsnValGluGlnMetLysAlaGln 73
                          --GTCTACCTGAACTTCCCTGTGTCCCGCAATGCCAACCTCAGCACCATCAGCAGCTG :::|||
Db   283 --GTCTACCTGAACTTCCCTGTGTCCCGCAATGCCAACCTCAGCACCATCAGCAGCTG 339

Qy   74 ValTrpLeuArgAlaLeuGluThrSerValSerAlaAspPheTyrHisArgLeu----Gly 92
             |||| :::
Db   340 CTGTGGCCACCGGCCCCAGTATGAGCCGCTC---------------TTCCATGTCAGTGGC 387

Qy   93 ProAspHisPheLeuLeu--LeuTyrGlnLysLysGlyGlnTrpTyrGlnIleIleTyrAsp 111
             ||||:||| |||
Db   388 CCCGAGGCCTATGTTCACCTGGCAGCAGCGGAGCAGCAAGAGCTGGAGGAC 447

Qy   112 LysTyrGlnValValGlnThrLeuAspCysLeuArgTyrTrpLysValLeuHisArgSer 131
             ||:| |||
Db   448 GAGCAACGG--------CGTCGTGTGACGTGCAGCCCTTCCGCCCGTCCTG--------- 492

Qy   132 ProGlyGlnIleHisValValGlnArgHisAlaProSerGluThrLeuAlaPheGln 151
             |||| :::
Db   493 ---------------CGCCTGGCCCGTGAGGGGCGCACCCGCGTGAAGAGAAGCTC---ATCAAC 537

Qy   712 ----------ArgPheAlaValIleLeuGluAlaTyrLeuArgGlyCysGlyThrAlaMet 728
                      :::|||
Db 2173 GTGGCCCTGCGGCTTCGGCCTCATCCTGAGGGGCTACTGCAGGGGC---AGCACCACCAC 2229

Qy   729 LeuHisAspPheThrGlnGlnValGlnValGlnLysMetLeuGlnLysValThrIleAsp 748
             ::: |||
Db 2230 ATGAAGGTGCTGATGAAGCAGGGGAAGCACTGAGCAAACTG---AAGGCCCTGAATGAC 2286

Qy   749 IleLysSerLeuSerAlaGluLysTyrAspValSerSerGlnValIleSerGlnLeuLys 768
             ||||| |||
Db 2287 TTCGTCAAGCTGAGCTCCAGAGACCCCC---------------------AAG 2319

Qy   769 GlnLysLeuGluAsnLeuGlnAsnLeuAsnLeuProGlnSer------------------ 782
             |||| |||
Db 2320 CCCCAGACCAAGGAGCTGATGCACTTGTGCACGGCGGAGGAGGCCTACCTGAGGGCCCTC 2379

Qy   783 ------PheArgValProTyrAspValLeuLeuLysAlaGlyAlaLeuValIleGluLys 800
             ||| :::|||
Db 2380 TCCCACCTGCAGTCCCCAGACCACCCCGGTGGCTGAAGTCTGCCTGGACGCAG 2439

Qy   801 CysLysLysValMetAlaSerLysLysLysProLeuTrpLeuGluPheLysCysAlaAspPro 820
             |||| |||
Db 2440 TGCACCTTCATGAAGTCCAAGATGAAGCCCCTGTGGACGATCATGTAC------AGCAACGAG 2493

Qy   821 ThrAlaLeuSerAsnGluThrIleGlyIleIleGluPheLysHisGlyAspAspLeuArgGln 840
             |||| :::
Db 2494 GAGGCAGGCGGCGGCAGCCTGGGCATCATCTTAAGAACGGGGATGACCTTCCGGCAG 2553

Qy   841 AspMetLeuIleLeuGlnIleLeuArgIleMetGluserIleTrpGluThrGluSerLeu 860
             |||| |||:::
Db 2554 GACATGCTACCCTGCAGATGATCCAGCTCATGGACGTGTCCATGGAAGCAGGAGGGGCTG 2613

Qy   861 AspLeuCysSerLeuLeuProTyrGlyCysTyrIleSerSerThrGlyCysLysMetIleGlu 880
             |||| :::|||
Db 2614 GACCTGAGGATGACCCCCATGGCTGCTCCCCACCGGGACCGACAGGCCTCATTGAG 2673

Qy   881 IleValLysAspAlaThrLeuAlaThrLeuAlaLysSerIleGln------GlnSerThrValGlyAsn 898
             ::: ||||
Db 2674 GTGGTACTCCGTTCAGACACCATGGCCAACAACTCAACCAAGACGAGCAACATGGCCAGCC 2733

Qy   899 ThrGlyAlaPheLysAspPheGluValLeuSerHisTrpLeuLysGluLysCysProIleGlu 918
             |||| :::|||
Db 2734 ACAGCCGCCTTCAACAAGGATGCCCTGCTCAACTGGCTCAAGTCCAAGAACCCG---GGG 2790

Qy   919 GluLysPheGlnAlaAlaValGluArgPheValTyrSerCysAlaGlyTyrCysValAla 938
             |||| :::
Db 2791 GAGGCCCTGGATCGGCCATTGAGAGAGTTCACCCTCTCTGTCTGGCTATTGTGTGGCC 2850

Qy   939 ThrPheValLeuGlyIleGlyAspArgHisAsnAspAsnIleMetIleSerGluThrGly 958
             |||| |||:::
Db 2851 GTGGTACTCCGTTCAGACACCATGGCCAACAACTCAACCAAGACGAGCAACATGGCCAGCC 2910

Qy   959 AsnLeuPheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIle 978
             |||| :::|||
Db 2911 CAGTGTTCCACATTGATTTTGGCCACTTTCTGGGGAATTTCAAGAGCCAAGTTTGGAATC 2970

Qy   979 AsnLysGluArgValProPheValLeuThrProAspPheLeuPheValMetGlyThrSer 998
             |||| :::
Db 2971 AACCGCGAGCGCGTGTCCATTCCATCATCCTCACCTATGACTTTGTCCATGTCAGTGGCCACCAGGGG 3030

Qy   999 GlyLysLysThrSerLeuHisPheGlnLysValCysPheGlnAspPheLeuThrAlaTyrLeu 1018
             ||||:|| |||
Db 3031 AAGACTAATAATAGTGAGAAATTTGAACGGTTCCGGGGCTACTGTGAAGGGGCTACACC 3090

Qy 1019 AlaLeuArgHisHisThrAsnLeuIleIleLeuPheSerMetMetLeuMetThrGly 1038
             |||| :::|||
Db 3091 ATCCTGCGGGCCACGGGCTTCTCTTTGCCCATGCGGCGGCCGCAGGC 3150

Qy 1039 MetProGlnLeuThrSerLysGluLysTyrIleLysArgAspAlaLeuThrValGly 1058
             |||| :::|||
Db 3151 CTGCCTGAGCTCAGCTGACACCCTCCAAAGACATCCAGTATCTCCGGGCACTGGGG 3210

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Qy    152 ArgGlnLeuAsnAlaLeuIleGlyTyrAspValThrAspValSerAsnValHisAspAsp 171
              ||| |||:::|| |||||||||         :::       |||||
Db    538 TCACAGATCAGCCTCCATCGGCAAAGGCCTCAGAGTTTGACTCCTTGTGCGACCCA 597

Qy    172 GluLeuGluPheThrArgArgLeuValThrProArgMetAlaGluValAlaGlyValArg 191
              |||||::::                  :::
Db    598 GAAGTGAACGACTTTCGGCCACAAGATGTGC-----CAATTCTGCGAGGAGGGGCCGCC 651

Qy    192 AspProLysLeuTyrAlaMetHisProTrpValThr---SerLysProLeu-------- 207
              ||:::||                ||||||
Db    652 CGCCGGCAGCAGCTGGGCTGGGAGGCCTGGCTGCAGTACAGTTTCCCCCTGCAGCTGGAG 711

Qy    208 --------------ProGluTyrLeuLeuLysLysIleThrAsnAsnCysVal 220
                            |||  ::: |||
Db    712 CCCTGCGGCTCAAACCTGGGGGCCTGGTACCCTG------CGGCTCCCGAACCGGGCCCTT 765

Qy    221 PheIleValIle------HisArgThrSerGlnThrIleLysValSerAlaAsp 238
              |||||                ||| |||
Db    766 CTGGTCAACGTTAAGTTTGAGGGAGCCAGCGAGGAGAGCTTCACCTTCCAGGTGTCCACCAAG 825

Qy    239 AspThrProGlyThrIleLeuGlnSerPhePheThrLysMetAlaLys-----LysLys 256
              |||                  :::|||||
Db    826 GACCTGCCCTGGCGCTGATGGCGTGCCCTGTGCCCGGAGAAGGCCACAGTGTTCCGGCAG 885

Qy    257 SerLeuMetAspIleProGluSerGlnAsnGluArgAspPheValLeuArgValCysGly 276
              :::|||                  |||
Db    886 CCGGTGGTGAGCAGCCGGAA-----------GACTACACGGTGCAGGTGAACGAC 930

Qy    277 ArgAspGluTyrLeuValGlyGluThrProIleLysAsnPheGlnInTrpValArgGlnCys 296
              |||||| :::                 ||||||
Db    931 AGGGATGAGTACCTGTATGGCAACTACCCGCTCTGCAGTACAGTCAGCTGCTA 990

Qy    297 LeuLysAsnGlyGluGluIleHisLeuValLeu-------------------- 307
              :::
Db    991 CTGCACAGTGGGTGACCCTCACCTGACCATGGTCCATCCTCCCATCCTGCCATG 1050

Qy    308 --------AspThrProAspProAlaLeuAspCysAspValAlaArgLysGluTrpPro 324
                      |||  |||:::
Db   1051 CGGGATGAGCAGAGCAACCCTGCCCCCCAGGTCCAGGAAACCGGTGCCAAACCACCTCCC 1110

Qy    325 LeuValAspAspCysThrGlyValThrGlyTyrValHisGluHisThrIleHisGlyLys 344
              :::                  |||||||||
Db   1111 ---------------------------------ATTCCTGCGAAG 1122

Qy    345 AspHisGluSerValPheThrValSerLeuTrpAspCysAspArgLysPheArgValLys 364
              ::: ::::                 |||||
Db   1123 AAGCCTTCCT--------GTGTCCCCGTGGTCCCCAGGTCCGAGCAGCCGTTCCGCATCGAG 1173

Qy    365 ---IleArgGlyIleAspIleProValLeuProArgThrAlaAspLeuThrValPheVal 383
                 :::                  |||||
Db   1174 CTCATCCAGGGAGCAGAAGTGAACGCCGACGAGCGG-------ATGAAGCTGGTGGTG 1224

Qy    384 GluAlaAsnIleGlnTyrGlyGlnValCysGlnArgArgThrSerProLys--- 402
              :::                  ::::|||
Db   1225 CAGGCCGGCTTTTCCACGGCACGAGATGCTGTGCAAGACGGTGTCCAGCTCGGAGGTG 1284

Qy    403 ProPheThrGlyLeuGluValLeuTrpAsnValTrpLeuGlnPheSerIleLysLysAsp 422
              |||:::                 ||||| :::
Db   1285 AGCCGTGTCGCTGGAGCCCGTGTGGAAGCAGCAGCCGTTCCGCATCAACATCTGCCAC 1344

Qy    423 LeuProLysGlyAlaLeuLeuAsnLeuGlnIleTyrCysGlyLysAlaProAlaLeuSer 442
              ||||::::                 :::
Db   1345 CTGCCCCCGCATGGCCGTCTCGCTTTGCGCTGTACGCC-----------GTGATCGAG 1392

Qy    443 GlyLysThrSerAlaGluMetProSerProGluSerLysGlyLysAlaGlnLeuLeuTyr 462
              |||                  :::
Db   1393 AAAGCCAAGAAGGCTGCGTCCACCAAGAAGAAGAAGCCGGACTGCCCCATTGCC 1452

Qy    463 TyrValAsnLeuLeuLeuIleAspHisArgPheLeuLeuArgHisGlyGluTyrValLeu 482
              :::  |||||:::                 |||
Db   1453 TGGGCCACCTCATGGCTGTTTGACTACAAGGACCAGCTTAAGACCCGGGGGAACGCTGCCTC 1512

Qy    483 HisMetTrpGlnLeuSerGlyLysGlyLysGluAspGlnInGlySerPheAsnAlaAspLysLysLeu 502
              ||| :::
Db   1513 TACATGTGG------CCCTCCTCCCAGATGAGAAGGCGGAGCTGCTGAACCCCACGGGC 1566

Qy    503 ThrSerAlaThrAsnProAspLysLysGluAsnSerMetSerIleSerLeuSerLeuLeuAspAsn 522
              :::  :::::                 :::::
Db   1567 ACTGTGGCAGTAACCCCAACACGGATAGCGCCGGCGTGCCCTGCCATCTGCCTGCCCGAG 1626

Qy    523 TyrCys---HisProIleAlaLeuPro-------------LysHis 532
              ||||||                  :::||
Db   1627 GTGGGCCCCGGTACTACCCCGGAGAAGATCTTGGAGCTGGGCGACCAC 1686

Qy    533 ArgProThrProAspProGluGluGlyAspValArgAlaAlaGlyMetProAsnGlnLeuArg 552
                            |||:::
Db   1687 ----------------AGGGAGTGTGTGCATGTCACCGAGGAGGAGCAGCTG--- 1722

Qy    553 LysGlnLeuAlaIleIleIleAlaThrAspProLeuAsnProLeuThrArgAlaGluAspLys 572
                            :::::
Db   1723 ---CAGCTGCGGGAAATCCTGGAGCGGCGGGGGTCTGGGGAGCTGATGAGCACGAGAAG 1779

Qy    573 GluLeuLeuTrpHisProPheArgTyrGluSerLeuLysAsp---ProLysAlaTyrProLys 591
              |||                  :::||
Db   1780 GACCTGGTGTGGAAGCTGCGCCATGAAGTCGGGCGCCACAGGCCGCTAGCCCGG 1839

Qy    592 LeuPheSerSerValLysTrpGlyIleGlnGluIleValAlaLysThrTyrGlnLeuLeu 611
              ||||:::                 :::
Db   1840 CTGCCCGGTCACCAGGTGGACACCAGCATGGAGGACATGGGCCAGATGCTCTACCTGCTG 1899

Qy    612 AlaLysArgGluValTrpAspGlnSerArgAlaLeuAsnAspValGlyLeuThrMetGlnLeuLeu 631
              |||                  :::::
Db   1900 TGGTCC------------CTGCCCGTCCTGAGCCGCCTTGCGGAAACTG 1944

Qy    632 AspCysAsnPheSerAspGluAsnValArgAlaIleeAlaValGlnLysLeuGlnSerLeu 651
              :::                  :::::
Db   1945 GACTTCAGCTTCCCCGATTGCCACGTAGGCTCCTTCGCCATCAAGTCGCTGCGGAAACTG 2004

Qy    652 GluAspAspAspValAlaGluHisTyrLeuLeuGlnSerGlnLeuAlaValLysPheGluPro 671
              |||:::                  ::::|||
Db   2005 ACGGACCATGAGCTGTTCCAGTACCTGCTGGTGCAGTCCCAGCTGGCTGTCAAGTTCGAGCC 2064

Qy    672 TyrHisAspSerAlaLeuIleLeuGluAlaAlaTyrLeuArgGlyCysLeuArgAsnLysArgIle 691
              :::                  :::
Db   2065 TACCTGGACTGCGAGCTGACCAAATTCCTGCGGGAAGCACTGAGCAAACTG--AAGGCCCTGAATGAC 2124

Qy    692 GlyHisPheLeuPheTrpPheLeuArgSerGluIleAlaGlnInSerArgHisTyrGlnGln 711
              |||                  :::::
Db   2125 GGCCCACTTCCTTTCTCGGCACCTCCGGTCCGAGATG---------CACGTGCCGTCG 2172

Qy    712 ------------ArgPheAlaValIleLeuGluAlaTyrLeuArgGlyCysGlyThrAlaMet 728
                            :::
Db   2173 GTGGGCCCTGCGGCTTCGGCCTTCATCCTGGAGCGGGGC---AGCACCACCAC 2229

Qy    729 LeuHisAspPheThrGlnInValGlnInValIleValThrIleAsp 748
              :::                  :::||
Db   2230 ATGAAGGTGCTGATGAAGCAGGGGAAGCACTGAGCAAACTG---AAGGGCCCTGAATGAC 2286

Qy    749 IleLeuLysSerLeuAlaGluLysValTyrAspValSerSerGlnInValIleuLys 768
              |||                  :::
Db   2287 TTCGTCAAGCTGAGCCTCCAGAAGACCCCCC----------AAG 2319

Qy    769 GlnLysLeuGluAsnLeuGlnAsnLeuAsnLeuProGlnSer------------ 782
              :::                  :::
Db   2320 CCCCAGACCAAGGAGCTGATCGCACTTGTGCATGCGGCAGGAGGCCTACCTGGAGGCCCTC 2379

Qy    783 -----PheArgValProTyrAspProGlyLeuLysLysAlaGlyAlaLeuVallIleGluLys 800
                   |||||:::
Db   2380 TCCCAGCTCAGTGCCCACTCGACCCCAGCACCCTGCTGAAGTCGCTGTGGAGCAG 2439

Qy    801 CysLysValMetAlaSerArgLysLysProLeuTrpLeuGluPheLysCysAlaAspPro 820
              :::                  :::
Db   2440 TGCACCTTCATGGACCTCAAGATACCAAGATGAAGCCCGTGTGTCGATCATGTAC----AGCACGAG 2493

Qy    821 ThrAlaLeuSerAsnGluThrIleGlyThrIleIlePheLysHisGlyAspAspLeuArgArgGln 840
              |||                  |||||
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Db  2494  GAGGCAGGCAGCGGCGGCGGGCATCATCTTTAAGACGGGATGACCTCCGGCAG  2553

Qy   841  AspMetLeuIleLeuGlnIleLeuArgIleMetGluSerIleTrpGluThrGluSerLeu    860
               :::  |||:  ||||:  :::
Db  2554  GACATGCTGACCCCTGCCAGATGATCCAGCTCCATGGACGTCCCTGTGGAAGCAGGAGGGGCTG    2613

Qy   861  AspLeuCysLeuLeuProTyrGlyCysIleSerThrGlyArgIleSerThrGlyMetIleGlu   880
               |  :::   ||||||  ||||||||  |
Db  2614  GACCTGAGGATGACCCCCTATGCGCCTGCCTCCCACCGGGACACCGCAGGCCTCATTGAG    2673

Qy   881  IleValLysAspAlaThrThrIleAlaLysLysIleGln------GlnSerThrValGlyAsn    898
               :::|   |||||||  :::  |||
Db  2674  GTGGTACTCCGTTCAGACACCATCGCCAACATCCAACTCAACAGAGCAACATGGCAGCC    2733

Qy   899  ThrGlyLysPheLysPheLysAspAlaLysGluValLeuSerHisTrpLysLysCysProIleGlu   918
               |||   ||||||   |:::  ||||||||||
Db  2734  ACAGGCCGCTTCAACAAGGATGCCCTGCTCAACCTGGCTGAAGTCCAAGAACCCG--GGG   2790

Qy   919  GluLysPheGlnAlaAlaValAlaValGluArgPheValTyrSerCysAlaGlyPheTyrCysValAla   938
               |||   :::  |  ::|
Db  2791  GAGGCCCTGGATGCAGCCATTGAGGAGTTCACCCTCCTCCTGTCCTGGCTATTGTGTGGCC    2850

Qy   939  ThrPheValLeuGlyIleIleGlyTyrIleAspAsnIleMetIleSerGluThrGly    958
               |  |||  :::
Db  2851  ACATATGTGCTGGCATTGGCGGATCGCGGCACAGCGCACAACATCATGATCCGAGAGAGTGGG    2910

Qy   959  AsnLeuPheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIle   978
               |  |||   |||   ::|
Db  2911  CAGCTGTTCCACATTGATTTTGGCCACTTTCTGGGAAATTACAAGACCAAGTTTGAAATC   2970

Qy   979  AsnLysGluArgValProPheValLeuThrProAspPheLeuPheValMetGlyThrSer   998
               :|  :::
Db  2971  AACCGCGAGCGTGTCCCATTCATCCTCCACTATGACTTTGTCCATGTGATTCAGCAGGGG    3030

Qy   999  GlyLysLysThrSerLeuHisPheGlnIleLysPheGlnLysAspLysProSerAlaAspGlnIleHisArgGln   1018
               |||   |:::
Db  3031  AAGACTAATAATAGTGAGAAATTTGAACGGTTCCGGGGCTACTGTGAAAGGGCTCACACC    3090

Qy  1019  AlaLeuArgHisHisThrAsnLeuLeuIleIleLeuLeuPheSerMetMetLeuThrGly   1038
               |||   |||
Db  3091  ATCCTGCGGCGCCACACGGCCTTCCTGTCCCTGATGCGGCGGCAGGC    3150

Qy  1039  MetProGlnLeuThrSerLysGluSerLysIleGluGluTyrIleLeuArgAspAlaLeuThrValGly   1058
               |||   |:::  |
Db  3151  CTGCCTGAGCTGACTGCTCAGCCTGCTCCAAAGACATCCAGATCTCCAAGGACTCCCTGGCACTGGGG   3210

Qy  1059  LysSerGluGluAspAlaLysLysTyrPheLeuAspLysLeuIleGlyGlnIleGluGluGlnValCysArgArgAspLys   1078
               |||   |:::  |
Db  3211  AAAACAGAGGAGGAGGACGCACTGAAGAAGTACTTCCTGGATAAGTTAACGAAGCCCCTGTGAG   3270

Qy  1079  GlyTrpThrValGlnPheAsnTrpPheLeuHisLeuVal   1091
               :::  ||||||
Db  3271  AGCTGGAAAACCAAAGTGAACTGGCTGGCCACAACGTG   3309
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-162-160-2

Alignment Scores:
Pred. No.:                         6.45e-147                Length:           3387
Score:                             1349.50                  Matches:          361
Percent Similarity:                50.23%                   Conservative:     197
Best Local Similarity:             32.49%                   Mismatches:       404
Query Match:                       23.31%                   Indels:           149
DB:                                15                       Gaps:             39

US-09-974-573-1 (1-1102) x US-10-162-160-2 (1-3387)

Qy    38  IleProIleGluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAla    57
              :::   |||
Db    58  GTTGTGGTTGACTTCCTGCTTGCCCACAGGG--                                  --GTC    90

Qy    58  LeuLeuHis------ValAlaGlyHisGlyAsnValGluMetLysAlaGlnIleValTrp    75
              |||   :::  :::|||
Db    91  TACTTGAACTTCCCTGTCCGCAATGCCAACCTCAGCAACCATCAAGCAGCTGCTGTGG    150

Qy    76  LeuArgAlaLeuGluThrSerValSerAlaAspPheTyrHisArgLeu--GlyProAsp    94
              |||   :::|||
Db   151  CACCGCGCCCCAGTATGAGCCCCTC--------------TTCCACATGCTCAGTGGCCCCGAG    198

Qy    95  HisPheLeuLeu--LeuTyrGlnLysLysGlyGlnTrpTyrGluIleTyrArgAspTyr    113
              :::|||
Db   199  GCCTATGTGTTCACCTGCATCAACCAGACAGCGGAGCAAGAGCTGGAGGACGAGCAA    258

Qy   114  GlnValGlnThrLeuAspCysLeuArgTyrTrpLysValHisArgSerProGly    133
              :::   :::
Db   259  CGG-----CGCTCGTGTGACGTGCAGCCCCTTCCTGCGCCCTG---                297

Qy   134  GlnIleHisValValGlnArgHisAlaProSerGluGluThrLeuAlaPheGlnArgGln    153
              :::   :::
Db   298  ------CGCTCGTGTGGCCCCGTGAGGGCGACCGCGTGAAGAAGCTC--ATCAACTCACAG    348

Qy   154  LeuAsnAlaLeuIleGlyTyrArgAspValThrAspValSerAsnValHisAspGluLeu    173
              :::   :::|||:::
Db   349  ATCAGCCTTCCCTCATCGGCAAAGGCCTCCACGAGTTGACTCTTGTCGGACCCAGAAGTG    408

Qy   174  GlyPheThrArgArgLeuValThrProArgMetAlaGluValAlaGlyValAlaArgAspPro    193
              :::|||
Db   409  AACGACTTTCCGCCAAGATGTGC------CAATTCTGCGAGGAGCGGCGGGCCCCGCCGG    462

Qy   194  LysLeuTyrAlaMetHisProTrpValThr---SerLysProLeu                207
              :::   |||
Db   463  CAGCAGCTGGCTGGCTGGAGGCCTGGCTGCAGTACAGTTCCCCTGCAGTGGAGCCCTCG    522

Qy   208  ---------------ProGluTyrLeuLeuLysLysIleThrAsnAsnCysValPheIle    222
                         :::
Db   523  GCTCAAACCTGGGGGCGTACCCCTG------CGGCTCCCGCAACCGGGGCCTTCTGGTC    576

Qy   223  ValIle-----HisArgSerThrThrGlnThrIleLysValSerAlaAspAspThr    240
              :::   :::
Db   577  AACGTTAAGTTTGAGGGGCAGCGAGAGAGTTCACCTTCCAGGTGTTCCACCAAGGACGTG    636

Qy   241  ProGlyThrIleLeuGlnSerPhePheThrLysMetAlaLys-------LysLysSerLeu    258
              :::   :::|||
Db   637  CCGGTGACGATGGCTGGCCCTGTCCCTGCGGAAGAAGAGGCCAACAGTTCCGGCAGCCGCTG    696

Qy   259  MetAspIleProGluSerGlnAsnGluArgGluValCysGlyTyrArgValCysTyrArgAsp    278
              :::   |||
Db   697  GTGGAGCAGCCCGGAA-----------GACTACACGCTGCAGGTGAACGCAGGCCAGGCAT    741

Qy   279  GluTyrLeuValGlyGluThrProIleLysAsnPheGlnTrpProValArgGlnCysLysLys    298
              :::   :::|||
Db   742  GAGTACCTGTATGGAGCAGCTACCCGTCTCGCCAGTTCCAGTACATCTGCAGTGCCTGCAC    801

Qy   299  AsnGlyGluIleHisLeuValLeu---------                307
              :::|||
Db   802  AGTGGGTGACCCCTCACCTGACCATGTCCATTCCTCCTCATCCTCGCCATGCGGGAT    861
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RESULT 8
US-10-162-160-2
; Sequence 2, Application US/10162160
; Publication No. US2003009627A1
; GENERAL INFORMATION:
; APPLICANT: Van Hasebroeck, Bart
; APPLICANT: Waterfield, Michael D.
; TITLE OF INVENTION: No. US2003009627A1e1 Lipid Kinase
; FILE REFERENCE: 2332-1-002
; CURRENT APPLICATION NUMBER: US/10/162,160
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/194,640
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: 9611460.8
; PRIOR FILING DATE: 1996-06-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 3387

Right column:

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Qy   654  AspAspValLeuHisTyrLeuLeuGlnLeuValGlnAlaValLysPheGluProTyrHis  673
               ::::::::|||||||||||||::::::||||||::||||||||||:::::|||:||:
Db  1816  GATGAGCTGTTCCAGTACCTGCTCCAGTTGGTGCAGGTGCTCAAGTACGAGTCCTACCTG 1875

Qy   674  AspSerAlaLeuAlaArgPheLeuLysArgGlyLeuArgAsnLysArgIleGlyHis    693
               ::|:|||::|||||||||||||||||:::||||::||||||||||||:|||||||
Db  1876  GACTGCGAGCTGACCAAATTCCTGCTGAAGCGGGGCCTGCGCAACAAGCGGATCGGCCAC 1935

Qy   694  PheLeuPheTrpPheValSerLeuTrpAspCysAspArgPheArgValLys------Ile  711
               ||||||:|||||:||||||||||||:||||||||||:::::::::
Db  1936  TTCCTTTTCTGGACCACCCGCTCCGACTGCGACATG-----------CACGTGCCGTCGGTGGCC 1983

Qy   712  ---ArgPheAlaValIleLeuGluAlaTyrArgGlyCysGlyThrAlaMetLeuHis    730
                 ::::||::|||||||::||||||||::||||
Db  1984  CTGCGCCTTCGGCCTCATCCTGGAGGCCTACTGCAGGGGC---AGGACCCACCACATGAAG 2040

Qy   731  AspPheThrGlnIleValIleGlnValLysValThrIleAspMetIleLys         750
               :::|||||:|||||||::|||||||||:||||
Db  2041  GTGCTGATGAAGCAGGGGGAAGCACTGAGCAAACTG--AAGCCCTGAATGACTTCGTC    2097

Qy   751  SerLeuSerAlaGluLysTyrAspValSerSerGlnValIleSerGlnLeuLysGlnLys  770
               :::::::|||:::::::
Db  2098  AAGCTGAGCTCTCAGAGAGACCCC---------------AAGCCCCAG            2130

Qy   771  LeuGluAsnLeuGlnAsnLeuAsnLeuProGlnSer                       782
               :::|||
Db  2131  ACCAAGGAGCTGATGCACTTGTGCATGGCAGGAGGGCTACCTAGAGGCCCTCTCCCAC    2190

Qy   783  PheArgValProTyrAspProGlyLeuLysAlaAlaGlyAlaLeuValIleGluLysCysLys  802
               :::|||||||||
Db  2191  CTGCAGTCCCCACTCGACCCCGACACCCTGCTGGCTGGAGTCTGCGTGGACCAGTGCACC  2250

Qy   803  ValMetAlaSerIleLysLysProLeuTrpPheLeuGluPheLysCysAlaAspProThrAla  822
               :::||||
Db  2251  TTCATGGACTCCAAGATGAAGCCCCTGTGGATCATGTAC-----AGCAACGAGGAGGCA  2304

Qy   823  LeuSerAsnGluThrIleGlyIleIlePheLysHisGlyLysAspAspLysGlnAspMet  842
               |||:::||||
Db  2305  GGCAGCGGGCAGCGTGGGCATCATCTTTAAGAACGGGGATGACCTCCGGCAGGACATG    2364

Qy   843  LeuIleLeuGlnIleLeuArgIleMetGluSerIleTrpGluThrGluSerLeuAspLeu  862
               :::||||
Db  2365  CTGACCCTGCAGATGATCCAGTCATGGAGCGTCCTGTGGAAGCAGGAGGGGCTGGACCTG  2424

Qy   863  CysLeuProTyrGlyTyrCysIleSerSerThrGlyValAspLysIleGlyMetIleGluIleVal  882
               :::||||
Db  2425  AGGATGAACCCCATGGGCTGCCCCCCACCGGGGACCGGCGCCTCATTGAGGTGGTA    2484

Qy   883  LysAspAlaThrIleAlaLysIleGln------GlnSerThrValGlyAsnThrGly   900
               :::||||
Db  2485  CTCCGGTCAGAGACACCATGCCAACATCCAACTCAACAAGAGCAACATCATGATCTG  2544

Qy   901  AlaPheLysAspPheGlyValLeuSerHisIleProLeuLysLysCysIleGluGluLys  920
               :::|||
Db  2545  GCCTTCAACAAGAGACCCTGCTCAACTGCTGAAGTCCAAGAACCCG--GGGGAGGCC  2601

Qy   921  PheGlnAlaAlaValGluArgPheTyrSerCysAlaGlyTyrCysValAlaThrPhe  940
               :::||||
Db  2602  CTGGATCGAGCATTGAGGAGTTCACCCTCTCGTGTGGCTATTGTGTGGCCACATAT  2661

Qy   941  ValLeuGlyIleGlyAspHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeu  960
               :::||||
Db  2662  GTGCTGGGCATTGGCGATCACAACGACAACATCATGATCTCCGAGAGTGGGCAGCTG  2721

Qy   961  PheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyAsnLys  980
               :::||||
Db  2722  TTCCACATTGATTTTGGCCACTTTCTGGGAAATTACAAGAGTTTGGAATCAACCGC  2781

Qy   981  GluArgValProPheValLeuThrProAspPheLeuMetGlyThrSerGlyGlyLys  1000
               :::|||
Db  2782  GAGCGTGTCCCATTCATCCTCACCTACCGACTTTGTCCATGTGATCAGCAGGGGAAGACT  2841

Qy  1001  LysThrSerLeuHisPheGlnLysPheGlnAspValCysValLysAlaTyrLeuAlaLeu  1020
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Left column:

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Qy   308  ---AspThrProProAspProAlaLeuAspGluValArgLysGluGluTrpProLeuVal  326
               :::
Db   862  GAGCAGAGCAACCCTGCCCCCAGGTCCAGAAACCGGTGCCAAAACCACCTCCC------    915

Qy   327  AspAspCysThrGlyValThrGlyTyrHisGluGlnLeuThrIleHisGlyHisLysAspHis  346
               :::
Db   916  -----------------------ATTCCCTGCGAAGAAGCCT                     933

Qy   347  GluSerValPheThrValSerLeuTrpAspCysAspArgPheArgValLys---Ile  365
               :::
Db   934  TCCTCT-------GTGTCCCTGGTCCGTCCGCAGCCGTTCCGCATCGAGCTCATC  984

Qy   366  ArgGlyIleAspIleProValLeuProArgThrAlaAspPheValPheValGlnAla  385
               |||
Db   985  CAGGGCAGCAGAAAGTGAACGGCCGACGAGCGG-------ATGAAGCTGGTGGTGCAGGCC 1035

Qy   386  AsnIleGlnTyrGlyValGlnValLeuCysValAsnArgGlnThrSerProLys---ProPhe  404
               :::
Db  1036  GGGCTTTTCCACGGCAACGAGATGGCTGTGAAGACGGTGTCCAGCTCGGAGGTGAGCGTG  1095

Qy   405  ThrGluGlnValLeuValTrpAsnValTrpLeuGluPheSerIleLysGluLysAspLeuPro  424
               :::
Db  1096  TGCTCGGAGCCCGTGTGGAAGCAGCGGCTGGAGTTCAGCATCAAGCATCTGCGACCTGCCC  1155

Qy   425  LysGlyAlaAlaLeuLeuAsnLeuGlnIleTyrCysGlyLysAlaProAlaLeuSerGlyLys  444
               :::
Db  1156  CGCATGGCCCCGTCCTGCTTTGGCGTGTACGCC-------GTGATCGAGAAAAGCC    1203

Qy   445  ThrSerAlaGluMetProSerProGluSerLysGlyLysAlaGlnLeuLeuTyrTyrVal  464
               :::
Db  1204  AAGAGAGGCTGCTCCACCAGAAGAGTCCAAGAAGAGGCGACTGCCCATTGCCTGGGCC  1263

Qy   465  AsnLeuLeuLeuIleAspHisArgPheLeuLeuArgHisGlyLysTyrValLeuHisMet  484
               :::
Db  1264  AACCTCATGCTGTTGACTACAAGGACCCAGCTTAAGACCCGGGGACGCTGCCCTACATG 1323

Qy   485  TrpGlnLeuSerGlyLysLysGlyGluAspProSerPheAsnAlaAspLysLeuThrSer  504
               :::
Db  1324  TGG-------CCCTCCGTCCCAGATGAGAGAGGGGCAGCTGCTGGCAACCCCACGGGCACTGTG 1377

Qy   505  AlaThrAsnProAspLysGluAlaAsnSerMetSerIleSerLeuLeuAspAsnTyrCys  524
               :::
Db  1378  CGCAGTAACCCCACACGGATAGCGCCGTCGCCTGCCTGCCTGCCTCTGCCTGCCGAGGTGGCC 1437

Qy   525  ---HisProIleAlaLeuPro-------------------LysHisArgPro          534
               |||
Db  1438  CCGCACCCCGTGTACTACCCCGGAAGATCTTGGAGCTGGGGCGACAC---------    1491

Qy   535  ThrProAspProGluGlyGluArgAspArgValArgAlaGlyMetProAsnGlnLeuArgLysGln  554
               :::
Db  1492  ----------------AGCGAGTGTGTGCATGTCACCGAGGAGGAGCAGCTG------CAG 1530

Qy   555  LeuGluAlaIleIleIleAspThrAspProLeuAsnProLeuThrAlaGluAspLysGluLeu  574
               :::
Db  1531  CTGCGCGGGAAATCCTGGACGCGGCGGGGGTCTGGGGAGCTGTATGAGCACGAGAGAGACCCTG 1590

Qy   575  LeuTrpHisPheArgTyrGluSerLeuLysAsp---ProLysAlaTyrProLysLeuPhe  593
               :::
Db  1591  GTGTTGGAAGCTGCGGCATTGAGGAGTTCACCCTCTCGTGTGGCTATTGTGTGGCCACATAT 1650

Qy   594  SerSerValLysTrpProGlyGlnSerAlaGlnLeuGluIleValAlaLysThrTyrGlnLeuLeuAlaLys  613
               :::
Db  1651  CTGGTCACCAAGTGGAACATGAGGATGGAACGGCCCAGTCCTACCTGCTGCCTGTGCTCC  1710

Qy   614  ArgGluValTrpAspGlnSerAlaLeuAspAlaValGlyLeuThrMetGlnLeuLeuAspCys  633
               :::
Db  1711  -------TGGCCGGAG-----CTGCCCGTCCTGAAGCGTGCTGCTGCTAGACTTC  1755

Qy   634  AsnPheSerAspGluAsnValArgAlaIleAlaValAlaIleGlnLysLeuGluSerGluAsp  653
               :::
Db  1756  AGCTTCCCCAATGCCACGTAGGCTCCTTCCGCCATCAAGTCGCTGCGGAAACTGACGGAC  1815
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Db 2842 AATAATAGTGAGAAATTGAAGGGTTCCGGGGCTACTGTGAAAGGGCCTACACCATCCTG 2901

Qy 1021 ArgHisHisThrAsnLeuLeuIleIleLeuPheSerMetMetGlyMetPro 1040

Db 2902 CGGCGCCCACAGGGCTTCTCTTCCTCCACCTCTTTGCCCGTATGCGGCGGCGCAGGCCTGCCT 2961

Qy 1041 GlnLeuThrSerLysGluAspIleAspTyrIleArgAspAlaLeuThrValGlyLysSer 1060

Db 2962 GAGCTCAGCTGCTCCAAAGACATCCAGTATCTCAAGGACTCCCTGGCACTGGGGAAAACA 3021

Qy 1061 GluGluAspAlaLysLysTyrPheLeuAspGlnIleGluValCysArgAspLysGlyTrp 1080

Db 3022 GAGGAGGAGGCACTGAAGCACTTCCGAGTGAAGTTAACGAAGCCCCTCCGTGAGAGCTGG 3081

Qy 1081 ThrValGlnPheAsnTrpPheLeuHisLeuVal 1091

Db 3082 AAAACCAAAGTGAACTGGCTGGCTGGCCCACAACGTG 3114

Alignment Scores:
Pred. No.:   2e-145   Length: 3777
Score: 1337.50   Matches: 364
Percent Similarity: 49.65%   Conservative: 201
Best Local Similarity: 31.99%   Mismatches: 407
Query Match: 23.10%   Indels: 167
DB.:   13   Gaps: 38

US-09-974-573-1 (1-1102) x US-09-814-353-19587 (1-3777)

Qy   30 AlaSerLeuSerMetGluLeuIleProIleGluPheValLeuProThrSerGlnArg 49

Db   402 TCACCAGATAGCATCTGATGGCTCCATACCTGTGGATTTCCTTTTGCCCACTGGG------ 455

Qy   50 AsnThrLysThrProGluThrAlaLeuHisValPheValGluAlaAsnIleGlnTyrGlyGln 69

Db 1368 AACACCAGGAGAAACTGTAAAAGTTCATGTCAGGGCTGGTCTTTTTTCATGTGTACTGAGCTC 1427

Db   456 ------------ATTTATATCCAGTTGGAGGTACCTCGGGAAGCTACCATTCTTAT 500

Qy   70 MetLysAlaGlnValTrpLeuArgAlaLeuGluThrSerValSerAlaAspPheTyrHis 89
          ::::::::: |||
Db   501 ATTAAGCAGATGTTATGGAAGCAAGTTCACATTACCCAATG------------------ 542

Qy   90 ArgLeuGlyProAspHisPheLeuLeuTyrGlnLysLysGlyGlnLnTrpTyrGluIle 109
                                         ||||||||
Db   543 ------------TTCAACCTCCTTATGGATATTGGACTCCTATATGTTTGCATGT 584

Qy   110 TyrAspLysTyrGlnValValGlnThrLeuAsp----------Cys-------- 121
          :::::: ||||| |||
Db   585 GTGAATCAGACTGCTGTATATGAGGAGCTTGAAGATGAAACACGAAGACTCGTGATGTC 644

Qy   122 ----------LeuArgTyrTrpLysValValHisArgSer------ProGlyGlnIleHis 136
                    |||::: |||||:::
Db   645 AGACCTTTTCTTCCAGTTCTCAAATTAGTGACAAGAAGTTGTGACCCAGGGGAA 698

Qy   137 ValValGlnHisArgHisAlaProSerGluGlyThrLeuAlaPheLeuArgGlnLeuAsnAla 156
                                                            :::::::::
Db   699 ------------AAATTAGACTCAAAAATTGGAGTC 722

Qy   157 LeuIleGlyTyrAspValThrAspValSerAsnValHisAspAspGluLeu---GluPhe 175
          |||::: |||
Db   723 CTTATAGGAAAAGGTCTGCATGAATTTGATTCCTTGAGGATCCTGAAGTAAATGAATTT 782

Qy   176 ThrArg------------ArgLeuValThrProArgMetAlaGluValAlaAlaGlyArgAsp-- 192
          ::: |||:::
Db   783 CGAAGAAAATGCGCAATTCAGCGAGGAAAAAATCCTGTCACTGTGGGATTGTCTTGG 842

Qy   193 ---ProLysLeuTyrAlaMetHisProTrpValThrSerLysProLeuProGluTyrLeu 211
             ||| :::||||||
Db   843 ATGGACTGGCTAAAACAACATATCCACCAGGACCATGAACCATCCCTGAAAACTTA 902

Qy   212 LeuLysLysIleThrAsnAsnCysValPheIleValIleValIleHisArgSerThrSerGln 231
                      ||| :::|||||
Db   903 GAAGATAAACTTTATGGGGAAAGCTCATCGTAGCTGTTCATTTGAAAACTGCCAGGAC 962

Qy   232 ------ThrIleLysValSerAlaAspAspThrProGlyThrIleLeuGlnSerPhePhe 249
                  ::: |||:::
Db   963 GTGTTTAGCTTTCAAGTGTCTCCTAATATGAATCCTATCAAAGTAAATGAA---------- 1013

Qy   250 ThrLysMetAlaLysLysSerLeuMetAspIleProGluSerGlnAsnGluArgAsp 269
                      ||| :::|||
Db 1014 TTGGCAATCCAAAAACGTTTGACTATTCATGGGAAGGAAGATGAAGTTAGCCCCTATGAT 1073

Qy   270 PheValLeuArgValCysGlyArgAspAspArgTyrLeuValGlyGluThrProIleLysAsn 289
          ::::::::: |||
Db 1074 TATGTTTTGCAGTCAGCGGGAGAGTAGAATATGTTTTTGTGATCATCCACTAATTCAG 1133

Qy   290 PheGlnTrpValArgGlnCysLeuLysAsnGlyGluGluIleHisLeuValLeuAspThr 309
          |||||::::: |||
Db 1134 TTCCAGTATATCCGGAACTGTGTGATGAACAGAGCCCGCCCATTTTATACTT------ 1187

Qy   310 ProProAlaProAlaLeuAspArgValArgLysGluGluTrpProLeuValAspAspCys 329
          :::
Db 1188 ------------GTGGAATGC 1196

Qy   330 ThrGlyValThrGlyTyrHisGluGln----------LeuThrIleHisGlyLysAspHisGlu 347
          :::   ::::::
Db 1197 TGCAAGATCAAGAAAAATGTATGAACAGAAATGATTGCCATAGAGGCTGCCATAAATCGA 1256

Qy   348 SerValPheThrValSerLeu---------- 354
          ::: |||
Db 1257 AATTCATCTAAATCTCCTTCCATTACCACCAAAGAAAACACGAATTATTTCTCATGTT 1316

Qy   355 TrpAspCysAspArgLysPheArg---ValLysIleArgGlyIleAspIleProValLeu 373
          :::   :::::::::||||
Db 1317 TGGGAAAATAACAACCCTTTCCAAATTGTCTTGGTTAAGGGA------AATAAACTT 1367

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Qy   726 ThrAlaMetLeuHisAspPheThrGlnValGlnLeuTrpAsnVal 745
         :::       |||||
Db  2445 GTGGGGCACATGAAAGTGCTTTCTAAGCAGGTTGAAGCACTCAATAAGTTAAAAACTTTA 2504

Qy   746 Thr-----IleAspIleLysSerLeuSerAlaGluLysTyrArgSerSerGlnVal 763
         :::        ||| :::::::
Db  2505 AATAGTTTAATCAAACTGAATGCCGTGAAGTTAAACAGAGCCAAAGGGAAGGAGGCCATG 2564

Qy   764 IleSerGlnLeuLysGlnLys----------------LeuGluAsnLeuGlnAsnLeuAsn 778
         :::       |||
Db  2565 CATACCTGTTTAAAACAGAGTGCTTACCGGGAAGCCCTTCTGACCTGCAGTCA------- 2618

Qy   779 LeuProGlnSerPheArgValProTyrArgGlyLeuLysLysAlaGluValAlaGlyAlaLeuAlaLeuAlaLeuAlaValIle 798
         :::        :::
Db  2619 ------------CCCCTGACCCCATGTGTTATCCTCCAGAACCTCCATGTT 2657

Qy   799 GluLysCysLysValMetAlaSerLysLysValProLeuTrpLeuGluPheLysLysCysAla 818
         :::::::      ||| :::
Db  2658 GAAAAGTGCAAATACATGGATCCAAAATGAGCCCTTTGTGGCTGGTATAC-------- 2708

Qy   819 AspProThrAlaLeuSerAsnGluThrIleGlyThrIleIlePheLysHisGlyAspAspLeu 838
         :::       |||:::::
Db  2709 AATAACAAGGTATTTGGTGGAGGATTCAGTTGGAGTGATTTTTAAAAATGGTGATGATTTA 2768

Qy   839 ArgGlnAspMetLeuIleLeuGlnIleLeuArgIleMetGluSerIleTrpGluThrGlu 858
         ::::::||||||||||      :::::
Db  2769 CGACAGGATATGTTGACACTCCAAATGTTGGCTTGATGATTTACCTCTGGAAAGAAGCT 2828

Qy   859 SerLeuAspLeuCysLeuLeuProTyrGlyTyrCysIleSerGlyThrGlyAspLysIleGlyMet 878
         |||||||      :::
Db  2829 GGTTTGGATCTTCGGATGTTGCCTTATGGCTGTTTAGCAACAGGAGAGACTCGGCCTC 2888

Qy   879 IleGluIleValLysAspAlaThrThrIleAlaLysIleGln------GlnSerThrVal 896
         ||||||      :::
Db  2889 ATTGAAGTTGTGAGCACCTCTGAAACAATTGCTAAGATCCAGCTGACAGTAGCAATGTG 2948

Qy   897 GlyAsnThrGlyAlaPheLysAspTrpPheLeuValLeuSerHisTrpLeuLysGluLysCysPro 916
         |||||||      :::
Db  2949 GCTGCTGCAGCCTTCAACAAAGATGCCCTTCGAACTGGCTTAAAGATACAACTCT 3008

Qy   917 IleIleGluGluLysPheGlnAlaAlaAlaValGluArgPheValTyrSerCysAlaGlyTyrCys 936
         :::::      :::
Db  3009 GGGGATGAC---CTGGACCGAGCCATTGAAGGATTTACACTGTCTGTGGCTACTGT 3065

Qy   937 ValAlaThrPheValLeuGlyIleGlyIleLeuIleMetIleSerGlu 956
         :::::::||||::::
Db  3066 GTAGCTTCTTATGTCCTTGGGATTGGTACAGACATAGTGACAACATCATCATGTCAAAAAA 3125

Qy   957 ThrGlyLysAsnLeuPheHisIleLeuAspGlyHisIleLeuGluGlyAsnTyrLysSerPheLeu 976
         ||||||      ::::::
Db  3126 ACTGGGCCAGCTGTCCTTCCACATTGGACATATTCTTGGAAATTTCAAATCTAAGTTT 3185

Qy   977 GlyIleLysAsnLysGluArgValProPheValLeuProPheLeuProPheLeuPheValMetGly 996
         |||:::::||      ::::
Db  3186 GGCATTAAAAGGAGGCCAGTGCCTTTTATTCTTACCTATGATTTCATCCATGTCATTCAA 3245

Qy   997 ThrSerGlyLysLysThrSerLeuHisPheGlnLeuAsnIleProPheGlnLeuAsnAspValCysValLysAla 1016
         ||||||::::
Db  3246 CAAGGAAAAACAGAAATACAGAAAAGTTTGGCCGGTTCCGCCAGTGTTGTGAGGATGCA 3305

Qy  1017 TyrLeuAlaLeuArgHisHisThrAsnLeuGluLeuIleLeuPheSerMetMetGly 1036
         ||:::      :::
Db  3306 TATCTGATTTTACGACGGGATATGGGAGTGCCTTTTTATTCATCACTCTTTCGGCTGGACT 3365

Qy  1037 ThrGlyMetProGlnLeuThrSerLysGlyIleAsnIleGluTyrIleArgAspAlaLeuThr 1056
         ||:::::||||      :::
Db  3366 GCCAGGGCCTTCCTGAACTCACATCAGTCAAAGATATCAGTAATCTTAAGGACTCTCTTGCA 3425

Qy  1057 ValGlyLysSerGlnGluAlaLysAlaTyrPheLeuAspGlnIle---GluValCys 1075
         :::::
Db  3426 TTAGGGAAGAGTGAAGAGGAGAACAGCACTCAAACAGTTTAAGCAAAAATTTGATGAGGCGCTC 3485

Qy  1076 ArgAspLysLysGlyTrpThrValGlnPheAsnTrpPheLeuHisLeuValLeuGluGly 1093
```

```
Qy   394 LeuCysGlnArgArgThrSerProLys---ProPheThrGluGluValLeuTrpAsnVal 412
         :::       |||||||
Db  1428 CTGTGTAAAACCATCTAAGCTCAGAGGTATCAGGGAAAAATGATCATATTTGGAATGAA 1487

Qy   413 TrpLeuGluPheSerIleLysPheIleLysLysIleLysAspLeuProLysProGlyGlyAlaLeuAsnLeuGln 432
         ||||||      |||      :::
Db  1488 CCACTGGAATTGATATTAATATTTGTGACTTACCAAGAATGGCTCGATTATGTTTTGCT 1547

Qy   433 IleTyrCysGlyLysLysAlaProAlaLeuSerGlyLysLysThrSerArgAlaGluMetProSerPro 452
         :::      :::
Db  1548 GTTTAT---GCAGTTTGGATAAAGTAAAAACGAAGAAATCAACGAAAACTATTAATCCC 1604

Qy   453 ------------GluSerLysLysGlyGlyLysLysGlnIleLeuGlnIleLeuGlnLeuTyrTyr------ValAsn 465
         |||      :::::::
Db  1605 TCTAAATATCAGACCATCAGGAAAGCTGGAAAAGTGCATTATCCTGTAGCGTGGGTAAAT 1664

Qy   466 LeuLeuLeuIleLeuAspHisArgPheLeuLeuArgHisGlyHisGluTyrTyrValLeuHisMetTrp 485
         :::::::      |||
Db  1665 ACGATGGTTTTTGACTTTAAAGGACAATTGAGAACTGGAGACAATAATATTACACAGCTGG 1724

Qy   486 GlnLeuSerGlyGlyLysGlyGluAspGlnGlySerPheAsnAlaAspLysLeu--------- 502
         ||||||      :::
Db  1725 ---------------TCTTCATTT---CCTGATGAACTCGAAGGAAATG 1754

Qy   503 ------------ThrSerAlaThrArgAsnProAspLysGluAsnSerMetSerIleSer 517
         :::::::      |||
Db  1755 TTGAATCCAATGGGAAGTTGACTTCAAACAATTCCATATACTGAAAATGCAACAGCTTTGCAT 1814

Qy   518 IleLeuLeu--AspAsnTyrCysHisTyrCysIleSerProIleAlaLeuPro------------ 530
         :::      |||
Db  1815 GTTAAAATTTCCAGAGAATAAAAAAACAACCTTATTATTACCTCCCTTCGATAAGATTATT 1874

Qy   531 ---LysHisArgProThrProAspProGluGlyValAspArgAlaArgValAlaArgAlaGluMetProAsn 549
         |||      :::
Db  1875 GAAAAAGGCAGCTGAGATTGCAAGCAGTAGTGATGCTAAATGTGTCAAGTCGAGGTGGAAAA 1934

Qy   550 GlnLeuArgLysGlnLeuAsnLeuGluAlaIleIleGluIleAlaThrAspProLeuAsnProLeuAsnProThrArgAla 569
         ||:::||||      :::
Db  1935 AAGTTTCTCCTGTATTGAAAGAAATCTTGGACAGGGATCCCTTGTCTCAACTGTGTGAA 1994

Qy   570 GluAspLysGlyGluLeuTrpLeuTrpHisPheArgTyrGluSerLeuLys---AspProLysAla 588
         :::      :::
Db  1995 AATGAAAATGGATCTTATTTGGACTTTGCCACAAGACTGCCGAGAGATTTCCCACAATCA 2054

Qy   589 TyrProLysPheSerGlySerValLysSerTrpProGlnIleGlnLeuIleValAlaLysThrTyr 608
         |||||:::      :::
Db  2055 CTGCCAAAATTACTGCTGTCAATCAAGTGGAATAAACTTGAGGATGTTGCT------- 2105

Qy   609 GlnLeuLeuAlaLysAlaArgGluValTrpAspGlnSerAlaLeuAspValGlyLeuThrMet 628
         |||:::      :::
Db  2106 CAGCTTCAGGCGCGTGCTTCAGATTTGGCCTAA------CTGCCCCCGGGAGGCCCTA 2159

Qy   629 GlnLeuLeuAsnPheSerAspCysAsnPheSerAspAspPheGluAsnValArgAlaIleAlaValGlnLeuLysLeu 648
         ||||||      :::
Db  2160 GAGCTTCTGGATTTCAACATCCAGAACCACCAGTACGTTCGAGAATATGCTGTAGGCTGCCTG 2219

Qy   649 GluSerLeuGluAspAspAspAspValLeuHisIleTyrLeuLeuGlnLeuGlnLeuValGlnIleLeuValGlnGlnAlaAlaValLys 668
         :::      |||||||
Db  2220 CGACAGATGAGTGATGAGGAGAACTTTCTCAATATCTTTTACAACTGGTGCAGTGTAAAA 2279

Qy   669 PheGluProTyrHisAspSerPheArgAlaLeuArgPheLeuLeuLysGlyArgGlyLeuArgAsn 688
         :::      |||
Db  2280 TATGAGCCCTTTCCTGATTTGTGCCCTCTCCATTAGAAAAGAGCAACTTGGTAAT 2339

Qy   689 LysArgIleGluHisPheLeuTrpPheTrpPheTrpTrpTrpGlnIleAlaGlnSerArgHis 708
         :::      |||
Db  2340 CGGAGGATAGGCCAGTTTCTATTTGGCATCTTAGGTCAGAAGTG---------CAC 2387

Qy   709 ------------TyrGlnArgGlnPheAlaValIleLeuGluLeuAlaTyrLeuArgValCysGly 725
         :::::::      ||||||
Db  2388 ATTCCTGCTGTCTCAGTACAAATTTGGTGTCATCCTTGCAAGCATAACTGCCGGGGA---AGT 2444
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Db    3486 AGGGACAAGCT-GGACTACTAAAGTTGAACTGGATGGCCACACAGTTCCGGGA 3538
               ||||||||                  ::::::||||         |||       |||
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RESULT 10
US-10-092-219-1
; Sequence 1, Application US/10092219
; Publication No. US20020115114A1
; GENERAL INFORMATION:
; APPLICANT: Domin, Jan
; TITLE OF INVENTION: No. US20020115114Ale1 Lipid Kinase
; FILE REFERENCE: 1064HG/50947
; CURRENT APPLICATION NUMBER: US/10/092,219
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: PCT/GB98/00244
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 09/355,160
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 9701652.1
; PRIOR FILING DATE: 1997-01-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
;
; SEQ ID NO 1
; LENGTH: 5061
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(5058)
; OTHER INFORMATION:
US-10-092-219-1

Alignment Scores:
Pred. No.:   Length: 5061
Score: 3.01e-114   Matches: 309
Percent Similarity: 1074.00   Conservative: 178
Best Local Similarity: 45.60%   Mismatches: 343
Query Match: 28.93%   Indels: 238
DB: 18.55%   Gaps: 32
                    14

US-09-974-573-1 (1-1102) x US-10-092-219-1 (1-5061)

Qy   194 LysLeuTyrAlaMetHisProTrpValThrSerLysProLeuProGluTyrLeuLeuLys 213
              |||| ||::| ::: ||||||||
Db   1168 AAATTGAAGACCAACAAATTTCCATATACCAATCACCGCACCAAACCCAGGCTATTTGTTAAGT 1227

Qy   214 LysIleThr--------AsnAsnCysValPheIleValIleHisArgSerThrThrSer 230
              ||||||| :::||| |:::|:|:|||||:::::::||||::
Db   1228 CCAGTCACACAGCGCAAAGAAACATATGC----------------------GGAGAAAAT 1263

Qy   231 GlnThrIleLysValSerAlaAspAspThrProGlyThrIleLeuGlnSerPhePheThr 250
              ::|:||||||||||||||||::|||| |||||||||:|:
Db   1264 GCTAGTGTGAAGGTCCATT--GACATTGAAGGATTCAGTCACCAGTTACTTTTACG 1320

Qy   251 ----------------------LysMetAlaLysLysSerLeuMetAspIleProGlu 263
                                     :::|| ||| ::: :::
Db   1321 TGTGATGTGAGTTCTACTGTAGAAATCATTATAATGCAAGCCCCTTTGCTGGGTACATGAT 1380

Qy   264 SerGlnAsnGluArgAsp----------PheValLeuArgValCysGlyArgAspGluTyr 280
              ::::||| :::|:||:||:|:|:||||||||||:::
Db   1381 GACTTGAATCAAGTAGATGATGTTGGCAGCTATGTTCTAAAAGTTTGTGGTCAAGAGGAAGTG 1440

Qy   281 LeuValGlyGluThrProIleLysPheLysAsnPheGlnTrpValArgGlnCysLeuLysAsnGly 300
              ||| ||| :::: :::|:
Db   1441 CTGCAGAATAATCATTGCTTGGAAGTCATGAGCATATTCAAAAACTGTCGAAAATGGGAC 1500

Qy   301 GluGluIleHisLeuValLeu------------------------- 307
              ||||||:|||||:
Db   1501 ACAGAAAATTAGACTACAACTCTTGACCTTCAGTGCAATGTCAAAATCTGGCCGAACA 1560

Qy   308 AspThrProProAspProAlaLeuAspGluValArgLysGluGluTrp 323
              ::|||||||::| :|: :::
Db   1561 GCAGAAGATGATGAAACAAACACCCGTGGAT--------TTAAACAAAACCTGTAT 1605
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Right column (Qy/Db continuation):

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Qy    324 ProLeuValAspAspCysThrGly-----------------------ValThr 333
              :::||
Db   3486 CAAATAGAAAAAACCTGCAAAGAAGCCATGACGAGCAGCACCCTGTGAAGAACTCTTAGAT 1665

Qy    334 GlyTyrHisGluGln------------------LeuThrIleHisGlyLysAspHis------ 346
              ||||| |||                         |||  |||              :::
Db   1666 TCTTATCACACCAAGTAGACTGGCTTCAAATTGAAAACACCAGCAGTAGAT 1725

Qy    347 ----------------------------GluSerValPheThrValSer 353
                                         |||
Db   1726 CAAGTAATTAAAGTGTAAGAAAAATCTGTAGTGCTTTAGATGGTGTCGAGACTCTTGCC 1785

Qy    354 LeuTrpAspCysAspArgLysPheArgValLysIleArgGlyIleArgAspIleProValLeu 373
              ::::  |||              :::                 ||||||||
Db   1786 ATTACAGAATCAGTAAGAAAGCTAAAG--------AGAGCAGTAATCTTCCA---AGG 1833

Qy    374 ProArgThrAlaAspLeuThrValPheVal---------------------- 383
              |||||||||||:::
Db   1834 AGTAAAACTGCTGATGGACTTCTTTGTTGGAGGAGAAGACACTAGCAGGAGTTCAACT 1893

Qy    384 ----GluAlaAsnIleGlnTyrGlyGlnGlnLeuCysGlnArgArgThr-- 399
                   |||||
Db   1894 AGGGGTCACTTAATCCTGAAAATCCTGTCAAGTAAGCATAAACCAATTAACTGCAGCA 1953

Qy    400 -----------------------------SerPro---------------------------- 400
                                           |||||
Db   1954 ATTTATGATCTTCTCAGACTCCATGCAAATTCTGGTAGGAGTCCTACAGACTGTGCCCAA 2013

Qy    401 ------------------------------------------------------- 401
Db   2014 AGTAGCAAGAGTGTCAAGGAAGCATGGACTACAACAGAGCAGCTCCAGTTTACTATTTT 2073

Qy    401 ------------------------------LysProPheThrGluGluValLeuTrpAsnValTrpLeuGluPheSerIleLysIle 420
                                           |||  ::::|||||||
Db   2074 GCTGCTCATGGAATTTCAAGTAATGGGTATCAAATTAAAAATTATGAAAAATACTACTGATATGT 2133

Qy    402 --LysProPheThrGluGluValLeuTrpAsnValTrpLeuGluPheSerIleLysIle 420
              |||  ::::|||||||                     |||:::
Db   2194 TACAAGAATTTCTTCATCTTATTAAATGGGATGAACTAATCATTTTCCTATCCAGATA 2253

Qy    421 LysAspLeuProLysGlyValIleLeuAlaLeuAsnLeuGlnIleTyr-----CysGlyLysAla 438
              |||||:||::||                                      ::::::
Db   2254 TCACAATTGCCATTAGAATCAGTTCCTCACCTTACTCTTTTTGGAATTTAAATCAGAGC 2313

Qy    439 ProAlaLeuSerGlyLysLysThrSerAlaGluMetProSerProGluSerLysGlyLysAla 458
              :::|:|                       |||:::::|||||||
Db   2314 AGTGGAAGTTCCCCTGATTCTAATAGCAGAGAAAGGGACCAGAAGCTTTGGGCAAA--- 2370

Qy    459 GlnLeuLeuTyrTyrValAsnLeuLeuIleLeuAspHisArgPheLeuLysArgHisGly 478
              ||||||                                 :::
Db   2371 ------------GTTTCCTTACCTCTTTGTGACTTTGACGGTTTTTAACATGTGGA 2415

Qy    479 GluThrValLeuHisMetTrpGlnLeuSerGlyLysGlyGluArgProGluSerPheAsn 498
              |||:::::||                                      ||||||
Db   2416 ACTAAACTTCTATATCTTTGGACTTCATCA------------------------------ 2445

Qy    499 AlaAspLysLeuThrSerAlaThrAsnProAspLysGlyGluAsnSerMetSerIleSerIle 518
                                                      :::::::::
Db   2446 ----------------------CATACAAATTCTGTTCCTGGACAGTT 2472

Qy    519 LeuLeuAspAsnTyr---CysHisProIleAlaLeuProLysHisArgProThrPro--- 536
              |||:::                                    ::|:::
Db   2473 ACCAAAAAAGGATAGTCATGGAAAGATAGTGTCACAGGTTGATTTTCCTTCCTCTGCA 2532

Qy    537 ------------------------------AspProGluGlyAspValArgAlaGlu----- 546
                                           ::|||:
Db   2533 TTTGATTATTATTATACAACTCCTCAGTTGACAGAAGCATTATACAGCAACATAACTTA 2592

Qy    547 MetProAsnGlnLeuArgLysGlnLeuArgLeuGluAlaIleIleAlaThrAspProLeu 564
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RESULT 11
US-09-205-658-47
; Sequence 47, Application US/09205658
; Patent No. US2001029617A1
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; APPLICANT: Ogg, Scott
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
; FILE REFERENCE: 00786/351004
; CURRENT APPLICATION NUMBER: US/09/205,658
; CURRENT FILING DATE: 1998-12-03
; EARLIER APPLICATION NUMBER: 08/857,076
; EARLIER FILING DATE: 1997-05-15
; EARLIER APPLICATION NUMBER: 08/888,534
; EARLIER FILING DATE: 1997-07-07
; EARLIER APPLICATION NUMBER: US98/10080
; EARLIER FILING DATE: 1998-05-15
; SOFTWARE: FastSEQ for Windows Version 4.0
; NUMBER OF SEQ ID NOS: 328
; SEQ ID NO 47
; LENGTH: 3504
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
US-09-205-658-47

Alignment Scores:
Pred. No.:
Score: 7.99e-110   Length: 3504
                            1034.00   Matches: 313
Percent Similarity: 46.96%   Conservative: 227
Best Local Similarity: 27.22%   Mismatches: 400
Query Match: 17.86%   Indels: 210
DB: 9   Gaps: 44

US-09-974-573-1 (1-1102) x US-09-205-658-47 (1-3504)

```
Qy   369  AspIleProValLeuProArgThrLeuAspLeuThrValPheValGluAlaAsnIleGln  388
                 |||    |||        ::::  :::
Db  1273  ------------------GACTGGAATGTACGTTCGAATCGAATTCAGTGTATAT       1323

Qy   389  TyrGlyGlnValLeuCysGlnArgArgThrSerProLysProPheThrGluGluVal     408
                 |||       ||| :::
Db  1324  GTGGGGGACACTGACGCTGGCATCAAAATCTCACAACA---AAAGTGAATGCTCAATTGCA 1380

Qy   409  LeuTrpAspValTrpLeu---GluPheSerIleLysIleLysAspLeuProLysGlyAla  427
                 ||| :::::
Db  1381  AAAATGGAATAAGGAAATGTACACTTTGATCTATACATGAAGGAATGCCACCATCTGCA   1440

Qy   428  LeuLeuAsnLeuGlnIleTyrCysGlyLysLysAlaProAlaLeuSerGlyLysThrSerAla 447
                 :::::::||    |||||
Db  1441  GTACTCAGCATTCGTGTTGTTACGGAAA------------------------GTG       1473

Qy   448  GluMetProSerProGluSerLysGlyLysLysAlaGlnLeuTyrTyrValAsnLeuLeu  467
                 :::      :::
Db  1474  AAATTAAAAGTGAAGAATTCGAA---------GTTGGGTAAATATGTCC             1518

Qy   468  LeuIleAspHisArgPheLeuLeuArgHisGlyGluTyrValLeuHisSerMetTrpGlnLeu 487
                 |||       |||
Db  1519  CTAACCGATTGGAGATGAGTACGACAAGACAATTTTATTCCATCTGTGG------        1572

Qy   488  SerGlyLysGlyGluAspGlnGlnGlySerPheAsnAlaAspLysLeuThrSerAlaThrAsn 507
                 |||                :::      :::
Db  1573  -------------------------GTCCCTGAACCGACTGCCAATCGTAGT          1599

Qy   508  ProAspGluAsn------------------SerMetSerIleSerLeuLeuLeuAsp      521
                 :::                :::
Db  1600  AGGATCCGAGAAAATGGAGCAAGGATAGGCCACCAACGCGGTTACAATTGAAATCTCA    1659

Qy   522  AsnTyrCysHisProIleAlaLeuPro-----------------------LysHis      532
                 :::::::||
Db  1660  AGTTATGGTGGTAGAGTTCAGAGTCCGAGTGCAAGGACAATACACATATCTCGTCAGCAC  1719

Qy   533  Arg--------------ProThrProAspProGluGlyValArgGlyAlaGluMetPro   548
                 |||       :::
Db  1720  CGAAGTACTTGGACGGAAACTTGAATAATATGGGTGATGACTATGTGTCGTGTATCAGA   1779

Qy   549  AsnGlnLeuArgLysAlaGlnLeuGlnLeuAlaIleAlaIleLeuAlaThrAspProLeuAsnProLeuThr 568
                 :::
Db  1780  GATCCAGGAATATAAGAGCTTCAGATGCTTGTCAGGAAGCATGAATCTGGAATTGTATTA  1839

Qy   569  AlaGluAspLysGlu--------LeuLeuTrpIleHisPheArgTyrGluSerLeuLysAsp 585
                 :::::::
Db  1840  GAGGAAGATGAACAACCATGTCGATGTGGAG---AGATACATTCAAAAGCAGGAG        1896

Qy   586  ProLysAlaTyrProLeuPheSer---SerValLysTrpGlyInGlnIleVal        604
                 |||||| :::::::
Db  1897  CCTGATTTGCTCATTGTGCTCTTCCGAACTCGGCATTGTGTGTGGACTGGTGAGAACTT   1956

Qy   605  AlaLysThrTyrGlnLeuLeuLeuAspGlu------ArgGluValTrpProGlnSerAlaLeuAspVal 624
                 :::
Db  1957  TCCGAGCTCATGTGATGCTTGAAAAA--------TGGAAACCGCCGAGTGTGCAGCC     2007

Qy   625  GlyLeuThrMetGlnLeuLeuLeuAspGlu------AspCysAsnPheSerAspCysAsnPheArgAlaIleAla 644
                 ::: :::
Db  2008  GCGTTGACT--------TTGCTTGGAAAAGTTGCACGGATCGTGATTCGAAGTTTGCA    2061

Qy   645  ValGlnLysLeuGluLysLeuGluLeuGlnAspAspValLeuHis---TyrLeuGlnLeu  663
                 :::
Db  2062  GTGGAGAAGTTGAATGACGACAGCTGAGCCCGGTCACATTCCATCTTTCATATTGCCTCTC 2121

Qy   664  ValGlnAlaValLysPheGluProTyrHisAspSerAlaLeuAlaArgPheLeuLeuLeuLys 683
                 ||||:::
Db  2122  ATACAGGCGTTGGAAGTACGAACCGGTCGTACCGGGTTGGAATGATGCTCTTGACT      2181

Qy   684  ArgGlyLysArgAsnLysLysArgIleGlyHisLeuPheLeuTrpPheLeuArgLeuSerGluIle 703
                 :::
Db  2182  AGAGCCTCTGCGATTATCGAATTGGAACATCGACTTTCTGCGTCTCCGTGACGAGATT    2241

Qy   704  AlaGlnSerArg--------------------HisTyrGlnArgPheAlaValIleLeuLeu 717
```

```
Qy    78  AlaLeuGluThrSerValSerAlaAlaAspPheTyrHisArgLeuGlyProAspHisPheLeu 97
                 ::::::      :::
Db   265  TCGCTAGAAATCAAGCTATCA---GATTTCAAACATCAACTT                     309

Qy    98  LeuLeuTyrGlnLysLysGlyInTrpTyrGluIleTyrAspLysTyrGlnValValGln    117
                 |||||       :::
Db   310  TTGATTGCTCCGATGAAGTGGGGAACATATTCCGTAAAGCCACAGGATTATGTGTTCAGA   369

Qy   118  ThrLeuAspCysLeuArgTyrTrpLysTrpLeuHisArgSerProGlyGlnIleHisVal   137
                 ||| :::::
Db   370  CAGTTGAATAATTTCGGCAAATGAAGTTATATTAACGACGATCAACCCCTGTCGAAA      429

Qy   138  ValGlnHisArgHisAlaProSerGluGluThrGluThrLeuAlaPheGln-----      151
                 :::::||
Db   430  TTAGAGCTCCACGCCACTTCCCAATGCTTTTCTCTACCAACCTGATGGAATAAAACAGG   489

Qy   152  -----ArgGlnLeuAsnAlaAlaLeuIleGlyTyrAspValThrAspValSer         166
                 :::
Db   490  GATAAAGAATTAATGAGTGATATAAGTCATTGTCTAGGATACTCACTGGATAAACTGGAA   549

Qy   167  AsnValHisAspAspGluLeu---GluPhe----------ThrArgArg             178
                 ||||:::
Db   550  GAGAGGCCTCGATGAGGAACTCCGTCAATTTCGTGCTTCTCTCTGGCGTCGTACGAAGAAA 609

Qy   179  ArgLeuValThr-----------                                       182
                 |||
Db   610  ACGTGCTTGACACGTGGACTTGAGGGTACCAGTCACTACGCGTTCCCCGAAGAACAGTAC  669

Qy   183  -------------ProArgMetAlaGluValAlaGlyLysArgAspProLysLeu       195
                 ||||:||||
Db   670  TTGTGTGTGGTGAATGCGTGCCCGAAAGATTTGGAATCAAAAGTCAAGGCTGCCAAGCTG  729

Qy   196  TyrAlaMetHisProTrpValThrSerLysProLeuProGluTyrLeuLeuLysLysIle  215
                 :::
Db   730  AGTTATCAGATGTTTTGGGAAAACGTAA----------GCGGAAATC               768

Qy   216  ThrAsnAsnCysValPheIleValIleHisArgSerThrThrSerGlnThrLysVal     235
                 :::
Db   769  AATGGAGTTTGC-------------GAGAAAATGATGAAGAATTCAAATTGAATTC       810

Qy   236  SerAlaAspThrProGlyThrIleLeuGlnSerPhePheThrLysMetAlaLysLys     255
                 :::::|||||
Db   811  AATCCGAACGAAATCTCCGAAATCTCTGCTTCACACGTTTCTTCTCTACGAAATGCGAAAA-- 867

Qy   256  LysSerLeuMetAspIleProGluSerGlnAsnGluArgAsp------PheValLeuArg  273
                 :::
Db   868  ---------TTGGATGTATACGATACCGATGATCCTGCAGATGAAGGATGGTTTCTTCAA   918

Qy   274  ValCysGlyArgAspGluTyrLeuValGly--GluThrProLeuLysAsnPheGlnTrp   292
                 ||||:::::::
Db   919  TTGGCTGGACGTACCACGTTTGTTACAAATCCAGAATGTCAAACTTACGTCTTATGATGGT 978

Qy   293  ValArgGlnCysLeuLysAsn------------GlyGluIleHis----------Leu    305
                 :::
Db   979  GTCCGTTCCGAAGACTGGAAAGCTATCGATGCCCTTGGATTCGTTGTTCCGCGACAATCACTA 1038

Qy   306  ValLeuAsp----------ThrProProAspProAlaLeuGlu----ValArgLysGlu   321
                 :::::|||||
Db  1039  GTCCTCAAAGACTATTGTCGCCCAAAACCACTTACGAACCACCATTATGTGAGAGCACAC  1098

Qy   322  GluTrpProLeuValAlaAspCysTyrGlyValThrGlyTyrHisGluLeuThrIle     341
                 :::
Db  1099  GAACGAAAACTTGCTCTAGACGTGCTCTAGACGTGTCT-----ATAGATAGCACACCAAAA 1152

Qy   342  HisGlyLysAspHisGluSerValPheThr---                            351
                 ||||:::::
Db  1153  CAGAGCAAGACAGTGACATGGTTATGACTGATTTTCGTCGACAGCTTCACTCAAACAA    1212

Qy   352  ValSerLeuTrpAspCysAspArgLysPheArgValLys-------IleArgGlyIle   368
                 ||||:::::
Db  1213  GTTTCACTTTGGGACCTTGGGACCTTTATGATACGGCGTGTGATAATTTTCTGGATTC    1272
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Db  2242  |||::::          |||                 :::::|||
          GCTCGTTGAGAGATTGTGATCTGAAAAGTGAAGAAATATCGCCGTATCCACTTCTGATG  2301

Qy   718  GluAlaTyrLeuArgGlyCysGlyThrAlaMetLeuHisAspPheThrGlnGlnValGln  737
          |||||||||:::||||         :::
Db  2302  GAAGCTTACCTCCGTGGA---AATGAAGAGGCACATCAAGATCATCACCCGACAAGTTGAC  2358

Qy   738  ValIleAspMetLeuGlnLysValThrIleAspIleLysSerLeuSerAlaGluLysTyr  757
          :::||||   :::||:        |||
Db  2359  ATGGTTGATGAGCTCACACGACTCAGCACTCTTGTCAAAGGAATGCCAAAA---------  2409

Qy   758  AspValSerSer--------GlnValIleSerGlnLeuLysGlnLysLeuGluAsn  773
          |||:::          :::                    :::|||||||||
Db  2410  GATGTTGCTACGATGAAACTGCGTGACGAGCTTCGATCGATTAGTCATAAAATGGAAAAT  2469

Qy   774  LeuGlnAsnLeuAsnLeuProGlnSerPheArgValProTyrAspProGlyLeuLysAla  793
          :::              |||||||||
Db  2470  ATGGATTCT--------------------------CCACTCGGATCCTGTGTACAAACTG  2502

Qy   794  GlyAlaLeuValIleGluLysCysLysValMetAlaSerLeuLysLysLysProLeuTrpLeu  813
          |||||||          :::||:||||
Db  2503  GGTGAAATGATAATCGACAAAGCCATCGTCCTAGGAGTGCAAAACGTCCGTTAATGCTT  2562

Qy   814  GluPheLysCysAlaAspProThrAla---LeuSerAsnGluThrIleGlyTyrIleIlePhe  832
          :::|||       :::       |||
Db  2563  CACTCGGAAGAACAAAAATCCAAAGAGTGACCTGCACCTTCCGTTCTGTGCAATGATCTTC  2622

Qy   833  LysHisGlyAspAspLeuArgGlnAspMetLeuIleLeuLeuArgIleMetGlu  852
          |||||||||                :::
Db  2623  AAGAATGGAGACGATCTTCGCCAGGACATGCTGTTTCTTCAAGTTCTCGAAGTTATGGAT  2682

Qy   853  SerIleTrpProGluThrGluSerLeuAspLeuCysLeuLeuProTyrGlyCysIleSerThr  872
          :::|||||||:::||     :::||:
Db  2683  AACATCTGGAAGGCTGCAAACATTGATTGCTGTTGAACCCGTACGCAGTTCTTCCAATG  2742

Qy   873  GlyAspLysIleGlyMetIleGlyLeuIleValLysAspAlaThrThrIleAlaLysIleGln  892
          |||||||||:::|||||              :::
Db  2743  GGAGAAAATGATTGGAATTATTGAAGTTGTGCCTAATTGTAAAACAATATTCGAGATTCCA  2802

Qy   893  GlnSerThr---ValGlyAsnThrGly------AlaPheLysAspGluValSerHis  909
          :::              :::
Db  2803  GTTCGAACAGAGGATTCATGAATACAGCAGTTCGGAGTATTGATCCTTCGTTTATGAATAAG  2862

Qy   910  TrpLeuLysGluLysCysProIleGluGlu--------  919
          :::||||          :::
Db  2863  TGGATTCGGAAACAATGCCGGAATTGAAGATGAAGAGAAAAAGCAAAAAGGACTCTACG  2922

Qy   920  --------LysPheGlnAlaAla  924
                          |||
Db  2923  AAAAATCCCATCGAAAAGAAGAGAGATTGATAATACTCAAGCCATGAAGAGARATATTTTGAAGT  2982

Qy   925  ValGluArgPheValTyrSerCysAlaGlyTyrCysValAlaThrPheLeuLeuGlyIle  944
          ||||:::||||:::|||||       |||||:::
Db  2983  GTCGGATCGGATTCCTATACTCGTGTTGTTGGATATTCAGTTGCCACGTACATAATGGGAATC  3042

Qy   945  GlyAspArgHisAsnAspAsnIleMetLeuSerGlyThrGlyAsnLeuPheHisIleAsp  964
          |||||||||:::
Db  3043  AAGGATCGTCACGGTAATAATCTGATGTCCACTGGAGATGGAAAATATGTCCACATTGAT  3102

Qy   965  PheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLysGluValProIle  984
          |||||||||:::|||||       :::|||
Db  3103  TTCGGTCACATTTTGGGACACGGAAAAGACCAAACTTGGAGGTCCAGCGGATCGTCAACCCG  3162

Qy   985  PheValLeuThrProAspPheLeuValMet-----GlyThrSerGlyLysLysThr  1002
          |||||||       :::|||
Db  3163  TTTATTCTAACCGAACACTTTATGACAGTGATTCGATTCGATCGGGTAAATCTGTGGATGGAAAT  3222

Qy  1003  SerLeuHisPheGlnLysPheGlnAsnLysPheValCysValLysAlaTyrLeuAlaLeuArgHis  1022
          ||||:::          :::|||
Db  3223  TCGCATGAGCTACAAAAATTCAAAACGTTATGCGTCGAAGCCTACGAAGTAAATGTGGAAT  3282

Qy  1023  HisThrAsnLeuIleIleLeuLeuPheSerMetMetLeuThrGlyMetProGlnLeu  1042
          :::  :::      |||||||||
Db  3283  AATCGAGATTGTTCGTTCCTTGTTCACCTGATGCTCGGAATGGAGTTGCTGAGCTG  3342
```

```
Qy  1043  ThrSerLysGluAspGlnTyrIleArgHisAspAlaLeuThrLeuGln---GlyLysSerGlu  1061
          ||||:::|||                                    |||
Db  3343  TCGACGAAAGCGGATTGGATCATTGAGAGAAAAACCCTTCTGCAATGGAGAAAGCAAA  3402

Qy  1062  GluAspAlaLysLysTyrPheLeuAspLysGlnIleIleGluValCysArgArgAspLysTrpThr  1081
          |||:::|||                    :::|||
Db  3403  GAAGACGCAGAAAGTTTTTCGCTTGGAATCTACGAAGAAGCCTTCAATGGATCATGGTCT  3462

Qy  1082  ValGlnPheAsnTrpPheLeuHisLeuVal  1091
          :::|||
Db  3463  ACCAAAACGAATTGGCTCTTCCACGCAGTC  3492
```

RESULT 12

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US-09-844-353A-47
; Sequence 47, Application US/0984353A
; Patent No. US2002003758SA1
; GENERAL INFORMATION:
;  APPLICANT: Ruvkun, Gary
;  APPLICANT: Kimura, Koutarou
;  APPLICANT: Patterson, Garth
;  APPLICANT: Ogg, Scott
;  APPLICANT: Paradis, Suzanne
;  APPLICANT: Tissenbaum, Heidi
;  APPLICANT: Morris, Jason
;  APPLICANT: Koweek, Allison
;  TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
;  TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
;  FILE REFERENCE: 00786/351005
;  CURRENT APPLICATION NUMBER: US/09/844,353A
;  CURRENT FILING DATE: 2001-04-27
;  PRIOR APPLICATION NUMBER: US 08/857,076
;  PRIOR FILING DATE: 1997-05-15
;  NUMBER OF SEQ ID NOS: 114
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 47
;  LENGTH: 3504
;  TYPE: DNA
;  ORGANISM: Caenorhabditis elegans
US-09-844-353A-47

Alignment Scores:
Pred. No.:                                   Length:            3504
Score:                 7.99e-110             Matches:            313
                       1034.00               Conservative:       227
Percent Similarity:    46.96%                Mismatches:         400
Best Local Similarity: 27.22%                Indels:             210
Query Match:           17.86%                Gaps:                44
DB:                    9

US-09-974-573-1 (1-1102) x US-09-844-353A-47 (1-3504)
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```
Qy   78  AlaLeuGluThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeu  97
         ::||||||          :::|||
Db  265  TCGCTAGAAATCAAGCTATCA---GATTTCAAACATCAACTT-----------TTCGAA  309

Qy   98  LeuLeuTyrGlnLysGlyGlnTrpTyrGluIleTyrArgLysValValGln  117
         :::||||||:::||
Db  310  TTGATTGCTCCGATGAGGTGGGAACATATTCCGTAAAGCCACAGGATTATGTGTTCAGA  369

Qy  118  ThrLeuAspCysLeuArgTyrTrpLysValLeuHisArgSerProGlyIleHisVal  137
         ::||||||          |||
Db  370  CAGTTGATAATTCGGCAGAAATTGAAGTTATATTAACGACGATCAACCCCTGTCGAAA  429

Qy  138  ValGlnArgHisAlaProSerGluGluThrLeuAlaPheGln-----------  151
         :::|||
Db  430  TTAGAGCTCCACGGCACTTTCCCAATGCTGTTTTCTCACCAACTGATGGAATAAAACAGG  489

Qy  152  -----------ArgGlnLeuAsnAlaLeuLeuGlyTyrAspValThrAspValSer  166
                    :::
Db  490  GATAAAGAATTAATGAGTGATATAAGTCATTGTCTAGGATAAGTCATTGATAAAACTGGAA  549

Qy  167  AsnValHisAspAspGluLeu--GluPhe  178
         :::  :::                |||
```

```
Db  1519  CTAACCGGTTGGAGAGATGACTACGACAAGGACAATTTTATTCCATCTGGG------  1572
                ||||:::||||||                    ||||||||
Qy   488  SerGlyLysGlyGluAspGlnGlySerPheAsnAlaAspLysLeuThrSerAlaThrAsn  507

Db  1573  ------------------------------------------GCTCCTGAACCGACTGCCAATCGTAGT  1599
Qy   508  ProAspLysGluAsn---                                 SerMetSerIleSerIleMetLeuAsp  521

Db  1600  AGGATCGAGAAAATGGAGCAAGGAATAGGCACCAACCAGCCGGTTACAATTGAAATCTCA  1659
                                                        :::
Qy   522  AsnTyrCysHisProIleAlaLeuPro------                 LysHis  532

Db  1660  AGTTATGGTGGTAGAGTTCGAATGCCAGGTCAAGGACAATACACATATCTCGTCAAGCAC  1719
                :::|||
Qy   533  Arg------                    ProThrProAspProGluGluValAspValAlaArgArgValAlaGluMetPro  548

Db  1720  CGAAGTACTTGGACGGAAACTTTGAATATTATGGGTGATGACTATGAGTCGTGTATCAGA  1779
Qy   549  AsnGlnLeuArgLysGlnLeuGluAlaIleIleIleAlaThrAspProLeuAsnProLeuThr  568

Db  1780  GATCCAGGATATAGGAAGCTTCAGATGCTTGTCAGGACATGAAATCGGAATTGTTATTA  1839
                :::                ::::::::
Qy   569  AlaGluAspLysGlyGlu------                 LeuLeuTrpHisPheArgTyrGluSerLeuLysAsp  585

Db  1840  GAGGAAGATGAACAACGTCATGTCTGGATGGGAGG--                AGATACATTCAAAAGCAGGAG  1896
                |||                :::
Qy   586  ProLysAlaTyrProLysLeuPheSer------                 SerValLysTrpGlyGlnGluLeuVal  604

Db  1897  CCTGATTGCTCATTGTGTCCGACTCGGACTGGATCGTGGAGAACTTT  1956
                :::
Qy   605  AlaLysThrTyrGlnLeuLeuAlaLysArgGluValTrpAspGlnSerAlaLeuAspVal  624

Db  1957  TCCGAGCTCTATGCTTGAAAA--                TGGAAACCGCCGAGTGTGGCAGCC  2007
                ||||
Qy   625  GlyLeuThrMetGlnLeuLeuAspCysAsnPheSerAspGluAsnValArgAlaIleAla  644

Db  2008  GCGTTGACT------                TTGCTTGGAAAACGTTGCACGGATCGTGTGATTCGAAAGTTTGCA  2061
                :::
Qy   645  ValGlnLysLeuGluSerLeuGluAspAspAspValLeuHis---                TyrLeuLeuGlnLeu  663

Db  2062  GTTGGAGAAGTTGAATGAGCAGCTGAGCCCGGTCACATTCCATTCCATCTTTCATATTGCCTCTC  2121
Qy   664  ValGlnAlaValLysPheGluProTyrHisAspSerAlaLeuAlaArgPheLeuLeuLys  683

Db  2122  ATACAGGCGGTTGAAGTACGAACCGCGTGCTCAATCGGAAGTTGGAATGATGTCTTGACT  2181
Qy   684  ArgGlyLeuArgAsnLysArgIleArgIle------                GlnValIleSerGlnLeuAsn  703

Db  2182  AGAGCCTGCTGGATTATCGAATTGGACATCGATCTTTCTGCTGCTCCGCTGCAGAGATT  2241
                :::                :::
Qy   704  AlaGlnSerArg------                HisTyrGlnArgPheAlaValIleLeu  717

Db  2242  GCTCGTTGAGAGATTGGATCTGAAAAGTGAAGAAGATATCGCGTATCTCACTTCTGATG  2301
                :::::::::
Qy   718  GluAlaTyrLeuArgGlyCysGlyGlyThrAlaMetLeuHisAspPheThrGlnGlnValGln  737

Db  2302  GAAGCTTACCCTCCGTGGA--                AATGAAGAGACAATCAAGAATCATCACCCGACAAGTTGAC  2358
Qy   738  ValIleAspMetGlnLeuGlnIleGlyValAsnValThrIleAspIleLysSerLeuSerLysTyr  757

Db  2359  ATGGTTGATGAGCTCACCACGAATCAGCACTCTTGTCAAGGAAATGCCAAA------  2409
                ::::::
Qy   758  AspValSerSer------                GlnValIleSerGlnIleLeuLysGlnLeuGluAsn  773

Db  2410  GATGTTGCTACGATGAAACTGCGTGACGAGCTTCGATCGATTAGTCATAAAATGGAAAAT  2469
Qy   774  LeuGlnAsnLeuAsnLeuProGlnSerPheArgValProTyrAspProGlyLeuLeuLysAla  793

Db  2470  CCACTGGATCCTGTGTACAACTG  2502
                :::::
Qy   794  GlyAlaLeuValIleGluLysCysLysValMetAlaSerLysLysProLeuTrpProLeu  813

Db  2503  GGTGAAATGATAATCGACAAAGCCATCCTCCTAGGAGTGCAAAACGTCCGTTAATGCTT  2562
```

```
Db   550  GAGAGGCCTCGATGAGGAACTCCGTCAATTTCGTGTCTTCTCTCTCGGGCGTCGTACGGAAGAAA  609
                ||||:::|||||||                    |||||
Qy   179  ArgLeuValThr------  182

Db   610  ACGTGCTTGACACGTGGACTTGAGGTACCAGTCACTACGGCGTTCCCGAAGAACAGTAC  669
                |||||::                :::
Qy   183  ------                ProArgMetAlaGluValAlaLaGlyArgAspProLysLeu  195

Db   670  TTGTGTGTGGTGAATCGTCCCGGAAGATTTGGAATCAAAAGTCAAGGCTGCCAAGCTG  729
                :::
Qy   196  TyrAlaMetHisProTrpValThrSerLysProLeuProGluTyrLeuLeuLysLysIle  215

Db   730  AGTTATCAGATGTTTTGGAGAAAACGTAAA------                GCCGAAATC  768
                ::|||
Qy   216  ThrAsnAsnCysValPheIleValIleHisArgSerThrSerGlnThrIleLysVal  235

Db   769  AATGGAGGTTGC------                GAGAAAATGATGAAGAGATTCAAAATTGAATTC  810
                |||:::
Qy   236  SerAlaAspAspThrProGlyThrIleLeuGlnLeuSerPhePheThrLysMetAlaLeuLys  255

Db   811  AATCCGAACGAAAACTCCGAAATCTCTGCTTCACACGTTTCTCTACGAAATGCGAAAA---  867
                :::::::::                ::::::
Qy   256  LysSerLeuMetAspIleProGluSerGlnInArgGluArgAsp------                PheValLeuArg  273

Db   868  ------                TTGGATGTATACGATCCGATGATCCTGCAGATGAAGAGATGGTTTCTTCAA  918
                |||                :::
Qy   274  ValCysGlyArgAspGluTyrArgLeuValGly---                GluThrProIleLysAsnPheGlnTrp  292

Db   919  TTGGGCTGGACTACCACGTTTTGTTACAAATCCAGATGCTAAACTTACGTCTTATGATGGT  978
                :::::::
Qy   293  ValArgGlnCysGluLeuLysAsn------                GlyGluGluIleHis------                Leu  305

Db   979  GTCCGTTCCGGAACTGGAAAGCTAATCGATGCCCTGGATTCGTTGTTCGCCGACAATCACTA  1038
                |||||||
Qy   306  ValLeuAsp------                ThrProAlaAspProAlaLeuAspGlu------                ValArgLysGlu  321

Db  1039  GTCCTCAAAGACTATTGTGTCGCCCAAAAACCACTCACGAACCACCATTATGTGAGAGCACAC  1098
Qy   322  GluTrpProLeuValAspCysAspThrGlyValThrGlyValThrTyrHisGluGlnLeuLeuThrIle  341

Db  1099  GAACGAAAACTTGCTCTAGACGTGCTCAGCGTGTCT------                ATAGATAGCACACCAAAA  1152
                :::
Qy   342  HisGlyLysAspHisGlySerValPheThr------  351

Db  1153  CAGACCAAGAACAGTGACATGGTTATGACTGATTTTCGTCCGACAGCTTCACTCAAACAA  1212
Qy   352  ValSerLeuTrpAspCysAspAspArgLysPheArgValLys------                IleArgGlyIle  368

Db  1213  GTTTCACTTTGGGAACTTGACGCGGAATCTTATGCAACGGCCTGTGAATATTTCTGGATTC  1272
                :::::::::
Qy   369  AspIleProValLeuProArgThrAlaAspLeuThrValPheValGluAlaAsnIleGln  388

Db  1273  GATTTCCCCGGCC------                GACGTGGATATGTACGTTCGAATTCAGTCAGTGTATAT  1323
                |||                ::::::
Qy   389  TyrGlyLysGlnInValLeuCysGlnArgArgThrSerProPheProGlnThrGluGluVal  408

Db  1324  GTGGGGACACTGACCGACCGTTTGGCCATCATCAAAATCTACACA---                AAAGTGAATGCTCAATTTGCA  1380
Qy   409  LeuTrpAspValTrpLeu--                GluTyrLysIleLysLysGlyLysAspLeuProLysGlyValAla  427

Db  1381  AAATCGGAATAAGGAAAATGTACACTTTTGATCTATACATGAGAGGATATGCCACCATCTGCA  1440
                :::
Qy   428  LeuLeuAsnLeuGlnIleLeuTyrCysGlyLysAlaProAlaLeuSerGlyLysThrSerAla  447

Db  1441  GTACTCAGCATTCGTTTTTGTACGGAAAA------                GTG  1473
                :::::
Qy   448  GluMetProSerProGluSerGlyLysGlyLysAlaGlnLeuLeuTyrTyrValAsnLeuLeu  467

Db  1474  AAATTAAAAGTGAAGAATTCGAA------                GTTGGTTGGGTAAAATATGCC  1518
                :::::
Qy   468  LeuIleAspHisArgPheLeuLeuArgHisGlyLeuTyrValLeuHisMetTrpGlnLeuLeu  487
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```
;   TITLE OF INVENTION:  IMPAIRED GLUCOSE TOLERANCE CONDITIONS
;   FILE REFERENCE: 00786/351004
;   CURRENT APPLICATION NUMBER: US/09/963,693
;   CURRENT FILING DATE:  2001-09-25
;   PRIOR APPLICATION NUMBER: US/09/205,658
;   PRIOR FILING DATE:  1998-12-03
;   PRIOR APPLICATION NUMBER: 08/857,076
;   PRIOR FILING DATE:  1997-05-15
;   PRIOR APPLICATION NUMBER: 08/888,534
;   PRIOR FILING DATE:  1997-07-07
;   PRIOR APPLICATION NUMBER: US98/10080
;   PRIOR FILING DATE:  1998-05-15
;   NUMBER OF SEQ ID NOS: 328
;   SEQ ID NO 47
;     LENGTH: 3504
;     SOFTWARE: FastSEQ for Windows Version 4.0
;     TYPE: DNA
;     ORGANISM: Caenorhabditis elegans
US-09-963-693-47

Alignment Scores:
Pred. No.:                              Length:               3504
Score:                  7.99e-110       Matches:              313
Percent Similarity:     1034.00         Conservative:         227
Best Local Similarity:  46.96%          Mismatches:           400
Query Match:            27.22%          Indels:               210
DB:                     17.86%          Gaps:                 44
                        13

US-09-974-573-1 (1-1102) x US-09-963-693-47 (1-3504)

Qy      78  AlaLeuGluThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeu  97
                :::||||||      ||| ||| :::|:||||   :::||||| |:|
Db     265  TCGCTAGAAATCAAGCTATCA---GATTTCAAACATCAACTT--------------TTCGAA 309

Qy      98  LeuLeuTyrGlnLysLysGlyGlnTrpTyrGluIleTyrArgLysTyrGlnValValGln 117
                ||:::                   :|| ||||||| |::||| |||:
Db     310  TTGATTGCTCCGATGAAGTGGGGAACATATTCCGTAAAGCCACAGGATTATGTTCAGA 369

Qy     118  ThrLeuAspCysLeuArgTyrTrpLysTrpLysLysValLeuHisArgSerProGlyGlnIleHisHisVal 137
               |||||||         :::|||:||        :|||||||
Db     370  CAGTTGAATAATTCGGCGAAATTGAGTTATATTTAACGACGATCAACCCTGTCGAAA 429

Qy     138  ValGlnArgHisAlaProSerGluGluThrLeuAlaPheGln- 151
                :::|| |||
Db     430  TTAGAGCTTCCACGGCACTTCCCAATGCTTTTTCTCCACCAACCTGATGGAATAAACAGG 489

Qy     152  ----------------ArgGlnLeuAsnAlaLeuIleGlyTyrAspValThrAspValSer 166
                                   :::|||||
Db     490  GATAAAGAATTAATGAGTGATATAAGTCATTGTCTAGGATACTCACTGGATAAACTGGAA 549

Qy     167  AsnValHisAspAspGluLeu---GluPhe- 178
                ::||||| :::|||
Db     550  GAGAGCCTCGATGAGGAACTCCGTCAATTTCGTGCTCTTCCTCTGGGCTCGTACGAAGAAA 609

Qy     179  ArgLeuValThr- 182
                :::|||
Db     610  ACGTGCTTGACACGTGGACTTGAGGGTACCAGTCACTACGGTTCCCGAAGAACAGTAC 669

Qy     183  ---------------ProArgMetAlaGluValAlaAlaGlyArgAspProLysLeu 195
                               |||
Db     670  TTGTGTTGGTGAACTGTGCCCGAAAGATTTGGAATCAAAAGTCAAGGCTGCCAAGCTG 729

Qy     196  TyrAlaMetHisProTrpValPheSerLysProLeuProGluTyrLeuLeuLysLysIle 215
                |||         :::|||
Db     730  AGTTATCAGATGTTTTGGAGAAACGTAAA------------------------GCGGAAATC 768

Qy     216  ThrAsnAsnCysValPheIleValIleHisArgSerThrThrSerGlnThrIleLysVal 235
                :::|||      |||:::
Db     769  AATGGAGTTGC-----------------------GAGAAAATGATGAAGATTCAAATTGAATTC 810

Qy     236  SerAlaAspAspThrProGlyThrIleLeuGlnSerPhePheThrLysMetAlaLysLys 255
                :::|| ::::|||:::||||
Db     811  AATCCGAACGAACTCCGAAATCTCGTCTTCACCGGTTTCTTCCTACGAAATCGCGAAA---- 867
```

```
Qy     814  GluPheLysCysAlaAspProThrAla---LeuSerAsnGluThrIleGlyIleIlePhe 832
                :::||    :::       |||
Db    2563  CACTGGAAGACAAAAATCCAAAGAGTGACCTGCACCCTTCCGTTCGTGTCGAATGATCTTC 2622

Qy     833  LysHisGlyAlaAspLeuArgGlnAspMetLeuIleLeuGlnIleLeuArgIleMetGlu 852
                :::|||    ||| :::|||:::
Db    2623  AAGAATGGAGACGATCTTCGCCAGAACATGCTTGTTCTTCAAGTTCTCCAAGTTATGGAT 2682

Qy     853  SerIleTrpGluThrGlySerLeuAspLeuCysLeuLeuProTyrGlyCysIleSerThr 872
               :::||||||          :::|||          :::
Db    2683  AACATCTGGAAGGGCTGCAAACATTGATTGCTGTTGAACCCGTACGCAGTTCTTCCAATG 2742

Qy     873  GlyAspLysLysIleGlyGlyMetIleGluIleLysValLysAspAlaThrThrIleAlaLysIleGln 892
               :::||||| :::                ::   :::||||||
Db    2743  GGAGAAATGAGATTATTGAAGTTGTGCCTAATTGTAAAACAATATTCGAGATTCAA 2802

Qy     893  GlnSerThr---ValGlyAsnThrGly---------AlaPheLysAspGluValLeuSerHis 909
               |||       |||                   :::
Db    2803  GTTGAACAGGATTCATGAATACAGCAGTTCGGAGTGATTCCTTCGTTTATGAATAAG 2862

Qy     910  TrpLeuLysGluLysCysProIleGluGlu------------------- 919
               ||||||::::::||:::||| ||:::
Db    2863  TGGATTCGGAAACAATGCGAATTGAAGATGAAAAAGAAGAAAAGACTCTACG 2922

Qy     920  ---------------LysPheGlnAlaAla 924
                              |||||||
Db    2923  AAAAATCCCATCGAAAAGAAGAATTCGATAATACTCAAGCCATGAAGAAATATTTTGAAAGT 2982

Qy     925  ValGluArgPheValTyrSerCysValAlaGlyTyrCysValAlaThrPheValLeuGlyIle 944
               ||:::||||::::|||:::|||||| |::||||||   |:||||| :::||:::|||
Db    2983  GTCGTAGCGGATTCCCTATACCTCGTGTGTTGGGATATTCAGTTGCCCACGTACATAATGGGAATC 3042

Qy     945  GlyAspArgHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeuPheHisIleAsp 964
                |||:::||||||  :::|||:::|||:::
Db    3043  AAGGATACGTCACAGTGATATCTGATGCTCACTGAGCTCCACCATTGAT 3102

Qy     965  PheGlyHisIleLeuLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLysGluValPro 984
               ||:::           ||||||:::||:::
Db    3103  TTCGGTCACATTTGGGACCGGAAAGACCAAACTTGGATCCAGCGAGATCGTCAACCG 3162

Qy     985  PheValLeuThrProPheLeuPheValMet-----GlyThrSerGlyLysLysThr 1002
                |||:::                    :::
Db    3163  TTTATTCTAACCGAACACACTTTATGACGTGATTCGATTCCATTCGTGGATGGAAAT 3222

Qy    1003  SerLeuHisPheGlnLysPheGlnAspValCysValAlaTyrLeuAlaLeuArgHis 1022
                :::||                   ||| :::
Db    3223  TCGCCATGAGCTACAAAAAATTCAAAACGTTATTAGCGTCGGAAGCCTACGAAGTCAATGTGGAAT 3282

Qy    1023  HisThrArgLeuIleLeuLeuIleLeuLeuPheSerMetMetLeuMetThrGlyMetProGlnLeu 1042
               :::||||||||           |||||||
Db    3283  AATCGAGATTTGTTCGTTGTTCCTTGTTCACCTTGATGCTCGGAATGGAGTTGCCTGAGCTG 3342

Qy    1043  ThrSerLysGluAspIleGluTyrIleArgAspAlaLeuThrVal--GlyLysSerGlu 1061
               :::|||:::          ||||| :::|||
Db    3343  TCGACGAAAGCGAAAAGTTTTCGCTGGAATCATTGAAGAAAACCCTCTTCTGCAATGGAAAGCAAA 3402

Qy    1062  GluAspAlaLysLysTyrPheLeuAspLysTyrPheLeuGluGluValCysArgAspLysTrpThr 1081
               :::|||:::|||        ||:::||||||
Db    3403  GAGGAAGCCGAGAAAGTTTTTCGCTGGAATCTACGAAGAAGCCTTCAATCGATCATGGTCT 3462

Qy    1082  ValGlnPheAsnTrpPheLeuHisLeuVal 1091
               ::: |||        ||||||
Db    3463  ACCAAAACGAATTGGCTCTTCCACGCAGTC 3492
```

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RESULT 13
US-09-963-693-47
; Sequence 47, Application US/09963693
; Publication No. US20030181364A1
; GENERAL INFORMATION:
;   APPLICANT: Ruvkun, Gary
;   APPLICANT: Ogg, Scott
;   TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
```

```
Qy   256  LysSerLeuMetAspIleProGluProGluSerGlnAsnGluArgAsp------PheValLeuArg      273
               ::||:::  ::|::                          :::     |||
Db   868  ------TTGGATGTATACGATACCGATGATCCTGCAGATGAAGGATGGTTTCTTCAA               918

Qy   274  ValCysGlyArgAspGluTyrLeuValGly---GluThrProIleLeuLysAsnPheGlnTrp         292
          |||                                :::
Db   919  TTGGCTGGACGTACCACGTTGTTACAAATCCAGATGCTCAAACTTACGTCTCTATGATGGT          978

Qy   293  ValArgGlnCysLeuLysAsn------------GlyGluGluIleHis---Leu                 305
          ||||                            |||              |||
Db   979  GTCCGTTCCGGAACTGGAAAGCTATCGATGCCCTGGATTCGTTGTTCGCCGAACAATCACTA        1038

Qy   306  ValLeuAsp------ThrProAspProAlaLeuAspGlu------ValArgLysGlu             321
          |||||                                      :::    ||||||
Db  1039  GTCCTCAAAGACTATTGTCGCCCAAAACCACTCTACGACCACCATTATGTGAGAGCACAC          1098

Qy   322  GluTrpProLeuValAlaAspCysCysAspArgLysPheArgValLys------IleArgGlyIle     341
          ||||                                :::
Db  1099  GAACGAAAACTTGCTCTAGACGTGCTCAGCGTGTCT------ATAGATAGCACACCAAAA          1152

Qy   342  HisGlyLysAspHisGlnSerValPheThr------                                   351
          ||||         :::   :::
Db  1153  CAGACCAAGAACAGTGACATGGTTACGACTCGAGTTTCGTCCGACAGCTTCACTCAAACAA         1212

Qy   352  ValSerLeuTrpAspCysPheAspArgLysPheArgValLys------IleArgGlyIle          368
          |||                                :::
Db  1213  GTTTCACTTTGGGACTGCACGGAATCTTATGATACGGCCTCTGAATATTTCTGGATTC            1272

Qy   369  AspIleProValLeuProArgThrAlaAspLeuThrValPheValGluAlaAsnIleGln          388
          |||                                    :::
Db  1273  GATTTCCCGGCC------GACGTGGATATGTACGTTCGAATCAGTTCAGTGTATAT               1323

Qy   389  TyrGlyGlnValLeuCysGlnAsnArgArgThrSerProLysProPheThrGluGluVal          408
          |||                                        :::
Db  1324  GTGGGGACACTGACGCGCTGGCACATCAAAATCTACACACA---AAAGTGAATGCTCAATTGCA     1380

Qy   409  LeuTrpAsnValTrpLeu--GluPheSerIleLysLysLysAspLeuProLysGlyAla          427
          :::        ||                          :::
Db  1381  AAATCGAATAAGGAAAATGTACACTTTGATCTATACATGAAGGAGGATATGCCACCATCGCA       1440

Qy   428  LeuLeuAsnLeuGlnIleTyrCysGlyLysLysAlaProAlaLeuLeuSerGlyLysThrSerAla    447
          :::||||||::::::
Db  1441  GTACTCAGGATTCGTGTTTGTACGGAAAA------GTG                                1473

Qy   448  GluMetProSerProGluSerLysGlyLysGlyAlaGlnLeuLeuTyrTyrValAsnLeuLeu       467
          :::||                      ::::|||||:::
Db  1474  AAATTAAAAGTGAAGAAATTCGAA------GTTCGTTGGGTAAATATGTCC                   1518

Qy   468  LeuIleLeuAspHisArgPheLeuLeuArgHisGlyGluTyrArgValLeuGluHisMetTrpGlnLeu 487
          |||
Db  1519  CTAACCGATTGGAGAGATGAACTACGACAAGGACAATTTTTATTCCATCGTGG------          1572

Qy   488  SerGlyLysGlyLysGluAspGlnGlyLysSerPheAsnAlaAspLysLeuThrSerAlaThrAsn    507
          :::                            |||    :::
Db  1573  ------GCTCCTGAACCGACTGCCAATGCGTAGT                                    1599

Qy   508  ProAspLysGluAsn------SerMetSerIleSerIleLeuGluLeuLeuAsp                521
          |||||
Db  1600  AGGATCGGAGAAAATGGAGCAAGGATAGGCACCACCAGCCGGTTACAATTGAAATCTCA          1659

Qy   522  AsnTyrCysHisProIleAlaLeuPro------LysHis                              532
          :::||                          ||||||
Db  1660  AGTTATTGGTGCTAGAGTTGGAATGCCGAGTCAAGGACAATACACATATCCGTCAAGCAC         1719

Qy   533  Arg------ProThrProAspProGluProGlyLysAspArgValArgAlaGluMetPro        548
          |||                                :::
Db  1720  CGAAGCTACTTGGACGGAACGGAAACTTTGAATATATTGGGTGGTGACTATGAGTCCGTGTATACAGA 1779

Qy   549  AsnGlnLeuArgLysGlnGlnLeuGlnLeuAlaIleLeuIleAlaThrAspProLeuArgAspLeuThr 568
          :::                            :::::::
Db  1780  GATCCAGGATATAAGAGAAGCTTCAGATGCTTGTCAAGAAGCATGAAATCTGGAATTGTATTA      1839
```

```
Qy   569  AlaGluAspLysGlu------LeuLeuTrpHisPheArgTyrGluSerLeuLysAsp            585
          ||||:::                                            :::::
Db  1840  GAGGAGGATGAACACGTCATGTCTGGATGTGAGG---AGATACATTCAAAAGCAGGAG           1896

Qy   586  ProLysAlaTyrProLysLeuPheSer---SerValLysTrpGlyGlnGlnIleVal           604
          |||                          :::
Db  1897  CCTGATTTGCTCATTGTGCTTCCGAACTCGCCATTTGTGTGGACTGATCGTGAGAACTTT        1956

Qy   605  AlaLysThrTyrGlnLeuLeuLeuAlaLysArgGluValTrpAspGlnSerAlaLeuAspVal     624
          |||                                      :::          :::
Db  1957  TCCGAGCTCTATGTGATGCTTGAAAAA------TGGAAACCCGCCGAGTGTGGCAGCC           2007

Qy   625  GlyLeuThrMetGlnLeuLeuAspCysAsnPheSerAspGluAsnValArgAlaAlaIleAla     644
          |||                                      :::
Db  2008  GCGTTGACT----TTGCTTGGAAAACGTTGCACGGATGTGTGATTCGAAAGTTTGCA          2061

Qy   645  ValGlnLysLeuGluSerLeuGluAspAlaAspValLeuHis---TyrLeuLeuGlnLeu        663
          |||                                      |||
Db  2062  GTGGAGAAGTTGAATGACGAGCAGCTGACCCGGTCACATTTTCATATTGCCTCTC            2121

Qy   664  ValGlnAlaValLysPheGluProTyrHisAspSerAlaLeuAlaArgPheLeuLeuLys        683
          :::||                                    :::
Db  2122  ATACAGGCGTTGAAGTACGAACCGCCGTCTCAATCGGAAGTTGAATGATGCTCTTGACT         2181

Qy   684  ArgGlyLeuArgAsnArgIleGlyHisPheLeuPheTrpPheLeuArgSerGluIle          703
          :::                                  :::
Db  2182  AGAGCTTCTCTGCGATTATCGACGTTTCTGGGTGCTCCGTCCGTGCAGAGATT              2241

Qy   704  AlaGlnSerArg------HisTyrGlnGlnArgPheAlaValIleLeu                    717
          :::               |||
Db  2242  GCTCGTTTGAGAGATTGTGATCTGAAAAGTGAAGAAATATCCCGTATCTCACTTCTGATG       2301

Qy   718  GluAlaTyrLeuArgGlyCysGlyThrAlaMetLeuHisAspPheThrGlnGlnValGln        737
          |||                                      :::
Db  2302  GAAGCTTACCTTCCGTGA---AATGAAGAGCACATCAAGATCATCACCCGACAAGTTGAC       2358

Qy   738  ValIleAspMetLeuGlnLysValThrIleAspIleLysSerLeuSerAlaGluGluLysTyr     757
          :::||                                                :::
Db  2359  ATGGTTGATGAGCTCACACGAATCAGCACTCTTGTCAAAGGAATGCCAAAA------          2409

Qy   758  AspValSerSer------GlnValIleSerGlnLeuLysGlnLysLeuGluAsn             773
          :::                |||
Db  2410  GATGTTGCTACGATGAAACTGCGTGACGAGCTTCGATCGATTAGTCATAAAATGAAAAT        2469

Qy   774  LeuGlnAsnLeuAsnLeuProGlnSerPheArgValProTyrAspProGlyLeuLysAla       793
          :::                                      :::
Db  2470  ATGGATTCT------CCACTGGATCCTGTGTACAAACTG                             2502

Qy   794  GlyAlaLeuValIleGluLysCysLysValMetAlaSerLysLysProLeuTrpLeu          813
          |||                                      :::
Db  2503  GGTGAAATGATAATCGACAAAGCCATCGTCCTAGGAGTGCAAAAGTCCTTAATGCTT          2562

Qy   814  GluPheLysCysAlaAspProThrAla---LeuSerAsnGluThrIleGlyTyrIleIlePhe     832
          |||                          :::           :::
Db  2563  CACTCGAAGAACAAAATCCAAAGAGTGACCTGCACCTTCCGTTCTGCAATGATCTTC          2622

Qy   833  LysHisGlyAspAspLeuArgGlnAspMetLeuIleLeuGlnIleIleLeuArgIleMetGlu     852
          |||                                      :::
Db  2623  AAGAATGGAGACGATCTTCGCCAGGACATGCTTGGTTCTTCAAGTTCTGAAGTTATGGAT       2682

Qy   853  SerIleTrpGluThrGluSerLeuAspLeuCysLeuLeuProTyrGlyCysIleSerSerThr     872
          |||                                      :::
Db  2683  AACATCTGGAAGGCTGCAAACATTGATTGCTTGTTTGAACCCGTACGCAGTTCTTCCAATG      2742

Qy   873  GlyAspLysIleGlyMetIleGluIleValLysAspAlaThrIleAlaThrIleAlaLysIleGln  892
          |||                                      :::
Db  2743  GGAGAAATGATAATTATTGAAGTTGTGCTAATTGAAAACAATATTCGAGATTCAA             2802

Qy   893  GlnSerThr---ValGlyAsnThrGly------AlaPheLysAspGluValLeuSerHis        909
          :::        :::                  :::
Db  2803  GTTGGACAGGATTCATGAATACAGCAGTTCGGAGTATTGACCTTCGTTTGATGAATAAG        2862

Qy   910  TrpLeuLysGluLysGluSerProIleGluGlu---                                 919
```

US-09-974-573-1 (1-1102) x US-10-101-235A-1 (1-627)

```
Qy    536  ProAspProGluGlyAspArgValArgAlaGluMetProAsnGlnLeuArgLysGlnLeu  555
               |||||::::|  ||||||||||||||||||||
Db     48  CCCGAT--AGCCCTGACGCGGGTTCGAGCAGAAATGCCAACCAGCTTCGCAAGCAATTG  104

Qy    556  GluAlaIleIleAlaThrAspProLeuAsnProLeuThrAlaGluAspLysGluLeuLeu  575
               |||||::::||          ||||||||::
Db    105  GAGGCGATCATAGCCACTGATCCACTTAAC------------GACAAGAAATGCTC  149

Qy    576  TrpHisPheArgTyrGluSerLeuLysAspProLysAlaTyrProLysPheSerSer  595
               ||||||::::|||  :::|||||||::
Db    150  TGGCATTTTAGATACGAGAAGCCTTAAGCACCCAAAGCATATCCTAAGCTATTAGTTCA  209

Qy    596  ValLysTrpGlyGlnGluLeuPheTyrGlnLeuLeuAlaLysThrTyrGlnLeuArgGlu  615
               |||||:::||::  |||::
Db    210  GTGAAATGGGGACAGCAAGAAATTGTGGCCAAAACATACCAATTGTTGGCCAGAAGGGAA  269

Qy    616  ValTrpAspGlnSerAlaLeuAspValGlyLeuThrMetGlnLeuLeuAspCysAsnPhe  635
               ||||::::||||  :::|||
Db    270  GTCTGGGATCAAAGTGCTTGGATGTTGGGTTAACATGCAGCTCCTGGACTGCAACTTC  329

Qy    636  SerAspGluAsnValArgAlaLeuArgHis  655
               ::::||||
Db    330  TCAGATGAAAATGTAAGAGCCATTAAGAGC  389
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;  PRIOR APPLICATION NUMBER: US 60/303,459
;  PRIOR FILING DATE: 2001-07-09
;  NUMBER OF SEQ ID NOS: 1740
;  SOFTWARE: PatentIn Ver. 2.1
;  SEQ ID NO 477
;  LENGTH: 5990
;  TYPE: DNA
;  ORGANISM: Rattus norvegicus
;  FEATURE:
;  OTHER INFORMATION: Genbank Accession No. US20020119462A1 AB009636
US-09-917-800A-477

Alignment Scores:
Pred. No.:              2.91e-96           Length:        5990
Score:                  922.00             Matches:        286
Percent Similarity:     45.21%             Conservative:   195
Best Local Similarity:  26.88%             Mismatches:     366
Query Match:            15.92%             Indels:         218
DB:                                        Gaps:            37

US-09-974-573-1 (1-1102) x US-09-917-800A-477 (1-5990)

Qy   90 ArgLeuGlyProAspHisPheLeuLeuLeuTyrGlnLysLysGlyGlnTrpTyrGluIle 109
           :::|||||
Db 1083 CAGCTTTCCCCAAAGAGTATCTTCTA-----------------------AGTATA 1115

Qy  110 TyrAspLysTyrGlnValValGlnThrLeuAspCysLeuArgTyrTrpLysValLeuHis 129
           :::|||||
Db 1116 TGCGGTTCTGAGGAATTTTACAGACGGATCACTGTCTAGGGAGCCACAAAATATTTCAG 1175

Qy  130 ArgSerProGly------GlnIleHisValValGlnArgHisAlaProSerGluThr 147
           :::||||  |||:||||
Db 1176 AAAAGTAAATCTGTCATTCCAT--CTCCAGAGAGCAGGAGCCACACTCCAGGAAAA 1232

Qy  148 LeuAlaPheGlnArgGlnLeuAsnLeuAlaLeuIleGlyTyrArgValThrAspValSerAsn 167
           |||:|:|||||||||
Db 1233 TTATCCCGGAAGAGGGAT----------------GATGACCGCAGTCGG 1265

Qy  168 ValHisAspAspGlu---LeuGluPheThrArgArgArgLeuValThrProArgMetAla 186
           |||||||||||||
Db 1266 GTCCATCTGAACCAACTTCTAGAATTTACA----------------------- 1295

Qy  187 GluValAlaGlyArgAspProLysLeuTyrAlaMetHisProTrpValThrSerLysPro 206
           |||:||:|||
Db 1296 ----------------------------------------CAIATTTGG 1304

Qy  207 LeuProGluThrTyrLeuLeuLysLysLysIleThrAsnAsnCysValPheIleValIle 224
           |||||||||
Db 1305 -----AAAATATCCAGACAATGCCTCTCCAAGTAATGAAAAGC 1343

Qy  225 ------------HisArgSerThrThrSerGlnThrIleLeuLysValSerAlaAspAsp 238
           :::|||
Db 1344 TACAACCTCCATGTCGAGCACCCTGTGAAAACCCAGGAGATGTG---------GAG 1391

Qy  239 AspThrProGlyThrIleLeuLeuGlnSerPhePheThr----------------------- 250
           :::|:|||||
Db 1392 GAGAAACCT--------CTGTCATCCATGTTTCCTGTGGCCGACACCCTCCTCAGCCA 1442

Qy  251 ----------LysMetAlaLysLysLysSerLeuMetAspIleProGlu 263
           :::
Db 1443 CATGGGAATGACACATTATTGAAGATGTTAGAAACATGCGTTCTGGGGTGTATTGAA 1502

Qy  264 SerGlnAsnGluArgAspPheValCysGlyValCysGlyValTyrIleLeuValGly 283
           :::|:::
Db 1503 ACCAAACAAGTTCAGATGCAGTA-----------AAAGAACTAACTCTAATTCTG 1547

Qy  284 GluThrProIleLeuLysAsnPheGlnTrpValArgGlnCysLeuLysAsnGly-------- 300
           :::  :::||||
Db 1548 CAGAGACCATCACAGAGAATTTCATCAGAGATTCAGAGACTTCAAAAAAAAGGCTTCATAGAG 1607

Qy  301 -------GluGluIleHisLeuValLeuAspProProAspPro 313
           :::|||
Db 1608 AACGTGACACATCGGGAACTGTCGAGGTCCCCCATCAGCTGGTTGACGTGTACTGCAGTAGC 1667

Qy  314 AlaAlaLeuAspGluValArgLysGluGluTrpProLeuValAspAspCysThrGlyValThr 333
           :::|||
Db 1668 TTTTGTACAGATTCCGGCTCGCGGCGCCACCT-------------------------GGAGGCGTCTCC 1712

Qy  334 ------GlyTyrHisGluGlnLeuThrIleHisGlyLysAspHisGluSerVal 349
           |||
Db 1713 CGGGACCACGCTGGGCTCCCACCTGAG-CTTCACGGT----------------GTG 1756

Qy  350 PheThrValSerLeuTrpAspCysAspArgLysPheArgValLysIleArgGlyIleIleAsp 369
           |||:||||
Db 1757 TTCCCTGCA----------CAATGTTCAGAAACTTGGCACACAGTACA----- 1798

Qy  370 IleProValLeuProArgThrAlaAspLeuThrValGluAlaAsnIleGlnThr 389
           :::||:|:
Db 1799 ------------AGCATTTCATTTCCTGCTGGCTCACATA 1828

Qy  389 rGlyGlnIleValLeuCysGlnArgArgThrSer---------ProLysProPh 404
           |||
Db 1829 TGCTGGGAAGAAGCTGTGCCAAGTGAAAAGCTGCAGTCCCTGCCAGTCACAAAGTCATT 1888

Qy  404 eThrGluGluValLeuTrpAsnValTrpLeuGluPheSerIleLeuSerIleLeuLysAspLeuPr 424
           |||:|||
Db 1889 CTCTTTTTCGGTGAACTGGATGAATGAAATAATCAATTTCCTCTTGAGATAAAGTCACTTCC 1948

Qy  424 oLysGlyAlaLeuLeuAsnLeuGlnIleTyrCysGlyLysLysGlyAlaProAlaLeuSerGlyLy 444
           |||
Db 1949 AAGAGAATCCATGCTCGTTATAAAGTGTTT-------------------GGGAT 1984

Qy  444 sThrSerAlaGluMetProSerProGluSerLysGlyLysLysAlaGlnLeuLeuTyrTyrVa 464
           |||||
Db 1985 TGACAGTGCC-----------ACCCACAGCCGCAAATCTGCTGGCCTGGAC 2023

Qy  464 lAsnLeuLeuLeu------------IleAspHisArgPheLeuLeuArgHi 477
           |||  |||
Db 2024 CTGCCTTCCACTATTCCAAAAGAAAAGTCTCCGCTGGGGTCTAGGCTTTCTC--------- 2075

Qy  477 sGlyGluTyrValLeuHisMetTrpGlnLeuSerGlyLysGlyGluAspGlnGlySerPh 497
           
Db 2075 ----------------------------------------------- 2075

Qy  497 eAsnAlaAspLeuThrSerAlaThrAsnProAspLysGluAsnSerSerIleSe 517
           :::|||
Db 2076 -------AGCATGACACTACAGAGTGAGCCTCTATAGAA---ATGATGGCTCCAGG 2122

Qy  517 rIleLeuLeuAspAsnTyrCysHisProIleAlaLeuProLysHisArgProThr------- 535
           |||
Db 2123 AGTATGGGAGGGATGGGAGCCAGCCTACCCCACTGACCCTGCAGATAGATTTTCAGCTGCCAC 2182

Qy  536 ----ProAspProGluGlyAspArgVal---ArgAlaGluMetProAs 549
           |||:||||
Db 2183 GTGGGAGTACGTGAAGAACCTGAACTGAAGAACAGAACTGACCACCAGAGCCCTCAAG 2242

Qy  549 nGlnLeuArgLysGlnLeuGluGluAlaIleIleGluLeuAlaThrAspProLeuAsnProLeuThrAl 569
           :::|||
Db 2243 AGAGTGTTTAAAACACCATGCCAGAATCGCCAAAGCAGCCTCCCTGCTACTTTCTGT 2302

Qy  569 aGluAspLysGlyLeuLeuLeuTrpHisPheArgGluSerLeuLeuLysAspProLysAlaTy 589
           :::|||
Db 2303 GGAAAGAGGAGGAGATATTTGTGGTTTTATCGTTTGGTGGGTGTATTGAA 2362

Qy  589 rProLysLeuPheSerSerValLysTrpGlyGlnGlnGlyIleLeuValAlaLysThrTyrGl 609
           :::|||
Db 2353 CCCTTGCTCTTGGGCAGCGCCCCTGGTTGGGATGGAAGGGACAGTTTCGGAAATGCATGC 2422

Qy  609 nLeuLeuAlaLysArgGluValGluValTrpAspValGlnSer---AlaLeuAspValGlyLeuThrMe 628
           :::  :::|||
Db 2423 CGTCTTGAGAAGG-------TGGACATTTTCCCATCCGTGGAA--------GCTCT 2464

Qy  628 tGlnLeuLeuAspCysAsnPheSerAspGluAsnValArgAlaLeuAlaValGlnLysSerLe 648
           :::|||
Db 2465 TGGCCTTTGACTTCCAGGTTTCCAGCACGTTCCAAGACAATTCGTGAAGTTGCCGTTCACAGTT 2524
```

```
Qy    648  uGluSerLeuGluAspAspValLeuHisTyrLeuGlnLeuValGlnAlaValLy  668
                |:::::||||||||||||||||||||||||||||||||||||||||||||||
Db   2525  AGACAACTTCTGACCGATGAGCTGTGGACTGCCTCCCAGAGTTCAGGCTGTCAA 2584

Qy    668  sPheGluProTyrHisAspArgAlaLeuAlaArgPheLeuLysArgGlyLeuArgAs  688
                ::||||  |||| ||||||||||||::||:|||||||  ||::::||
Db   2585  GTTTGAGTGGAGTCGAAAGTCCCTGGTGAAGTCCCTTGCAATCCCTTGCAAAG 2644

Qy    688  nLysArgIleGlyHisPheLeuPheTrpPheLeuArgSerGluIleAlaGlnSerArgHi  708
            :||||:|:|||||   ||||||||||||||||||| |||          :::||
Db   2645  CATCCGAGTGGCTCACCGCCTGTTCTCGGGCTGCTGCGGGAT------GCACAAGGTGAAGA 2698

Qy    708  sTyrGlnArgPheAlaValIleLeuGluAlaTyrLeuArgGlyGlyCys--GlyThrAl  727
                 ::||  :::    ||| ||| ||| ||::||::  ||| |||   ||
Db   2699  CTACTTTAAAAGCTGGTACCGAGGAGTTTTGGCCGTCTCCAGTTCGTGTCGCAGGAGAAGC 2758

Qy    727  aMetLeuHisAspPheThrGlnGlnValGlnAsnLeuGlnLysValThrIl  747
             :::||||:::  ||||||||||||::||:|||||||:::||:||||
Db   2759  CCTGATCGAGAGAGCTTTCTTAAAGATATAAAGACTTGCCATCTT------CC 2818

Qy    747  eAspIleLysSerLeu--SerAlaGluLysTyrAspValSerSerGlnValIleSerGl  766
            :::||||:::::    |||||:||||:||||:||:   ||| ::::||
Db   2819  AAAAGTGAAGTGCGGCTGGCGATGCTCAGAGAAGGATGTGCTAAAGAAGGAGATTGGCAG 2878

Qy    766  nLeuLysGlnLysLeuGluAsnLeuGlnAsnLeuAsnLeuProGlnSerPheArgValPr  786
            ::||||::::     ||||||||||| :::|||  ::
Db   2879  TCTAGAAGAATTCTTTAAAGATATAAAGACTTGCCATCTT------------CC 2920

Qy    786  oTyrAspProGlyTyrLeuGluGlyLysAlaLeuValAlaLeuValLysLysValMetAlaSe  806
            ||||||||||||||||  :::         ||| :: |||||||||||
Db   2921  TCTGAACCCGGCCTGTGCTAAAGGAATTGATCGGGATGCATGTTCATATTCCACATC 2980

Qy    806  rLysLysLysProLeuTrpLeuGluPheLysCysAlaAspProThrAlaLeuSerAsnGl  826
            ||||||||||||||||||||  :::||  |||||||||
Db   2981  TAATGCCTTGCCAATTGAAGATCACTTTCATCAATGCTAATCCA-------ATGGGCCA 3031

Qy    826  uThrIleGlyIleIlePheLysHisGlyAspLeuAspArgGlnAspMetLeuIleLeuGl  846
            ||  ||| ||||||||||||||||||||||||||:::
Db   3032  AAATATCAGTGTATTTTTTAAGGCCCGGCGAGATCTTCGGCAGGATATGCTTGTTCTGCA 3091

Qy    846  nIleLeuArgIleMetGluSerIleLeuTrpGluThrGluSerLeuLeuAspLeuCysLeuLeuPr  866
            ||||||||||||||||||||||||||||||||||::::::
Db   3092  GATTATTCAGTGATGGACAACGTTTGGCTTCAGGAGGGCCTCGATATGCAAATGATCAT 3151

Qy    866  oTyrGlyCysTyrSerThrGlyAspValPheLeuGlyIleLeuValLeuValAlaAspAlaTh  886
            ||||::::::::||||::  ||| |||||||||||||
Db   3152  TTATGGATGTCTAGCCACAGGAAAGGCTCAAGGATTCAATAGAGATGGTGCCTGATGCTGT 3211

Qy    886  rThrIleAlaLysIleGlnGlnSe-ThrValGlyAsnThrGlyAlaPheLysAspGluVa  906
            ::::   :::||| ||| ||||||| |||||||||||||||
Db   3212  AACGGCTTGCCAAGATCCATCTGCACTCT---GGGCTGATAGGAGACCCCTGAAAGAAAAACAC 3268

Qy    906  lLeuSerHisTrpLeuLysGluLysCysProIleGluGlnLeuLysPheGlnAlaAlaValGl  926
              ::: ::::||||   ::: |||||  :::|||| :::||:
Db   3269  CATCAAGAAGTGGTTCAGTCAGCACAACCACTTAAAGGAAGATTATGAAAAGGCCTTGAG 3328

Qy    926  uArgPheValTyrSerCysAlaGlyTyrCysValValLysLysValGluGlyIleGlyAs  946
            ||| |||||::::::|||||||||||::||||||||||||||||||:::
Db   3329  GAACTTTTTTTACTCTTGTCTGGCGTGGTGTGTGCATATCTTGGAGTCTGTGA 3388

Qy    946  pArgHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeuPheHisLeuAspPheGl  966
            ||||||||||||||||||||||||||:::|||||||||||
Db   3389  CCGACATAATGACAATATCATGTCTGACAAAGTCAGGGCCACATGTTTCATATTGACTTTGG 3448

Qy    966  yHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleLeuAsnLysGluArgValProPheVa  986
            |||||||||||||||  :::||||||||||||  ::::
Db   3449  AAAATTCTTGGGTCACGCGACAAACATTTGGCGTATAAAAGGACCGAGCGCCTTTCAT 3508

Qy    986  lLeuThrProAspPheLeuPheValMetGlyThrSerGlyLysLysThrSerLeuHisPh  1006
                ::||||||||||||   |||||||| ::  :::
Db   3509  TTTTACTTCAGATGGAGTACTTTATT--ACCGAGGGTGGGAAAAACACAGCATTT 3565

Qy   1006  eGlnLysPheGlnAspValCysValLysValAlaTyrLeuAlaLeuArgHisHisThrAsnLe  1026
```

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Db   3566  TCAAGACTTCGTGTGAACTCTGCTGCGAACATTGTGAGGAGGCACAGCCAACT 3625
                |||||   |||||     :::|||
Qy   1026  uLeuIleIleLeuPheSerMetMetLeuMetThrGlyMetProGlnLeuThrSerLysGl  1046
            |||||||||||||:::::|||:||||||||||:||||||
Db   3626  GCTCCTGAGCCTTCTAGAAATGATGCTGCATGCCGGGCTTCCTGAGCTGAGGGGGGATTGA 3685

Qy   1046  uAspIleGluTyrIleArgAspAlaLeuThrValGlyLysSerGluGluAspAlaLysSLy  1066
            ||||:::::::||  |||     :::||
Db   3686  AGACCTGAAATACGTACACGACAATCTCCGGCCACAAGACCACAGACCTGGAAGCCACAAG 3745

Qy   1066  sTyrPheLeuAspGlnIleGluValCysArgAspLysGlyTrpProValGlnPheAsnTr  1086
                 :::||||| :::||::   ::
Db   3746  TCATTTTACCACGAAGATAAAGCAGAGTCTGGAG---TGCTTCCCAGTTAAACTGAATAA 3802

Qy   1086  pPheLeuHis 1089
                :::|||
Db   3803  CCTGATCCAC 3812
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Search completed: February 15, 2004, 09:17:53
Job time : 1163 secs

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                    GenCore version 5.1.6
          Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:    February 15, 2004, 01:39:44 ; Search time 40 Seconds
                              (without alignments)
                              2649.447 Million cell updates/sec

Title:         US-09-974-573-1
Perfect score: 5790
Sequence:      1 MELENYEQPVVLREDNRRRR.........QFNWFLHLVLGIKQGEKHSA 1102

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:    283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters:        283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR 76:*
             1: pir1:*
             2: pir2:*
             3: pir3:*
             4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5222	90.2	1050	1	A57134	1-phosphatidylinos
2	1465.5	90.2	1068	1	A43322	1-phosphatidylinos
3	1460.5	25.2	1068	1	I38110	1-phosphatidylinos
4	1354.5	23.4	1070	1	A54600	1-phosphatidylinos
5	1319	22.8	1043	2	T43502	1-phosphatidylinos
6	1297	22.4	1570	2	T18272	1-phosphatidylinos
7	1283	22.2	1088	2	T13950	1-phosphatidylinos
8	1233	21.3	1858	2	T18273	1-phosphatidylinos
9	1136.5	19.6	1585	2	T18274	1-phosphatidylinos
10	1076.5	18.6	1658	2	T42642	phosphoinositide 3
11	1031	17.8	1164	2	S71792	phosphatidylinosit
12	1021	17.6	1634	1	JC5500	phosphoinositide 3
13	876	15.1	1506	2	JC5985	phosphoinositide 3
14	873.5	15.1	1876	2	T13801	phosphoinositide 3
15	720.5	12.4	816	1	A59003	phosphoinositide 3
16	714.5	12.3	801	1	T52538	1-phosphatidylinos
17	701.5	12.1	664	2	PC4002	phosphatidylinosit
18	701.5	12.1	1607	2	T21982	hypothetical prote
19	693.5	12.0	887	1	S57219	1-Phosphatidylinos
20	672	11.6	814	2	T07761	phosphatidylinosit
21	669	11.6	812	2	T07745	phosphatidylinosit
22	657.5	11.4	814	1	B96630	Phosphatidylinosit
23	649.5	11.2	875	1	A36369	1-phosphatidylinos
24	646	11.2	873	2	T25442	hypothetical prote
25	626	10.8	897	2	T43628	phosphatidylinosit
26	562	9.7	1020	2	T18260	1-phosphatidylinos
27	508	8.8	732	2	T08420	1-phosphatidylinos
28	435.5	7.5	2028	2	T52022	1-phosphatidylinos
29	432	7.5	2051	2	F96529	probable Phosphati
30	410	7.1	1466	2	S65741	1-phosphatidylinos
31	408.5	7.1	133	2	PC4348	phosphoinositide 3
32	404	7.0	2121	2	T27406	hypothetical prote
33	402	6.9	854	2	A55404	1-phosphatidylinos
34	397.5	6.9	131	2	PC4346	phosphoinositide 3
35	397.5	6.9	131	2	PC4345	phosphoinositide 3
36	390.5	6.7	1877	2	T40550	probable phosphati
37	380	6.6	1900	2	S45530	probable 1-phospha
38	364	6.3	525	2	F96547	probable phosphati
39	361.5	6.2	131	2	PC4347	phosphoinositide 3
40	328.5	5.7	828	2	JC5706	1-phosphatidylinos
41	326	5.6	1121	2	T52631	1-phosphatidylinos
42	315	5.4	379	2	T07007	probable 1-phospha
43	314.5	5.4	1093	2	T18275	1-phosphatidylinos
44	277	4.8	1066	2	A49335	1-phosphatidylinos
45	274.5	4.7	604	2	F89453	protein F35H12.4 [

ALIGNMENTS

```
RESULT 1
A57134
1-phosphatidylinositol 3-kinase (EC 2.7.1.137) gamma isoform - human
N;Alternate names: p110-gamma protein
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A57134
R;Stoyanov, B.; Volinia, S.; Hanck, T.; Rubio, I.; Loubtchenkov, M.; Malek, D.; Stoyanov
  Wetzker, R.
Science 269, 690-693, 1995
A;Title: Cloning and characterization of a G protein-activated human phosphoinositide-3
A;Reference number: A57134; MUID:95350661; PMID:7624799
A;Accession: A57134
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1050 <STO>
C;Cross-references: GB:X83368
C;Genetics:
A;Gene: GDB:PIK3CG
A;Cross-references: GDB:370920
A;Map position: 3q26.3-3q26.3
C;Superfamily: phosphatidylinositol 3-kinase
C;Keywords: phosphotransferase

Query Match      90.2%;       Score 5222;   DB 1;   Length 1050;
Best Local Similarity   90.2%;       Pred. No. 0;
Matches 990;   Conservative 20;   Mismatches 30;   Indels  0;   Gaps  0;

Qy     35  MELIPIEFVLPTSQRNTKTPETALLHVAGHGNVEQMKAQVWLRALETSVSADFYHRLGPD   94
               MELIPIEFVLPTSQRNTKTPETALLHVAGHGNVEQMKAQVWLRALETSVSADFYHRLGP
Db      1  MELIPIEFVLPTSQRKCKSPETALLHVAGHGNVEQMKAQVWLRALETSVAADFYHRLGPH   60

Qy     95  HFLLLYQKKGQWYEIYDKYQVVQTLDCLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRQL  154
               HFLLLYQKKGQWYEIYDKYQVVQTLDCLRYWK:LHRSPGQIHVVQRHPPSEESQAFQRQL
Db     61  HFLLLYQKKGQWYEIYDKYQVVQTLDCLRYWKATHRSPGQIHLVQRHPPSEESQAFQRQL  120

Qy    155  NALIGYDVTDVSNVHDDELEFTRRRLVTPRVAEVAGRDPKLYAMHPWVTSKPLPEYLLKK  214
               TALIGYDVTDVSNVHDDELEFTRRGLVTPRMAEVASRDPKLYAMHPWVTSKPLPEYLWKK
Db    121  TALIGYDVTDVSNVHDDELEFTRRGLVTPRMAEVASRDPKLYAMHPWVTSKPLPEYLWKK  180

Qy    215  ITNNCVFIVIHRSTTSQTIKVSADDTPGTIIQSFFTKMAKKKSLMDIPESQNERDFVLRV  274
               IANNCIFIVIHRSTTSQTIKV:SPDDTPGAILQSFFTKMAKKKSLMDIPESQSEQDFVLRV
Db    181  IANNCIFIVIHRSTTSQTIKVSPDDTPGAILQSFFTKMAKKKSLMDIPESQSEQDFVLRV  240

Qy    275  CGRDEYLVGETPIKNFQWVRQCLKNGEEIHLVLDTPPDPALDEVRKEEWPLVDDCTGVTG  334
               CGRDEYLVGETPIKNFQWVRHCLKNGEEIHVVLDTPPDPALDEVRKEEWPLVDDCTGVTG
Db    241  CGRDEYLVGETPIKNFQWVRHCLKNGEEIHVVLDTPPDPALDEVRKEEWPLVDDCTGVTG  300

Qy    335  YHEQLTIHGKDHESVFTVSLWDCDRKFRVKIRGIDIPVLPRTADLTVFVEANIQYGQQVL  394
               YHEQLTIHGKDHESVFTVSLWDCDRKFRVKIRGIDIPVLPRNTDLTVFVEANIQHGQQVL
Db    301  YHEQLTIHGKDHESVFTVSLWDCDRKFRVKIRGIDIPVLPRNTDLTVFVEANIQHGQQVL  360
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Qy    23  MKPRSTAASLSSMELIP----IEFVLPTSQRNTKTPETALLHVAGHGNVEQMKAQVWLRA   78
Db     1  MPPRPSSGELWGIHLMPPRILVBCLLPNGMVT------LECLREATLITIKGHELFKEA    53

Qy    79  LETSVSADFYHRLGPDHFLLLYQKKGQWYEYDKYQVVQTLDCLRYWKVLHRSPGQIHVV   138
Db    54  RKYPL-----HQLLQDESSYIFVSVTQEABREEFPDETRRLCDLRLFQPF-----LKVI   102

Qy   139  QRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRLVTPRMAEVAGRD------  192
Db   103  EPVGNRBEKI-LNREIGFAIGMPVCEFDMVKDPEVQDFRRNILNVCKEAVDLRDLNSPHS  161

Qy   193  PKLYAMHPWTSKP-LPEYLLKKITNNCVFIVI------HRSTTSQTIKVSADDTPGTIL   245
Db   162  RAMYVYPPNVESSPELPKHIYNKLDKGQIIVVIWVIVSPNNDKQKYTLKLNHDCVPEQVI  221

Qy   246  QSFFTKMAKKKSLMDIPES------QNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKN  299
Db   222  AEAIRK--KTRSMLLSSEQLKLCVLEYQGKYILKVCGCDEYFLEKYPLSQYKYIRSCIML  279

Qy   300  GEEIHLVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLT----IHGKDHESVFTVSL   354
Db   280  GRMPNLML------MAKESLYSQLFM--DCFTMPSYSRRISTATPYMNGE---TSTKSL   327

Qy   355  WDCDRKFRVK--------IRGIDIPVLPRTADLIVFVEBANIQYGGQVLCQRRTSPKPF   404
Db   328  WVINSALRIKILCATYVNVNIRDID----------KIYVRTGIYHGGEPLCDNVNTQRVP  377

Qy   405  TEEVLWNVWLEFSIKIKDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYYV  464
Db   378  CSNPRWNEWLNVDIYIPDLPRAARLCLSI-C----SVKGRKGA------KEEHCPLAWG   425

Qy   465  NLLLIDHRFLLRHGEYVLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYC  524
Db   426  NINLFDYTDTLVSGKMALNLWFVPHGLED--LLNPIGVT-GSNPNKE-TPCLELEFDWFS  481

Qy   525  HPIALPKHRPTPDPEGDRV----------RAEMPNQLR---KQLEAIIATDPLN       565
Db   482  SVVKFPDMSVIEHAHWSVSREAGFSYSHAGLSNRLARDNELRENDKEQLRAICTRDPLS   541

Qy   566  PLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQQEIVAKTYQLLAKREVWDQSALDVG  625
Db   542  EITBQEKDFLWSHRHYCVTIPEILPKLLSVKWNSRDEVAQMYCL----VKDWPPIKPE   596

Qy   626  LTMQLLDCNFSDENVRAIAVQKLES-LEDDDVLHYLLQLVQAVKFEPYHDSALARFLLKR  684
Db   597  QAMBLLDCNYPDMVRGFAVRCLEKYLTDDKLSQYILQLVQVIKYEQYLDNLLVRFLLKK   656

Qy   685  GLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAYLRGCTAMLHDFTQQVQVIDMLQK   744
Db   657  ALNQRIGHFFFWHLKSEM-HNKTVSQRFGLLLESSYCRACGMYLKH-LNRQVEAMEKLIN  714

Qy   745  VTIDIKSLSAEKYDVSSQVISQLKQKLENLQN--LNLPQSFRVPYDPGLKAGALVIEKC   801
Db   715  LI-DI--LKQEKKDETQKV--QMKFLVEQMRRPDFMDALQGFLSPLNPAHQLGNLRLEEC  769

Qy   802  KVMASKKKPLWLEFKCADPTALS------NETIGIIFKHGDDLRQDMLILQLIRIMESIW  855
Db   770  RIMSSAKRPLWLNWE--NPDIMSELLFQNNE---IIFKNGDDLRQDMLTLQIIRIMENIW  824

Qy   856  ETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTGA--FKDEVLSHWLKE  913
Db   825  QNQGLDLRMLPYGCLSIGDCVGLIEVRNSHTIMQI-QCKGGLKGALQFNSHTLHQWLKD   883

Qy   914  KCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNLFHIDFGHILGNYK  973
Db   884  KNK-GEIYDAAIDLFTRSCAGYCVATFILGIGDRHNSNIMVDDGQLFHIDFGHFLDHKK   942

Qy   974  SFLGINKERVPFVLTPDFLFVMGTSGKK-TSLHFQKFQDVCVKAYLALRHHTNLLILF   1031
Db   943  KKFGYKRERVPFVLTQDFLIVISKGAQECTKTREFERFQEMCYKAYLAIRQHANLFNLF  1002

Qy  1032  SMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGWTVVFNWFLHLV 1091
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Qy   395  CQRRTSPKFFTEEVLWNVWLEFSIKIKDLPKGALLNLQIYCGKAPALSGKTSAEMPSPES  454
Db   361  CQRRTSPKFFTEEVLWNVWLEFSIKIKDLPKGALLNLQIYCGKAPALSGKTSAEMPSPES  420

Qy   455  KGKAQLLYVNLLLIDHRFLLRHGEYVLHMWQLSGKGEDQGSFNADKLTSATNPDKENSM   514
Db   421  KGKVRLLYVNLLLIDHRFLLRRGEYVLHMWQISGKGEDQGSFNADKLTSATNPDKENSM   480

Qy   515  SISILLDNYCHPIALPKHRPTPDPEGDRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKEL  574
Db   481  SISILLDNYCHPIALPKHQPTPDPEGDRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKEL  540

Qy   575  LWHFRYESLKDPKAYPKLFSSVKWGQQEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCN  634
Db   541  LWHFRYESLKHPKAYPKLFSSVKWGQQEIVAKTYQLLARREVWDQSALDVGLTMQLLDCN  600

Qy   635  FSDENVRAIAVQKLESLEDDDVLHYLLQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHF  694
Db   601  FSDENVRAIAVQKLESLEDDDVLHYLLQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHF  660

Qy   695  LFWFLRSEIAQSRHYQQRFAVILEAYLRGCGTAMLHDFTQQVQVIDMLQKVTIDIKSLSA  754
Db   661  LFWFLRSEIAQSRHYQQRFAVILEAYLRGCGTAMLHDFTQQVQVIEMLQKVTLDIKSLSA  720

Qy   755  EKYDVSSQVISQLKQKLENLQNLNLPQSFRVPYDPGLKAGALVIEKCKVMASKKKPLWLE  814
Db   721  EKYDVSSQVISQLKQKLENLQNSQLPESFRVPYDPGLKAGALAIEKCKVMASKKKPLWLE  780

Qy   815  FKCADPTALSNETIGIIFKHGDDLRQDMLILQLIRIMESIWETESLDLCLLPYGCISTGD  874
Db   781  FKCADPTALSNETIGIIFKHGDDLRQDMLILQLIRIMESIWETESLDLCLLPYGCISTGD  840

Qy   875  KIGMEIVKDATTIAKIQQSTVGNTGAFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAG   934
Db   841  KIGMEIVKDATTIAKIQQSTVGNTGAFKDEVLNHWLKEKSPTEEKFQAAVERFVYSCAG   900

Qy   935  YCVATFVLGIGDRHNDNIMISETGNLFHIDFGHILGNYKSFLGINKERVPFVLTPDFLFV  994
Db   901  YCVATFVLGIGDRHNDNIMTETGNLFHIDFGHILGNYKSFLGINKERVPFVLTPDFLFV   960

Qy   995  MGTSGKKTSLHFQKFQDVCVKAYLALRHHTNLLILFSWMLMTGMPQLTSKEDIEYIRDA  1054
Db   961  MGTSGKKTSPHFQKFQDICVKAYLALRHHTNLLIILFSWMLMTGMPQLTSKEDIEYIRDA 1020

Qy  1055  LTVGKSEEDAKKYFLDQIEV  1074
Db  1021  LTVGKNEEDAKKYFLDQIEV  1040
```

RESULT 2

A43322

1-phosphatidylinositol 3-kinase (EC 2.7.1.137) 110K chain - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A43322
R;Hiles, I.D.; Otsu, M.; Volinia, S.; Fry, M.J.; Dhand, R.; Panayotou, G.; Rui
Cell 70, 419-429, 1992
A;Title: Phosphatidylinositol 3-kinase: structure and expression of the 110 kd catalytic
A;Reference number: A43322; MUID:92354059; PMID:1322797
A;Accession: A43322
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA; protein
A;Residues: 1-1068 <HIL>
A;Cross-references: GB:M93252; NID:g163519; NID:g163252; PIDN:AAA30698.1; PIDN:g163520
A;Experimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBIP:110292)
C;Superfamily: phosphatidylinositol 3-kinase
C;Keywords: phosphotransferase

Query Match   25.3%; Score 1465.5; DB 1; Length 1068;
Best Local Similarity 33.5%; Pred. No. 2.3e-91;
Matches 382; Conservative 204; Mismatches 405; Indels 149; Gaps 39;

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Db   1003 SMMLGSGMPELQSFDDIAYIRKTLADKTEQEALEYFMKQMNDAHHGWTTKMDWIFHTI 1062
          |||| :||||: :||||| : ||| ||| |||||||||||||||||||| :||:||||
```

RESULT 3
I38110
1-phosphatidylinositol 3-kinase (EC 2.7.1.137) alpha isoform - human
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: I38110; S44127
R;Volinia, S.; Hiles, I.; Ormondroyd, E.; Nizetic, D.; Antonacci, R.; Rocchi, M.; Waterf
   Genomics 24, 472-477, 1994
A;Title: Molecular cloning, cDNA sequence, and chromosomal localization of the human pho
A;Reference number: A55636; MUID:95229146; PMID:7713498
A;Accession: I38110
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1068 <RES>
A;Cross-references: EMBL:Z29090; NID:g472990; PIDN:CAA82333.1; PID:g472991
C;Genetics:
A;Gene: GDB:PIK3CA
A;Cross-references: GDB:370915; OMIM:171834
A;Map position: 3q26.3-3q26.3
C;Superfamily: phosphatidylinositol 3-kinase
C;Keywords: phosphotransferase

Query Match   25.2%; Score 1460.5; DB 1; Length 1068;
Best Local Similarity   33.3%; Pred. No. 5.1e-91;
Matches 381; Conservative 206; Mismatches 400; Indels 157; Gaps 40;

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Qy    23 MKPRSTAASLSSMELIP----IEFVLPTSQRNTKTPETALLHVAGHGNVEQMKAQVWLRA  78
Db     1 MPPRPSSGELWGIHLMPPRILVECLLPNGMIVT------LECLREATLVTIKHELFKEA   53

Qy    79 LETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLDCLRYWKVLHRSPGQIHVV 138
Db    54 RKYPL-----HQLLQDESSYIFVSVTQEAEREEFFDETRRLCDLRLFQPF-----LKVI 102

Qy   139 QRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRLVTPRMAEVAGRD------ 192
Db   103 EPVGNREEKI-LNREIGFAIGMFVCEFDMVKDPEVQDFRRNILNVCKEAVDLRDLNSPHS 161

Qy   193 PKLYAMHPWVTSKP-LPEYLLKKITNNCVFIVI-----HRSTTSQTIKVSADDTPGTIL 245
Db   162 RAMYVYPHVESSPELPKHIYNKLDRGQIVVIWVIVSPNNDKQKYTLKINHDCVPEQVI 221

Qy   246 QSFPTKMAKKKSLMDIPES------QNERDFVLRVCGRDEYILVGETPIKNFQWVRQCLKN 299
Db   222 AEAIRK--KTRSMLLSSEQLKLCVLEYQGKYILKVCGCDEYFLEKYPLSQYKYIRSCIML 279

Qy   300 GEBIHLVLDTPPDPALDEVRKE----EWPLVDDCTGVTGYHEQLT-----IHGKDHBSVF 350
Db   280 GRM--------FNLKMMAKESLYSQLPM--DCFTMPSYSYSRRISTATPYMNGE----TS 323

Qy   351 TVSLWDCDRKFRVK---------IRGIDIPVLPRTADLTVFVEANIQYGQGVVLCQRRTS 400
Db   324 TKSLWVINRALRIKILCATYVNLNIRDID---------KIYVRTGIYHGGEPLCDNVNT 373

Qy   401 PKPFTEEVLWNVWLEFSIKIKDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQL 460
Db   374 QRVPCSNPRWNEWLNYDIYIPDLPRAARLCLSI-C-----SVKGRKGA------KEEHCP 421

Qy   461 LYYVNLLLIDHRPLLRHGEYVLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILL 520
Db   422 LAWGNINLFDYTDTPLVSGKMALNLWPVPHGLED--LLNPIGVT-GSNPNKE-TPCLBLEF 477

Qy   521 DNYCHPIALPKHRPTPDPEGDRV-------RAEMPNQLR----KQLEAIIAT 561
Db   478 DWFSSVVKFPDMSVIEEHANWSVSREAGPSYSHAGLSNRLARDNELRENDKEQLKAISTR 537

Qy   562 DPLNPLITAEDKELLLWHFRYESLKDPKAYPKLFSSVKWGGQEIVAKTYQLLAKREVWDQSA 621
Db   538 DPLSEITEQEKDFLWSHRHYCVTIPEILPKLLLSVKWNSRDEVAQMYCL------VKDWPP 592

Qy   622 LDVGLTMQLLDCNFSDENVRAIAVQKLES-LEDDVLHYLLQLVQAVKFEPYHDSALARF 680
Db   593 IKPEQAMELLDCNYPDMVRGFAVRCLEKYLTDDKLSQYLIQLVQVIKYEQYLDNLLVRF 652

Qy   681 LLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAYLRGGCTAMLHDFTQQYQVID 740
Db   653 LLKKALTNQRIGHFFWHLKSEM-HNKTVSQRFGLLESYCRACGMYLKH-LNRQVBAME 710

Qy   741 MLQKVTIDIKSLSAEKYDVSSQVISQLKQLENLQN--LNLPQSFRVPYDPGLKAGALV 797
Db   711 KLINLT-DI--LKQERKDETQKV--QMKFLVEQMRRPDFMDALQGLLSPLNPAHQLGNLR 765

Qy   798 IEBCKKVNASKKKPLWLEFKCADPTALS-----NETIGIIPKHGGDLRQDMLILQILRIM 851
Db   766 LKECRIMSSAXRPLWLNWE--NPDIMSELLFQNNE----IIFKNGDDLRQDMLTLQIIRIM 820

Qy   852 ESIWETESLDLCLLPYGCISTGDKIGMEIVKDATTIAKIQQSTVGNTGA--FKDEVLSH 909
Db   821 ENIWQNQGLDLRMLPYGCLSIGDCVGLIEVVRNSHTIMQI-QCKGGLKGALQFNSHTLHQ 879

Qy   910 WLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNLFHIDFGHIL 969
Db   880 WLKDKDNK-GEIYDAAIDLFTRSCAGYCVAFFILGIGDRHNSNIMVKDDGQLFHIDFGHFL 938

Qy   970 GNYKSFLGINKERVPPVLTPDFLFVMGTSGKK--TSLHFQXFQDVCVKAYLALRHHTNLL 1027
Db   939 DHKKKKFGYKRRRVPFVLTQDFLIVISKGAQBCTKFREFERFQEMCKAYAAIRQHANLF 998

Qy  1028 IILFSMWLMTGMPQLTSKEDIEYIRDALTVGKSEBDAKKYFLDQIEVCRDKGWTVQFNWF 1087
Db   999 INLFSMWLGSGMPELQSFDDIAYIRKTLALDKTEQEALEYFMKQMNDAHHGGWTTKMDWI 1058

Qy  1088 LHLIV 1091
Db  1059 FHTI 1062
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RESULT 4
A54600
1-phosphatidylinositol 3-kinase (EC 2.7.1.137) 110K chain beta isoform - human
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A54600
R;Hu, P.; Mondino, A.; Skolnik, E.Y.; Schlessinger, J.
   Mol. Cell. Biol. 13, 7677-7688, 1993
A;Title: Cloning of a novel, ubiquitously expressed human phosphatidylinositol 3-kinase
A;Reference number: A54600; MUID:94067128; PMID:8246984
A;Accession: A54600
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1070 <HU1>
A;Cross-references: GB:S67334; NID:g455759; PIDN:AAB29081.1; PID:g455760
A;Note: sequence extracted from NCBI backbone (NCBIN:140879, NCBIP:140880)
C;Genetics:
A;Gene: GDB:PIK3CB; PIK3C1
A;Cross-references: GDB:136233
C;Superfamily: phosphatidylinositol 3-kinase
C;Keywords: phosphotransferase

Query Match   23.4%; Score 1354.5; DB 1; Length 1070;
Best Local Similarity   31.8%; Pred. No. 8.5e-84;
Matches 361; Conservative 202; Mismatches 407; Indels 165; Gaps 37;

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Qy    30 ASLSSMELIPIEFVLPTSQRNTKTPETALLHVAGHGNVEQMKAQVWLRALETSVSADFYH  89
Db    22 SQIASDGSIPVDFLLPTG-------IYIQLEVPREATISYIKQMLWKQVHYPM-------  68

Qy    90 RLGPDHFLLLYQKKGQWYEIYDKYQVVQTLD------C-----LRYWKVLHRS-PGQIH 136
Db    69 ------FNLLMDISYMFACVNQTAVYEELEDETRRLCDVRPFLPVYLLVTRSCDPGE-- 120

Qy   137 VVQRHAPSEETLAFQRQLNALJGYDVTDVSNVHDDEL-EFTR--RRLVTPRMAEVAGRD- 192
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C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
C;Accession: T43502
R;Chantry, D.; Vojtek, A.; Kashishian, A.; Holtzman, D.A.; Wood, C.; Gray, P.W.; Cooper,
J. Biol. Chem. 272, 19236-19241, 1997
A;Title: P110delta, a novel phosphatidylinositol 3-kinase catalytic subunit that associa
A;Reference number: 222519; MUID:97382246; PMID:9235916
A;Accession: T43502
A;Status: Preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1043 <CHA>
A;Cross-references: EMBL:U86587; NID:g2331237; PIDN:g2331238; PIDN:AAC25676.1
A;Experimental source: spleen
A;Note: highly expressed in lymphocytes and lymphoid tissues
C;Superfamily: phosphatidylinositol 3-kinase
C;Keywords: phosphotransferase

Query Match          22.8%;  Score 1319; DB 2; Length 1043;
Best Local Similarity 31.9%; Pred. No. 2.1e-81;
Matches  354; Conservative  206; Mismatches  404; Indels  144; Gaps  40;
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Qy   38 IPIEFVLPTSQRNTKTPETALLH--VAGHGNVEQMKAQVWLRALETSVSADFYHRLG-PD   94
Db   20 VVVDFLLPTG----------VYLNFPVSRNANLST:KQVLWHRAQYEPL--FHMLSDPE   66

Qy   95 HFLL-LYQKKGQWYEIYDKYQVVQTLDCLRYWKVLHRSPGQIHVVQRHAPEETLAFQRQ  153
Db   67 AYVFTCVNQTAEQQELEDEQR--RLCDIQPPLPVL------RLVAREGDRVKKL-INSQ  116

Qy  154 LNALIGYDVTDVSNVHDDELEFTRRLVTPRMAEVAGRDPKLYANHPWVT-SKPLP----  208
Db  117 ISLLIAKGLHEFDSLRDPEVNDFRTKM--RQFCEEAAAHRQLGWVEWLQYSFPLQLEPS  174

Qy  209 ----EYLLKKITNNCVFIVI--HRSTTSQTIKVSADDTPGTILQSFFTKMAK--KKSLMD  260
Db  175 ARGWRAGLLRVSNRALLVNVKFEGSEESFFTQVSTKDMPLALMACALRKKATVFRQPLVE  234

Qy  261 IPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNGEBIHLVL-----------D  308
Db  235 QPE------EYALQVNGRHEYLYGNYPLCHFQYICSCLHSGLTPHLTMVHSSSILAVRDEQ  289

Qy  309 TPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRKFPRVK-IRG  367
Db  290 SNPAPQVQKPRAKPPP------------------IPAKKPSS--VSLWSLEQPFSIELIEG  330

Qy  368 IDIPVLPRTAD--LTVFVEANIQYGQQVLCQRRTSPK-PFTEEVLWNVWLEPSIKIKDLP  424
Db  331 RKV------NADERMKLVVQAGLFHGNEMLCKTVSSSEVNVCSEPVWKQRLEFDISVCDLP  385

Qy  425 KGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYYNLLIDHRFLLRHGEYVLHM  484
Db  386 RMARLCFALYAVVEKAKKARSTKK----KSKKADCPIAWANLMLFDYKDQLKTGERCLYM  441

Qy  485 WQLSGKGEDQGSFNADKLTSATNPDKENSMSISLLLDNYC-HPIALP----------  534
Db  442 W--PSVPDEKGELLNPAGTVRGNPNTESAAALVIYLPEVAPHPVYFPALEKILELGRH--  497

Qy  535 TPDPEGDRVR-AEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKD-PKAYPKL  592
Db  498 ------GERGRITEEELQLREILERRGSGE---LYEHEKDLVWKMRHEVQEHFPEALARL  548

Qy  593 FSSVKWGGQQEIVAKTYQLLAKREVNDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLE  652
Db  549 LLVTKWNKHEDVAQMLYLLCS---WPB--LPVLSALELLDSSFPDCYVGSPAIKSLRKLT  603

Qy  653 DDDVLHYLLQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFLFWLRSEIAQSRHYQQ-  711
Db  604 DDELFQYLLQLVQVLKYESYLDCELTKFLLGRALANRKIGHFLFWHLHSEM----HVPSV  659

Qy  712 --RFAVILEAYLRGCGTAMLHDFTQQVQVIDMLQKVT--IDIKSLSAEKYDVSSQVISQL  767
Db  660 ALRFGLIMEAYCRG-STHHMKVLMKQGEALSKLKALNDFVKVSSQKTTKPQTKEMWHMCM  718

Qy  768 KQK--LENLQNLNLPQSFRVPYDPGLKAGALVIEKCKVMASKKKKPLWLEFKCADPTALSN  825
```

```
Db  121 -------------KLDSKIGVLIGKGLHEFDSLKPEVNEFRRKVRKFSEEKIISLVGLSW  168
Qy  193 -PKLYAMHPWVTSKPLPEYILLKKITNNCVFIVIHRSTTSQ--TIKVSADDTPGTILQSFF  249
Db  169 MDWLKQTYPPEHEPSIPENLEDKLYGGKLIVAVHFENCQDVFSFQVSPNMNPIKVNE--  225
Qy  250 TKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNGEEIHLVLDT  309
Db  226 LAIQKRLTIHGKEDEVSPYDYVLQVSGRVEYVFGDHPLLQFQYIRNCVWNRALPHFII--  283
Qy  310 PPDPALDEVRKEEWPLVDDCTGVTGYHEQ--LTIHGKDHESVFTVSL------------  354
Db  284 --------------VECCKIKKMYEQEMIAIEAAINRNSSNLPLPPKKTRIISHV  326
Qy  355 WDCDRKFPR-VKIRGIDIPVLPRTADLTVFVEANIQYGGQVLCQRRTSPK-PFTEEVLWNV  412
Db  327 WENNNPFQIVLVKG--NKLNTEETVKVHVRAGLFHGTBLLCKTIVSSEVSGKNDHIWNE  383
Qy  413 WLEFSIKIKDLPKGALLNLQIYCGKAPALSGKISAEMPSP---ESKGKAQLLYY----VN  465
Db  384 PLEFDINICDLPRNARLCFAVY-AVLDKVKTKKSTKTINPSKYQTIRKAGKVHYPVAWVN  442
Qy  466 LLLIDHRFLLRHGEYVLHMWQLSGKGEDQGSFNADKL------TSATNPDKENSMSIS  517
Db  443 TMVFDFKGQLRTGDIILHSW----------SSF-PDELEEMLNPMGTVQTNPYTENACALH  492
Qy  518 ILL-DNYCHPIALP-------KHRPTPDPEGDRVRAEMPNQLRKQLEAIIATDPLNPLTA  569
Db  493 VKFPENKKQPYYYPPFDKIIEKAAEIASSDSANVSSRGGKKFLPVLKEILDRDPLSQLCE  552
Qy  570 EDKELLWHFRYESLK-DPKAYPKLFSSVKWGQQEIVAKTYQLLAKREVWDQSALDVGLTM  628
Db  553 NEMDLIWTLRQDCREIFPQSLPKLLLSIKWNKLEDVA--QLQALLQIWPK--LPPREAL  607
Qy  629 QLLDCNFSDENVRAIAVQKLESLEDDDVLHYLLQLVQAVKFEPYHDSALARFLLKRGLRN  688
Db  608 ELLDFNYPDQYVREYAVGCLRQMSDEELSQYLLQLVQVLKYEPFLDCALSRFLLERALGN  667
Qy  689 KRIGHFLFWFLRSEIAQSRH---YQQRFAVILEAYLRGCGTAMLHDFTQQVQVIDMLQKV  745
Db  668 RRIGQFLFWHLRSEV----HIPAVSVQFGVILEAYCRG-SVGHMKVLSKQVEALNKLKTL  722
Qy  746 T---IDIKSLSAEKYDVSSQVISOLKQK------LENLQNLNLPQSFRVPYDPGLKAGALVI  798
Db  723 NSLIKLNAVKLNRAKGKEAMHTCLKQSAYREALSDLQS-------PLNPCVILSELYV  773
Qy  799 EKCKVMASKKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQDMLLIQILRIMESTWETE  858
Db  774 EKCKYMDSKMKPLMIVY----NNKVFGEDSVGVIFKNGDDLRQDMLTIQMLRLMDLLWKEA  830
Qy  859 SLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQ--QSTVGNTGAFKDEVLSHWLKEKCP  916
Db  831 GLDLRMLPYGCLATGDRSGLIEVVSTSETIADIQLNSSNVAAAAFNKDALLNWLKEYNS  890
Qy  917 IEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNLFHIDFGHILGNYKSFL  976
Db  891 GDD-LDRAIEEFTLSCAGYCVASYVLGIGDRHSDNIMVKKTGQLFHIDFGHILGNFKSKF  949
Qy  977 GINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLALRHHTNLLLILFSNMLM 1036
Db  950 GIKRERVPFILTYDFIHVIQQGKTGNTEKFGRFRQCCEDAYLILRRHGNLFITLFALMLT 1009
Qy 1037 TGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEYCRDKGWTVQFNWFLHLV     1091
Db 1010 AGLPELTSVKDIQYIKDSLALGKSEEEALKQFKQKFDEALRESWTTKVNWMAHTV     1064
```

```
RESULT 5
T43502
1-phosphatidylinositol 3-kinase (EC 2.7.1.137) 110K chain - mouse
N;Alternate names: p110delta protein
C;Species: Mus musculus (house mouse)
```

```
Db   847  SIRBIKKPFRVKVMGSTRIPLSCIKDIDSSSVTVSISLYHGIECFSKAFTQPIPPPPAF  906
               |:.  .:||      .  :::.|||     :
Qy   405  ---TEEVLWNVLEF-SIKIKDLPKGALLNLQIYCGKRAPALSGKTSAEMPS----PESKG  456
               ::  :|| | :.  :|:.:.:|  .: :|.::|
Db   907  LAEFLSVDWCEWIVFTNIDYSNLPVDARLSISVYS------ANETVDDVEEIKNLDEATK  960
               || .  || ||:.|||||    :|::|:|| | :|::|:
Qy   457  KAQLLYYVNLLLIDHRFLLRHGEYVLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSI  516
               |.|.|.|.|||||||  :||  :|.|::  :      ::|
Db   961  KLTPIGWINVMITDFKYQLRQGMVELSLW---------PSDFSNPLGTCSNNPSSSQSVGL  1012
               :||.|:.:|  .:|:.||::
Qy   517  SILLDNYCHIPIALPKHRPTPDPEGDRVRAEMP----NQLRKQLEAIIATDPLNPLTAED  571
               ||.:|.||  : :  : :::|: .::|
Db  1013  TLEFEEFNLPVLFP--RKTKFSTSVSVIEQPPTNINSNEMREFFEQITALDDLSDLKQEK  1070
               :|||.|||.|.||| ::.|.||.|::..::
Qy   572  KELLMHFRYESLKDPKAYPKLFSSVKWGQQEIVAKTYQLLAKREVWDQSALDVGLTMQLL  631
               |:|. ::::||||  :::||  |:.:..:::|.| :  . :.|||| :
Db  1071  YNQLWTLRHYSILFPQVLPRLMLSVPWTQATAVDEAISLLDR---WPK--LKPYESLELL  1125
               ::  .::..:|||| || .|.:: :|::|.:::..||
Qy   632  DCNFSDENVRAIAVQKLESLEDDDVLHYLLQLVQAVKPEPYHDSALARFLLKGLRNKRI  691
               ||.:|:..::|  : ::|:.||::|:|. .:||||
Db  1126  DAKHANRKVREFAVTCLEDLSEDELLDILLQLVQVLKYEPFHDSKLSRFLIRKAILNRNI  1185
               |.|..::|:||..:|.|||.::::|:.:||:||.:.::|||
Qy   692  GHFLFWFLRSEIAQSRHYQQRFAVILEAYLRGCGTAMLHDFTQQVQVIDMLQKVTIDIKS  751
               ||.:||||:|:||:|  :||  .:.|::|:.|..: .::|:..:|.|::||::|
Db  1186  GHSFFWYLKSDLHDS-NLSERFGILLESYLYACGAHRI-ELLKQMEVINNLTEVAKKIKP  1243
               :..||:.|.: |  ||:||||.:|||::|:.|:||  :
Qy   752  LSAEKYDVSSQVISQLKQKLENLQNLNLPQSFRVPYDPGLKAGALVIEKCKVMASKKKPL  811
               |.::||.|::|:|.||.||:||.||:.|..||.||:|||||.|.:||.|.:||:|:||
Db  1244  LKDQ------------DRRBEMIKBFESLEWPKRFHLTLNPRPBSNGLIINKSKYMDSKKLPL  1294
               |||                :||::|||||.||||:||:|.|:...||||:::|:..:||
Qy   812  WLEFKCADPTALSNETIGIIFKHGDDLRQDMLIQIIRIMESIWETBSLDLCLLPYGCIS  871
               ||.|:.|:||.|||||||||||||||||||.||:|:|::|:|||:|||||.|:||||||
Db  1295  RLSFTNTDMNA---DPIEVIFKAGDDLRQDMLTLQMIRLMDKLWQKEGLDLKLSPYGCIS  1351
               :||:||:|||    :|||:|||||||||||||..|::|||.|:|::.|||:|..|||||
Qy   872  TGDKIGMIEIVKDATTIAKIQOSTVG-----NTGAFKDEVLSHWLKEKCPIBEKFQAAVE  926
               |||:||.|||::|||:|:|||:||:      |||.|:|||::|| |:|.|:|::|:..|
Db  1352  TGDMIGMIEVVLNSETTAKIQKSEGGGAFRFOVGSFGQLILQH---NKSDME--YQKAVD  1406
               |||:|||||:|:||||||||:|  |.|||.|:...|.|||:.|    |:|:|  ||:||
Qy   927  RFVYSCAGYCVATFVLGIGDRHNDNIMISETGNLFHIDFGHGILGNYKSFLGINKERVPFV  986
               ||:.|.||||.||.|||||||||:|||||||||||||||||||||||||:|||.:|:||||
Db  1407  TFILSCAGYCVATVVLGIGDRHNDNLMVTKGGRLFHIDFGHFLGNYKKKFGFKRERAPFV  1466
               ||:|||||||||.||||||||||:||..||.|.|||||||:|||||:|:|.|:|||.|||
Qy   987  LTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLALRHHTNLLJLIFSMLMTGMPQLTSKE  1046
               |||||:|.|||.|||.||:||:|:|.::|.|.|:|:|||||:||||||||.:||.|||
Db  1467  FTPDFCVVM---GGKESFKFSQFVNYCCTGYNIVRKNAKLFMNLFAMMVSTGIPELQSME  1523
               |||||.||    ||:||||:||.|:|.||||::|.||..:.|||:|:.::||||.||
Qy  1047  DIEYIRDALTVGKSEEDAKKYFLDQI-EVCRDKGWTVQFNWFLH  1089
               |:||:|||..|||:|..||:|:|.|  :.|.|.|||:||||||
Db  1524  DLNYLKESFSIELSDAKAREKFVALIHESLATK--TTQLNNFFH  1565
```

RESULT 6
T18272
1-phosphatidylinositol 3-kinase (EC 2.7.1.137) - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T18272
R;Zhou, K.; Takegawa, K.; Emr, S.D.; Firtel, R.A.
Mol. Cell. Biol. 15, 5645-5656, 1995
A;Title: A phosphatidylinositol (PI) kinase gene family in Dictyostelium discoideum: Bio
A;Reference number: Z06411
A;Accession: T18272
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1570 <ZHO>
A;Cross-references: EMBL:U23476; NID:g733519; PID:g733520; PIDN:AAA85721.1
C;Genetics:
A;Gene: PIK1
C;Keywords: phosphotransferase

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Query Match       22.4%;   Score 1297;   DB 2;   Length 1570;
Best Local Similarity  30.9%;   Pred. No. 1.3e-79;
Matches  347;  Conservative  203;  Mismatches  406;  Indels  168;  Gaps  37;
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RESULT 7
T13950
1-phosphatidylinositol 3-kinase (EC 2.7.1.137) - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
C;Accession: T13950
R;Leevers, S.J.; Weinkove, D.; MacDougall, L.K.; Hafen, E.; Waterfield, M.D.
EMBO J. 15, 6584-6594, 1996
A;Title: The Drosophila phosphoinositide 3-kinase Dp110 promotes cell growth.
A;Reference number: Z17828; MUID:97133288; PMID:8978685
A;Accession: T13950
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1088 <LEE>
A;Cross-references: EMBL:Y09070; NID:g1707447; PIDN:CAA70291.1; PID:g1707448
C;Genetics:
A;Cross-references: FlyBase:FBgn0015279
A;Map position: 3
C;Superfamily: phosphatidylinositol 3-kinase
C;Keywords: phosphotransferase

```
Query Match       22.2%;   Score 1283;   DB 2;   Length 1088;
```

```
Db   719  QSPLDPSTLLEEVCVEQCTFMDSKMKPLWIMYSSEBAGSAGN  772
               :|: . :  ||         ||:.| ||::::::.|  || |
Qy    40  IEFVLPTSQRNTKTPETALLHVAGHGNVEQMKAQVWLRALETSVSADFYH--RLGPDHFL  97
               :|:|      ||| |:|.:|.|.|.|| :.||:.:|:|.|.:|:  |||    :||.|:|
Db   826  ETIGIIFKHGDDLRQDMLLQILRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDA  885
               ||||||||||||||||||:|||:||||.||||:|||||||||||||||:||.|||:|||
Qy   536  ILFLMPNQSKK------ILQVKGSDTIENLKERIISDYLPNNSNNNNNCKYGADSYL  588
               ||||:|:.|:|     ||::|.:||::|||:||:|:||:|.||:||||:|...|:
Db   773  --VGIIFKNGDDLRQDMLTLQMIQLMDVLWKQEGLDLRMTPYGCLPTGDRTGLIEVVLHS  830
               |||||||||||||||||||:|::|||:.||:.|||||:|||||.||||:.|:||::|:
Qy    98  LL---------------------YQKKGQWYEIYDKYQVVQTLDCLRYWKVLHRSPGQIHVV  138
               ||                      :||.||.::||.||..:|.|:|:|.|:|.|.||:|::
Db   886  TTIAKIQ--QSTVGNTGAFKDEVLSHWLKEKCPIBEKFQAAVERPVYSCAGYCVATFVLG  943
               |||||:|   ||.||||.|:||::|||||||||||||:|.|.||:|||||||||||.|||
Qy   589  ILDFNDNPMERSLVLNKSDYILDXRAQ--GLIPKLKVIEKSTIIDSDPSDELSPSEYEII  646
               ||||:|||.:||::|:|||::||:|    ||:||:|::||::|::|||||||.|:|:||:
Db   831  DTIANIQLNKSNMAATAAFNKDALLNWLKSKNP-GEALDRAIEEFTLSCAGYCVATYVLG  889
               ||:|:||||.:|:|||.||||||||||:|:|.| ||||||||||||||||||||||.|||
Qy   139  QRHAPSEETLAFQRQLNALIGDVTDVSNVHDDLEFTRRRLVTPRMAEVAGRDPKLYAM  198
               ||:||..||:|.||||:|:||.|.|.||.||||:|:|||||::|:|.|.|||.|:|.|
Db   944  IGDRHNDNIMISETGNLFHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTS  1003
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   647  RKLIPIGTDTW--------RGEEVEYFRR--VTSRLR-------YEA  675
               |:|:|:||.| :       :|:||.:|::  |.||:|       |:|
Db   890  IGDRHSDNIMIRESGQLFHIDFGHFLGNFKTKFGINRERVPFILTYDFVHVIQQGKTNNS  949
               |||||.||||||:||.|||||||||||||:|:|.||||||||||||||||:|::||:||:
Qy   199  HPWVTS----------KPLPEYLLKKITNNCVFIVIHRSTT--SQTIKVSADDTPGTILQ  246
               ||||||         :||||||||::|:|.||:|::|||:   ||:||.|.||:|||:|:
Db  1004  LHFQKFQDVCVKAYLALRHHTNLLILFSXMLMTGMPQLTSKEDTEYIRDALTVGKSEED  1063
               ||||||||||||||||||||||:||:||.|||||||||||||:|||||||||||||||:
Qy   676  LPLIKGSIOSTLLVRLSPLP----IPIVGNKILISIFLPITQVTKTLDLELNETADQFTN  731
               ||||||:::||:|:||||||    :|:||||::||:|:|:||.||:||:|:|.|||:||
Db   950  EKFERFRGYCERAYTILRRHGLLIFLHLFALMRAAGLPELLSCSKDIQYLKDSLALGKTEBE  1009
               ||||||||:|||||||:|||.|||||:|:|.||||||||:|||||:|||||.|||||||
Qy   247  SFFTKMAKKXSLMDIPESQNERDFVLRVCGRDEVLVGETPIKNFQWVRQCLKNGEBIHLV  306
               |||:||||||.|||||.|||||||:|||:|||||||.||||||||||||.|||.|||:|:
Db  1064  AKKYPLDQIEVCRDKGWTVQFNWFLHLV  1091
               |||||||||||||||||||||||||||:
Qy   307  LDCTPPDPALDE---VRKEEWP---LVD-DCTGVTGYHQLT------IHGKDHESVFTV  352
               |||.|||.||:   ||.|:||   |:|  ||.|..||::|       :|||:|||:||
Db  1010  ALKHFRVKFNEALRESWKTKVNWLAHNV  1037
               ||||||||||||.||||||||:|||||:
Qy   353  SLWDCDRIKFRVKIRG---IDIPVLPRTADLTVFVEANIQYGQOVLCQRRTS---PKPF--  404
               |||.||:||||::||    :|:||.||:|.|:|.|||:|.|||.||.|||:    |||
```

C;Accession: T18273
R;Zhou, K.; Takegawa, K.; Emr, S.D.; Firtel, R.A.
Mol. Cell. Biol. 15, 5645-5656, 1995
A;Title: A phosphatidylinositol (PI) kinase gene family in Dictyostelium discoideum: Bio
A;Reference number: Z06411
A;Accession: T18273
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1858 <ZHO>
A;Cross-references: EMBL:U23477; NID:g733521; PID:g733522; PIDN:AAA85722.1
C;Genetics:
A;Gene: PIK2
C;Keywords: phosphotransferase

Query Match 21.3%; Score 1233; DB 2; Length 1858;
Best Local Similarity 29.6%; Pred. No. 3.7e-75;
Matches 338; Conservative 178; Mismatches 364; Indels 260; Gaps 31;

```
Qy    157 LIGYDVTDVSNVHDDELEFTRRRLVTPRMAEVAGRDPKLYAMHPWTSKPLPEYLLKKIT 216
          || :|  |:: ||       :  :  ||     ::  | ::::  || | ||  : ||
Db    768 LIGTSFTRVLDGQQEVVSF-RRDFAQFRLSNFTSTRNDLSQM-IYVSSEPLPLTIPNKIT 825

Qy    217 NNCVFIVIHRSTTSQTIKVSADDTPGTILQSFFTKMAKKSLMDIPESQ-NERDFVLRV 274
               :     ::|   |: | :   |   | |  ::: :    ::  :||||: ||
Db    826 -----IMVLLPGDGKIIK-RVDCCPNSSVGDVKKEIFKKPFAMIDRVHTQGKTQDDFVLKV 879

Qy    275 CGRDEYLV---------------------------GETPIKNFQWVRQCLKNGEEIHLVLDTPPDPA 314
                                                 ::| :    : ||| : :  | | :|| ||
Db    880 TGFREYILCIHELGNLTSRQRFYPTGSSGGDFSLMDYDYIRQCVGKNQTVELSLTNNSILS 939

Qy    315 LDEVRKEEWPLVD---DCTGVTGYHEQL-----------------------------TIHGKDHESVFTV- 352
          ||: :    : |     : | |  |                                :| | |:  ::
Db    940 LNQV-SEKVSFIDKILETSDPDYDEDLDSINSNSFPDLKQSICQQQQQIQTVINIKET 998

Qy    353 --------------------------------------------------------- 352
Db    999 NKENKDSNKENKDSSSNNNNNNNNNNNNNNNNNNNNNNNGNNGNNGNSNNNSNSNI 1058

Qy    353 SLWDCD------------------------------------------RKFVKIRGIDIPVLPR 375
          ::|  |                                          || |: | | |  | |
Db   1059 SRGSIDSEGNGSSGSNGSEQPTLIGVQNFSLPNNSKLPINIVKRLFRVNIAGLRNLNFNN 1118

Qy    376 TADL----------------------------------------------BEVLW 410
            :|                                              :|:
Db   1119 NEDARNKFADGKNNQPNVFVMAELYYGGELI----------TNP-VFTPIAQLASYGDGSVEFPNW 1173

Qy    411 NVWLEFSIKIKDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYVNLLLID 470
          | ||| |  |||| |  : :||:|| | |::  |  ::     :||: :| ||:| | :
Db   1174 EKGIAFTIPIRYLPRARARASFTVY--VTTISEALESQM--DEVVSKSIPIGWSNCLLMN 1228

Qy    471 HRFLLRHGEYVLHWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIA-- 528
          || | || |  : : || || ||::  ::::       | || : : | | | :
Db   1229 HKGMLRMGPTAFRLWDDGRRANPIG-------TCVDNQAAKQPIILLVEFSFSPIRPIVYV 1281

Qy    529 --------------------------------------------LPKHRPTPDPEGDRVRAEMPNQL 551
                                                      | : | |  ||||||:  :
Db   1282 DTALQSMVNDSSISSNGVESPSIVSFSSSAASSSPLPS-SPLPSPVGLK--KLDLDE 1337

Qy    552 RKQLEAIIATDPLNPLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYVNLLLID---- 611
          | :||     ||| |  |  |  |   | ||::||  ||| : |:||: :: || || :
Db   1338 ARRLKALMDSDPLVQLSABDKKLVYGYRHIYKSKPALAKFLLSVNWIDPDQVTDAY--- 1394

Qy    612 AKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYLLQIVQAVKFEP 671
          || :   | | |||:|  | |  :  |::  : |  || :||||  :|| |: | ||:
Db   1395 --RQMNDWALLKPVQALEILDAKFADEHVRNFAIKIINSFSDAEFSDFLLQLTQVLKYEP 1452

Qy    672 YHDSALARFLLKRGLRNK-RIGHFLFWFLRSEM-HTPEIERYGLLLEGYLRGCGTAMLH 730
          || ||| | |:| | |:  | | ||  ||:|:   :   | : : | :   | :|
Db   1453 YHNSDLTHILIQRALSNRSRIGHFFWFLKSEM-HTPEIEBRYGLLEGYLRSCGTHR-Q 1510

Qy    731 DFTQQVQIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLPQSFRVPYDPG 790
          |  ::  : | : : :  :   |  |  |  | :|   | : |:   ||   :|   | |
Db   1511 DLIKQNQYLKSLHTVAMAVKQTNGSS-----ERRKVLMEGLSKKFPDTFQLPLDPR 1562
```

```
Qy    791  LKAGALVIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQDMLILQILRI  850
                ||||| |: ::||  ||||| || ::|   | :|||:|||||||||||||:|:|||||
Db   1563  WEAKGLIIDKCRYMDSKKLPLWLVFENVEPHA---KPLIVIFKVGDDLRQDILTLQVLRI 1619

Qy    851  MESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTGAFKDE-VLsH  909
                |::||| |||:||||||||||||||| || :::| :|||||||||||||||:| :| :|
Db   1620  MDKFWKNSGMDLRLQLPYKCIATGDGIGMLEVLNANTIANINKD-AGGTGALLEEKTLVN 1678

Qy    910  WLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNLFHIDFGHIL  969
                |||||   ||| ::||| ||||||||||||||||||||||||||||||||||||||||||
Db   1679  WLKECNKTEAYNKAVETFILSCAGYVVATYVMGIGDRHSDNIMITKLGHLFHIDFGHFPL 1738

Qy    970  GNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHPQKFQDVCVKAYLALRHTNLLII 1029
                ||||||   ::|:  :|:|| |  |::|: :|  :||
Db   1739  GNYKKKYGPKRERAPPIFTQYMAIV---GGKDSENFKRFVTTCCSAYNILRKNTDLFIN 1795

Qy   1030  LFSWMLTMGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGWTVQFNWFLH 1089
                |:| :| :|||||||||||||||||||:|||||:||||||||| :||| :|||| |||||
Db   1796  LFQLMLSTGIPELQVAEDIDYLRKALAPGLSDEEAAEEFTKNISVALNTK-TVLLNDIFH 1854
```

RESULT 9
T18274
1-phosphatidylinositol 3-kinase (EC 2.7.1.137) 3 - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T18274
R;Zhou, K.; Takegawa, K.; Emr, S.D.; Firtel, R.A.
Mol. Cel. Biol. 15, 5645-5656, 1995
A;Title: A phosphatidylinositol (PI) kinase gene family in Dictyostelium discoideum: Bio
A;Reference number: Z06411
A;Accession: T18274
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1585 <ZHO>
A;Cross-references: EMBL:U23478; NID:g733523; PID:g733524; PIDN:AAA85723.1
C;Genetics:
A;Gene: PIK3
C;Keywords: phosphotransferase

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Query Match             19.6%;  Score 1136.5;  DB 2;  Length 1585;
Best Local Similarity   28.2%;  Pred. No. 1.1e-68;
Matches  337;  Conservative 214;  Mismatches 413;  Indels 231;  Gaps  41;

Qy      2  ELENYEQPVVLRE-----DNRRRRRMKP----RSTAASLS---SMELIPIE--------F   42
                                : ::                   ::|          |: :
Db    411  KLENEEREKILKERNEIDNLKKKKNHLSKGYFMRACNASNDDGLEEEDIPLQDEHWETNVI 470

Qy     43  VLPTSQRNTKTPETALLHV-------------AGHGNVEQMKAQVWLRALETSVSADFYH   89
                   | |:  :|   :||                ||   | :|| : |: |: : :| | :
Db    471  VLLPCRHHVKVPGSSSSSSIDSIRQLAWASGKMQGHLNLEKDEKFFTLRWCNKDVVFDQDT 530

Qy     90  RLGPDHFLLLYQKKGQWYEIYDKYQVVQTLDCLRYWKVLHRSPGQIHV-VQRHAPSEETL 148
                :|                                :|::| :   ::|| |
Db    531  PLG--HLI-------------------------------QYNLNYNNPTQKPNIKLELVLEDEL 562

Qy    149  AFQRQLNALIGYDVTDVSNVH-------DDELEFTRR------RLVTPRMAEVAGRDPKL 195
                 | :| |:|| |:  |::  :         ||: |          :| | : :|| ::|
Db    563  CKER---LVDLQSLEINNGRPSIWKSHIDDDVLSFNRKLRELAMLAKFQSNVPAAR--- 614

Qy    196  YAMHPWVTSKPLPEYLLKKITNNCVFIVIHRSTTSQTIKVSADDTPGTILQSFFTKVAKK 255
                 |   :|: :   : ::|       |:     : :|  :   :  ||:| |: |:| ||
Db    615  --LTPYPPPKTIPEPFV------IRVHLFKNQTKSLRCANNHTAFSLMTILSEKLKN 663

Qy    256  KSLMDIPESQNERDPVLRVCGRDEYLVGETPIKNFQWRVQCLKNGEEIHLV-------- 306
                |:|  |  : |   ||: |        |   |: :  :|: :  : | :|
Db    664  TTPFD-----PTQRFLITGINQYVDPNVPLLSVEYIVEKIKRKGEIDLTMVELLSLGL 717

Qy    307  ---------------------LDTPPDP--------ALDEVRKEEWPL--VDDCTGVTGYH 336
                                         :                                :|
Db    718  IIQQQQQQQQQQQQQQQQIENIDDENILKLNNGILNVLSKIEKPIREKDNCISSLTVT 777
```

```
Qy    337  EQLTIHGKDHESVFTVSLWDCDRKFRVKIRGIDIPVLPRTADLITVPVEANIQYGQQVLCQ  396
                :|| ::  ::||:|||| ||: ::  : : |||| | | :: : |:  | :::| :|| :|
Db    778  ENLQVRLLHAHEIFASK--------ASEIIGTDSP------SIQLFIEAAVVFGGELLAT  823

Qy    397  RRTSPKPFTEEVLMNVWLEFSIKIKDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKG  456
                      :        |: : : : :| |||   |:|            ::
Db    824  QSSKLVSFQDTVVWNEWVNIPLAVSNIPNGARMCLGL-------------NARYRG  866

Qy    457  KAQLLYVNLLLIDHRFLLR-HGEYVLHMWQLSGKGBDQGSFNADKLTSATNPDKENSMS  515
                ||   : :: :::  : ||  |:  |  :  :    ::   :  :
Db    867  DIFNIGWCGHRLFDSKGILNTFAPFSLLLW---PGKINPIGTC-VDNLES------KDQAII  918

Qy    516  ISILLDNYCHPIALPKHRPTPDPEGDRV----RAEMPNQL---------RKQLEAIIATDPL  564
                |:| |:: |    |  :  | :  : :        :: :|            ::| | : :|
Db    919  IAPEFKDY----VVPK---TIHYEDDLIELISKDENGNELPVTMEEMDRVEQIIIQDPL  971

Qy    565  NPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGGQQEIVAKTYQLLAKREVWDQ-SALD  623
                ::|  |:  :  :|: :  |  :: ::| :  ||    |  || :::  :: :|  :: | |
Db    972  YSLNKEERLLIWKSRYFCHTKPQALSKLLQSVEWTNYKQVGBAFQLL---KIWPTLSAVD 1028

Qy    624  VGLTMQLLDCNFSD-ENVRAIAVQKLESLEDDDVLHYLLQLVQAVKFEPYHDSALARFLL  682
                                                                     ::| | |: :|
Db   1029  ---ALELLDPKFADCVEIREYTVKCLDQMSDYELEIYILLQLVQAIKHDVFHNSVLSLFLI 1085

Qy    683  KRGLRNKRI-GHFLFWFLRSEIAQSRHYQQRFAVILEAYLRGCGTAMLHDFTQQVQVIDM  741
                   |  |::  || ||: |:  |     :  :: |::| |  ::::|  |||  ||::  |
Db   1086  GRVWQNMQVLGHPFWHIRADI-DNQEVCERRFRVLSSGFLRYAPTQIMESFKREITTLRI 1144

Qy    742  LQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLPQSFR-----VPYDPGLKAGALV  797
                |:|     :   ||::|  :::: :||||||  | :|       :|  ::::   : |  :
Db   1145  LENLAKRVKEVPVEK--------RKQYVEN--NLREEQSPFTELFVPFDPSIRILNII 1192

Qy    798  IEKCKVMASKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQDMLILQILRIMESIWET  857
                |||||||||||||||||||||||||||||||||||||||||||||||||||| :  :|:
Db   1193  PEKCKSNMDSAKVPLWVTFKNADPFA---PPLQMIAKTGDDLRQDILTLQLLRLMDHMWKS 1249

Qy    858  ESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTGAFKDEVLSHWLKEKCPI  917
                ::|:|  |        | :  ::|  |   |  | ||:  :  |  | |   : ||:
Db   1250  QDLDLHMTIYRCIATGMGTGLIEVVPNSETARIQAGAGGVSGAFKQTPIANWLKNHNQT 1309

Qy    918  EEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNLFHIDFPGHILGNYKSFLG  977
                :|| :|||| || |||| ||   || |||||:||||  :|||| ||||  || | | |  :
Db   1310  ENSYQKAVSKFTLSCAGYCVATYVLGIGDRHNDNIMVDIHGHLFHIDFHGHFLGNFKTFAG 1369

Qy    978  INKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLALRHTNLLILLFSMMLMT 1037
                :  | |  |:| |  ::|  | |   |   :   |:   :|| :: :||:||  |::|:
Db   1370  FQREKAPFVLTPDFVVVI---GGKDSPNFAFFVDICCKAFNIIRSNAHVFINMFELMLST 1426

Qy   1038  GMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKG-WTVQPNWFLHLV 1091
                | :| ::|:|: ||::| ||:|:  ||: |:| ||  |: :  :  |: :  :|:
Db   1427  GIPELRSENDIVYLRDKFRLDLTDAEASEYFKKLIH--ESIGTLTTTINFAIHIM 1479
```

RESULT 10
T42642
phosphoinositide 3-kinase (EC 2.7.1.-) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-May-2000
C;Accession: T42642
R;Molz, L.M.; Chen, Y.W.; Hirano, M.; Williams, L.T.
J. Biol. Chem. 271, 13892-13899, 1996
A;Title: Cpk is a novel class of Drosophila ptdins 3-kinase containing a C2 domain.
A;Reference number: Z17659; MUID:96278830; PMID:8862856
A;Accession: T42642
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1658 <MOL>
A;Cross-references: EMBL:U52193; NID:g1272421; PID:g1272422; PIDN:AAC52604.1
A;Experimental source: strain balb c
C;Genetics:
A;Gene: cpk
C;Superfamily: HsC2 phosphatidylinositol 3-kinase; protein kinase C C2 region homology
C;Keywords: phosphotransferase

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Query Match      18.6%;   Score 1076.5; DB 2;  Length 1658;
Best Local Similarity   28.0%;   Pred. No. 1.4e-64;
Matches  330;   Conservative  198;   Mismatches  381;   Indels  269;  Gaps  39;

Qy    108 EIYDKYQVVQTLDCLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRQLN--ALIGYDVTDV 165
              :::    ::::    : :    :  :::     : : :::  :: :::::::::
Db    932 CAGYCVATFVLGIGDRHNDNIMISTGNLPHIDFGHILGNYKSFLGINKERVPFVLTPDF 991

Qy    259 QISPKSEDINKFD-----W--LDLDPWDAVLLEERSPS---CHLERKVNGKSLSGATVTRS 309
               ::::::       :  :::  :: :    :  ::   :::  :::: :  ::
Db   1208 CAGCCVATYVLGICDRHNDNIMLRSTGHMFHIDFGKPFLGHAQMFGSFKRDRAPFVLTSDM 1267

Qy    166 SNVHDDELEFTRRRLVTPRMAEVAGRDP------------------------K 194
             ::  : :   ::::  ::  ::
Db    992 LFVMGTSGKKTSLHFQKFQDVCVKAYLALRHHTNLLIILFSMMLMTGMPQLTSKEDIEYI 1051

Qy    310 QSLIIRTAQFTKAQ-------GQVSQKDPNGTSSLPTGSSLLQEFEVQNDEVAAFCQSIMK 363
              :::   ::  :        :
Db   1268 AYVI-NGGEKPTIRFQLFVDLCCQAYNLIRKQTNLFLNLLSLMIPSGLPELTSIQDLKFV 1326

Qy    195 LYAMHPWVTSKPLPEYLLKKIT---NNCVFIVIHRSTTSQTIKVSADDTPGTILQSFFT- 250
                :     :::   :  :::                ::    :::   :
Db   1052 RDALTVGKSEEDAKKYFLDQIEVCRDKGWTVQFNWFLH 1089

Qy    364 LKTKFPYTDHCTNPGYLLSPVTVQRNMC-------GENASVKVSI-BIEGLQLPVTFTC 414
                ::                 :  :      :::    ::
Db   1327 RDALQPQTTDABATIFFTRLIESSLGSIAT-KFNFFIH 1363

Qy    251 ---KMAKKKSLMDIPESQNERD---FVLRVCGRDEYLVGETPIKNFQWVRQCLKNGE 301

RESULT 11
S71792
phosphatidylinositol-3-OH kinase AGE-1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 12-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 01-Dec-2000
C;Accession: S71792; T31476, T18707
R;Morris, J.Z.; Tissenbaum, H.A.; Ruvkun, G.
Nature 382, 536-539, 1996
A;Title: A phosphatidylinositol-3-OH kinase family member regulating longevity and diapa
A;Reference number: S71792; MUID:96320556; PMID:8700226
A;Accession: S71792
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1164 <MOR>
A;Cross-references: EMBL.U56101
R;Williams, L.
submitted to the EMBL Data Library, October 1999
A;Reference number: Z21038
A;Accession: T31476
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-263,'YEMR', 270-285,'L','Q',289-307,324-328,'LESY',332-1164 <WIL>
A;Cross-references: EMBL.AL110499; PIDN:CAB57914.1; CESP:B0334.8
A;Experimental source: clone Y62F5A
R;Swinburne, J.
submitted to the EMBL Data Library, October 1995
A;Reference number: Z19009
A;Accession: T18707
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1089-1164 <WI2>
A;Cross-references: EMBL.Z66519; NID:g1044812; PIDN:CAA91377.1; GSPDB:GN00020; CESP:B033
C;Genetics:
A;Gene: CESP:B0334.8
A;Experimental source: clone B0334
A;Map position: 2
A;Introns: 22/2; 117/3; 307/3; 748/2; 835/2; 960/2; 1077/2; 1121/3
C;Superfamily: phosphatidylinositol 3-kinase

Query Match      17.8%;   Score 1031;   DB 2;   Length 1164;
Best Local Similarity   27.1%;   Pred. No. 1e-61;
Matches  316;   Conservative  221;   Mismatches  406;   Indels  222;  Gaps  43;

Qy    302 EIHLVLDT----------PPDALDEVRKE---EWPLVDDCTG------VTGYHEQL 339
              ::                ::  :  ::         ::::::
Db     78 ALETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLDCLRYWKVLHRSPGQIHV 137

Qy    475 EIKLQLLTLSAMCQNLARTAEDDEAPVDLNKYLYQIEKPYKEVMTRHPVBELLDSYHYQV 534
              :::   :  :    :          ::  :    ::::   :::
Db     68 SLEIKLS-DFKHQL----FELIAPMKWGTYSVKPQDYVFRQLNNFGEIEVIFNDDQPLSK 122

Qy    340 TI---HGKDHESVFTVSLWDCDRKFRVKIRGIDIPV------------LPR--TADLT- 380
                  :::    :::   :   : :                      :     ::
Db    138 VQRHAPSEETLAFQ-------RQLNALIGYDVTDVSNVHDDEL-EF-------TRR 178

Qy    535 ELALQTENQHRAVDQVI--KAVRKICSALDGVBTPSVTBAVKKLKRAVNLPRNKSADVTS 592
               : :         :     :::::    :::     :  ::::
Db    123 LELHGTFPMLFLYQPDGINRDKELMSDISHCLGYSLDKLEESLDERLRQFRASLWARTKK 182

Qy    381 ---------VFVEANIQYGQQVL---------------------CQRRT-------- 399
                                                         :
Db    179 RLVT------------------------PRVAEVAGRDPKLYAMHPWVTSKPLPEYLLKKI 215

Qy    593 LSGSDTDRKNSTKGSLNPENPVQVSMDHLTTAIYDLLRLHANSSRCSTGCPRGSRNIKEAW 652
               :: :  :      :         : :   :  : :
Db    183 TCLTRGLEGTSHYAPPEEQYLCVGGSCPKDLESKVKAAKLSYQMFWRKRK------AEI 235

Qy    400 ----------------------------------------SPKPFTEEVL 409
                                                      :
Db    216 TNNCVFIVIHRSTTSQTIKVSADDTPGTILQSFFTKM-AKKKSLMDIPESQNERDFVLRV 274

Qy    653 TATEQLQFTVYAAHGISSNWVSNYEKYYLICSLSHNGKDLFKPIQSKKVGTYKNFFYLIK 712
               ::  :   :     :   :    :  : :::  :
Db    236 NGVC------------EKMMKIQIEFNPNETPKSLLHTFLSRTNAIKLDVVTDPDADEGWFRSEL 289

Qy    410 WNVWLEFSIKIKDLPKGALLNLQIY--CGKAPALSGKTSAEMPSPESKGKAQLLYYVNLL 467
                :::    :    ::  ::   :   ::         :  :   :       ::
Db    275 CGRDEYLVGETPIK---------------NFQWVR-----QC--LKNGEEIHLVLD 308

Qy    713 WDELIIFFPIQISQLPLESVLHLTLFGVLNQSSGSSPDSNKQRKGPEALGK-----VSLT 766

Qy    468 LIDHRFLLRHGEYVLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPI 527

Qy    767 LPDFKRFLTCGTKLLYLWTSSHTNSIPGAI-----------PKKSYVMERIVLQVDF---- 812

Qy    528 ALPKHRPTP-------DPEGDR--VRAE----MPNQLRKQLEAIIATDPLNPLTADEKEL 574

Qy    813 -----PSPAFDIIYTSPQIDRNIIQQDKLETLESDIKGKLLDIIHRDSSFGLSKEDKVF 866

Qy    575 LWHFRYESLKDPKAYPKLFSSV---KWGQQOEIVAKTYQLLAKREVWDQSALDVGLIMQLL 631

Qy    867 LWENRYYCLKHPNCLPKILASAPNWKWAN--LAKTYSLLHQ---W--PPLCPLAALELL 918

Qy    632 DCNFSDENVRAIAVQKLESLEDDDVLHYLLQLVQAVKFEPYHDSALARFLLKRGLRNKRI 691

Qy    919 DAKFADQGVRSLAVSWMEAISDDELADLLPQFVQALKYEIYLNSSLVRFLLSRALGNIQI 978

Qy    692 GHFLFWFLRSEIAQSRHYQQRFAVILEAYLRGGTAMLHDFTQQVQVIDMLQKVTIDIKS 751

Qy    979 AHSLYWLLKDAL-HDTHFGSRYEHVLGALLSVGGKGLREELSKQMKLVQLLGGVABKVRQ 1037

Qy    752 LSAEKYDVSSQVISQLKQLENLQNLNLPQSFRVPYDPGLKAGALVIEKCKVMASKKPL 811

Qy    1038 ASGS---TRQVV--LQKSMERVQSFFLRNKCRIPLKPSLVAKELNIKSCSFFSSNAMPL 1091

Qy    812 WLEFKCADPTALSNETIGIIFKHGDDLRQDMLIIQILRIMESIWETBSLDLCLLPYGCIS 871

Qy    1092 KVIMWNADFL--GEEINVMFKVGEDLRQDMLALQMDKIIMDKIWLKEGLDLRMVIFRCLS 1148

Qy    872 TGDKIGMIEIVKDATTIAKIQQSTVGNTGAFKDEVLSHWLKEKCPIEKFQAAVERFVYS 931

Qy    1149 TGRDRGMVELVPASDTLRKIQVE-YGVTGSFKDPLAEWLRKYNPSEEEYEKASENFIYS 1207
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A;Reference number: JC5500; MUID:97289668; PMID:9144573
A;Accession: JC5500
A;Molecule type: mRNA
A;Residues: 1-1634 <BRO>
A;Cross-references: GB:Y11312; NID:g2808446; PIDN:CAA72168.1; PID:g2076604
A;Experimental source: breast cell
C;Comment: This enzyme is involved in receptor signal transduction, in a signalling com
ival.
C;Genetics:
C;Gene: GDB:PIK3C2B, C2-PI3K, PI3K-C2beta
A;Cross-reference: GDB:9837703; OMIM:602838
A;Map position: 1q32-1q32
C;Superfamily: HsC2 phosphatidylinositol 3-kinase; protein kinase C C2 region homology
C;Keywords: phosphotransferase
F;156-162,169-174/Domain: SH3 #status predicted <SH3>
F;1037-1320/Domain: catalytic #status predicted <CAT>
F;1498-1612/Domain: protein kinase C C2 region homology <KC2A>

Query Match          17.6%;  Score 1021;  DB 1;  Length 1634;
Best Local Similarity 28.0%;  Pred. No. 8.4e-61;
Matches  304;  Conservative 178;  Mismatches 391;  Indels 212;  Gaps  29;
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Db    290  AGRTTF-VTNPDVKLTSYDVRLQQNIFVQLKLNFGVRSERRLRCPGFVVRRQSIVLKDY  348
                 :  :|            :       |||
Qy    159  GYDVTDVSNVHDDELEFTRRRLVTPRMAEVAGRDPKLYAM--HPWVTSKPLPEYLLKKIT  216

Db    309  TPPPDALDE--VRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFT----------VSLWD  356
                      |||                              ||||||
Qy    322  GHELFEVSEERDEVAAFCHMLDILR---SGSDIQDYFLTGYVWSAVTPSPEHLGDEV-  376

Db    349  CRPKPLYEPHVRAHERKIALDVLSVS--IDSTPKQSKNSDMVMTDFRPTASLKQVSLWD  406
                 |||| ||              : :          :           ||||||
Qy    217  NNCVFIVIHRSTTSQTIKVSADDTPGTILQSFFTKMAKKKSLMDIPSQNERDFVLRVCG  276

Db    357  CDRKFRVK---IRGIDIPVLPRTADLITVFVEANIQYGQVLCQRRTSPKPFTEEVLWNVW  413
                :  |    :  ||: ::  ::|:  |||: :|| : | :     :       ::
Qy    377  NLKVTVLCDRLQEALTFTCNCSSTVDLLI--YQTLCYTHDDLRNV---DVGDFVLKPCG  430

Db    407  LDANLMIRPVNISGPDFPA---DVDMYVRIEFSVVGTLTLASKSTT-KVNAQFAKWNKE  462
                 |:  :| :::         :::|:| :      :::   ::|   :
Qy    277  RDEYLVGETPIKNFQWVRQCLK--                                      298

Db    414  L-EFSIKIKDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYVNLLLIDHR  472
              :|  ||       :      :     :  ::|        :  ::|:  :::
Qy    431  LEEFLQNKHALGSHEYIQYCRKFPDIDIRLQLMEQKVVRSDLARTVNDDQSPSTLNVLVHL  490

Db    463  MYTFDLYMKDMPPSAVLSIRVLYGK----------VKLKSEEFE------VGWVNMSLTDWR  508
               :||  ||:     :: ::||               :|:|             |:: ::
Qy    491  QERPVKQTISRQALSLLFDTYHNEVDAFLLADGDFPLKADRVVQSVKAICNALAAVETPE  550

Db    509  DELRQGQFLFHLW------------------------APEPTANRSRIGENGARIGTNAAVTIEISSYGGR  555
                :|||  |                                ::          :   :|  : ::  :|
Qy    551  ITSALNQLPPCPSRMQPKIQKDPSVLAVRENREKVVEALTAAILDLVELYCNTFNADFQT  610

Db    527  IALP--------------KJR---PTPDPEGDRVRAEMPNQLRKQLRAIIATDPLNPLTAEDKE  573
              :|                :       |:|||  |       ::  : :|:: |  |
Qy    277  RDEYLVGETPIKNFQWVRQCLK--                                      298

Db    556  VRMPSQGQYTYLVKHIRSTWTETLNIMGDDYESCIRDPGYKKLQMLVKKHESGIVLEEDEQ  615
                 :|   :|    |         ::  :  :| :      ::  ::     :: |:
Qy    299  -----------NGEEIHLVLDT----------                             309

Db    574  ---LLWHFRYESLKDPKAYPKLFS-SVKWGQQEIVAKTYQLLARKREVWDQSALDVGLTMQ  629
                  ||::| :| ::    | :|  :|:  :|   :|   :|:  :    ||::   :::
Qy    491  QERPVKQTISRQALSLLFDTYHNEVDAFLLADGDFPLKADRVVQSVKAICNALAAVETPE  550

Db    616  RHVWMWR-RYIQKQEPDLLIVLSELAFVWTDRENFSELYVMLEK--WKPPSVAAALT--   669
                ||:    : || ::     :  : |     | :        :   |:::
Qy    310  -----------------DPALDEVRKEEWPLV-----------                330

Db    630  LLDCNFSDENVRAIAVQKLESLEDDVLH-YLLQLVQAVKFEPYHDSALARFLLKRGLRN  688
              ||:  :|:| |  :: :: :::| :::|  :| ||::|:: :   ||     ||  :
Qy    551  ITSALNQLPPCPSRMQPKIQKDPSVLAVRENREKVVEALTAAILDLVELYCNTFNADFQT  610

Db    670  LLGKRCTDRVIRKFAVEKLNEQLSPVTFHLFILPLIQALKYEPRAQSEVGMLLTRALCD  729
               :|:|   :  |: :: ||:  |  |     :  ::|  :|: |::   :|:::| |
Qy    331  GVTGYHEQLTIHGKDH---ESVFTVSLWDCDRKFRVKIRGIDIPVLPRTADLITVFVEANI  387

Db    689  KRIGHPLFWFLRSEIAQSR------HYQQRFAVILEAYLRGCGTAMLHDFTQQVQVIDML  742
              |: | |||:|::: |            ||:|  : | | | :  :|: :: ::|:::|
Qy    611  AVPGSRKHDLVQEACHFARSLAFTV-YATH------IPIIWATSYEDFYLSCSL       658

Db    730  YRIGHRLFWLLRAEIARLRDCDLKSEEYRRISLLMEAYLRG-NEEHIKIITRQVDMVDEL  788
               |: | |||:|:|:|  |      |::|   |:::: :| |           ::|: ::|
Qy    388  QYGQQVLC------QRRTSPKPFTEEVLWNVWLEFSIKIKDLPKGALLNLQIYC--GKAPA  440

Db    743  QKVTIDIKSLSAEKYDVSS----QVISQLKQKLENLQNLNLPQSFRVPYDPGLKAGALVI  798
               :|  ::|:::| |           : :|:| :::   |  :| | | |     || :
Qy    659  SHGGKDMCSPLQTRRAHFSKYLFHLIVWDQQICFPVQVNRLPRETLLCATLYALPIPPPG  718

Db    789  TRISTLVKGMPK---DVATMKLRDELRSISHKMENMDS----------PLDPVVKLGEMII  836
               |:|| |:          |:||::|:|::: :                |:|:  |:|::
Qy    441  LSGKTSAEMPSPESKGKAQLLYVNLLLIDHRFLLRHGEYVLHMWQLSGKGEDQQGSFNAD  500

Db    799  EKCKYMASKKKPLWLEFKCADPTA-LSNETIGIIFKHGDDLRQDMLIQILRIMESTWET  857
              |:|:  |::   ||:|   |     ||  |:|:|  |||| ||:| : | |  :   |
Qy    719  SSEANKQRRVPEALG--------WVTTPLFNFRQVLTCGRKLLGLWPATQE------NPS  765

Db    837  DKAIVLGSAKRPLMLHWKNKNQNPKSLHLPFCAMIPKNGDDLRQPMLVLQVLEVMDNIWKA  896
              ||||:||:||:| |:||:|:  :|:|   | : || ||| :|: :: : : :::|:|:
Qy    501  KLTSATNPDKENSMSISILLDNYCHPIALPKHRPTDPPEGDRVR-----AEMPNQLRKQL  555

Db    858  ESLDICLLPYGCISTGDKIGMIEIVKDATTIAKIQQST-VGNTG--AFKDEVLSHWLKEK  914
              |||::|  :|| ||  |::|:   ||: ||   ::|:    |: |   :|::|   ::|:
Qy    766  ARWSAPNFHQPDSVILQIDFPTSAFDIKF------TSPPGDKFSPRYEFGSLREEDQRKL  819

Db    897  ANIDCCLNFYAVLPMGEMIGIIEVVPNCKTIFEIQVGTGFMNTAVRSIDPSFMNKWIRKQ  956
               |:  ::|::|:| |  ::|:  ||  :|:   :: |  :  ::::: ||:  :::|::|
Qy    556  EAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQQEIVAKTYQLLAKRE  615

Db    915  CPIEB-----------------------KFQAAVERFVYSCAGYCVATFVLGIGDRHN  949
                                          |: :|   || |  | |  :|: | | :
Qy    820  KDIMQKESLYWLTDADKKRLWEKRYYCHSEVSSLPLVLASAPSWEWACLPDIYVLLKQ--  877

Db    957  CGIEDBKKKSSKKDSTKNPIEKKIDNTQAMKKYFESVDRFLYSCVGYSVATYIMGIKDRHS  1016
               |:|:|:|::::  |:  :|::   : ::|  || ::  ::   || :|  :::|:| |
Qy    616  VW-----DQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDVLHYLLQLVQAVKFEP  671

Db    950  DNIMISETGNLFHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVM--GTSGKKTSLHFQ  1007
              ||:: |  :|||:|||| || :| ||:::|:|:  ::   :| :    : :|:|:| ||
Qy    672  YHDSALARFLLKRGLRNKRIGHPLFWFLRSEIAQSRHYQQRFAVILEAYLRGCGTAMLHD  731

Db    1017 DNLMLTEDGKYFHIDFGHILGHGKTKLGIQRDRQPFILTEHFMTVIRSGKSVDGNSHELQ  1076
              ||::  ||| |:|||||| || ||  ||::|:: ||: |   :|:|      |: |::|
Qy    732  FTQQVQVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENL-QNLNLPQSFRVPYDPG  790

Db    1008 KFQDVCVKAYLALRHHTNLLILFSMMLMTGMPQLTSKEDIEYIRDALTV-GKSEEDAKK  1066
              |: :|  :|  :|       |:::   : | | |::|  : :|| :|   |:||:|:|
Qy    1067 YFLDQIEVCRDKGWTVQFNWFLHLV  1091

Db    1077 KFKTLCVEAYEVMNNRDLFVSLFTLMLGMELPELSTRADLDHLKKTLFCNGSKEEARK  1136
              || | |  ||:|: :||||:||  ||| |:|  |: :||: |::| |: |:| |::|
Qy    1137 FFAGLYEEAFNGSWSTKTNWLFHAV  1161

RESULT 12
JC5500

phosphoinositide 3-kinase (EC 2.7.1.-) - human
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: JC5500
R;Brown, R.A.; Ho, L.K.F.; Weber-Hall, S.J.; Shipley, J.M.; Fry, M.J.
Biochem. Biophys. Res. Commun. 233, 537-544, 1997
A;Title: Identification and cDNA cloning of a novel mammalian C2 domain-containing phosp
```

```
Db    523  TDFQPVHTPGGVSHVHAGL----QSHLSFTVCSLHNVPETWAHSYKAFSF-----------    568
            :.:    ::::. .::        ::: ::.. ::.:::.. :. . ::
Qy    381  VFVEAANIQYGQQVLCQ-RRTSPKPFTEE----VLMNVWLEFSIKIKDLPKGALLNLQIYC   435

Db    569  ---SCWITYAGKKLCQVKSCRPLPVTKSFSLLVNWNBIINFPLEIKSLPRESMLVIKLF-    624
              : .:. ::::  :.. ::     :: : .: :::: ..     .  :::
Qy    436  GKAPALSGKTSAEMPSPESKGKAQLLYYVNLLLIDHRFLLRHGEYVLHMWQLSGKGEDQG   495

Db    625  ------------------------------------AWTCLPLFPPRQE            648
                                                .  :  : .
Qy    496  SFNADKLTSATNPDKENSMSISILLDNYCHPIALPKGHRPTPD-------PEGDRVRA---   545

Db    649  SVLGSRLFSVTLQSEEPIEMIAPGVWDGSQSPLTLQIDFPDAGWEYLKPESEENRTDHE   708
            ::.:::: :.: ::: . .  ::       ..  :: ..  ::: : .:. : :::
Qy    546  EMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQQEIVA   605

Db    709  EPPRECLKHIAKLSQKKSPLLSEEKRRYLWFYRLYCNNENSSLFLVLGASPGWDEETVS   768
            :   . :::.: ..:.: :..  ::  : : . :    .  : . :: .  ::. ::.
Qy    606  KTYQLiAK---REVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKESLEDDVLHYLLQ   662

Db    769  --------AlGLLISRFPPQDIREVAVQQlDTLLITDELLDCLPQ            820
                    . :: :. :. . :.  ::. .:    :. :::::::
Qy    663  LVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAYLR   722

Db    821  LVQAVKFEWNLESPLVELLPRRPLQSIRVARClYWLLRD--AQGEAYFKSWYQELLAALQ   878
            :::::::: .:::: ::.:: ::  :: . : ::::.:    :::.:::.:: :::.::
Qy    723  GC-GTAMLHDFTQQVVQIDMLQKVTIDIKSLS-ABKYDVSSQVISQLKQKLENLQNLNLP   780

Db    879  FCAGEALNEELSKEQKLVKLLGDIGEKVKSASDPQRKDVLKKBIGSLEEFFKDIKTCHL-   937
            :  :: ::.:. ::.::.:: .:: :.:: .    ::. : .:  :::::::.:   :
Qy    781  QSFRVPVYDPGLKAGALVIEKCKVMASKKKPlWLEFKCADPTALSNETIGIIFKHGDDLRQ   840

Db    938  ---PLNPALCIKGIDRDACSYFTSNASPLKITFINANP--MGKNISVIFKAGDDLRQ   989
               ::: :::::.  :. .:: ::. ::. ::: ..    :::.::.::::::::::
Qy    841  DMLILQILRIMBSIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG   900

Db    990  DMLALQIIQVMDNAWLQBGLDMQMITYGCLSTGRAQGFIEMVPDAVTLAKIHLHS-GLIG  1048
            :::::: :.:.:::: :..:  :. :::::::: : .:: ::: :.:::.  . ::::
Qy    901  AFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISBTGNL   960

Db   1049  FLKENTIKKKWFSQHNHLKBDYEKALRNFFYSCAGWCVVTFLGVCDRHNDNIMLTKSGHM  1108
            : :.:  :.: . ::.:::.:::.:::::::.::::: : .  ::::::::::. . :
Qy    961  FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKPQDVCVRAYLAL  1020

Db   1109  FHIDFGKFLGHAQCTFGGIKRDRAPFIFTSEMEYFI-TEGGKNIQHQDFVELCCRAYNIV  1167
            :::::::.::. ..: ::.::::::.:::::::::.  . .:.:::::::::. ::: ..
Qy   1021  RHHTNLLIILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW  1080

Db   1168  RGhSQLILSLLEMLLHAGLPELRGIEBLKVVHNNLRPQDTDLEATHSFTKKIKESLE-CF  1226
            :: ::::::: :::::::::  :::.: . . :: : ::. ::: :.  .:.:.:: ::
Qy   1081  TVQFNWFLH            1089

Db   1227  PVKLNNLIH            1235
```

```
RESULT 13
JC5985
phosphoinositide 3-kinase C2gamma - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-May-1998 #sequence_revision 29-May-1998 #text_change 30-Apr-1999
C;Accession: JC5985
R;Misawa, H.; Ohtsubo, M.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Yoshimura, A.
Biochem. Biophys. Res. Commun. 244, 531-539, 1998
A;Title: Cloning and charaterization of a novel class II phosphoinositide 3-kinase conta
A;Reference number: JC5985; MUID:98189216; PMID:9514948
A;Accession: JC5985
A;Molecule type: mRNA
A;Residues: 1-1506 <MIS>
A;Cross-references: DDBJ:AB008791
A;Experimental source: liver
A;Comment: This protein exclusively expressed in the liver,and a N-terminal truncated fo
C;Genetics:
A;Map position: 6
C;Superfamily: HsC2 phosphatidylinositol 3-kinase; protein kinase C C2 region homology
F;978-1239/Domain: catalytic #status predicted <CAT>

Query Match      15.1%;  Score 876;  DB 2;  Length 1506;
Best Local Similarity   25.4%;  Pred. No. 5.6e-51;
Matches  277;  Conservative 195;  Mismatches 407;  Indels 210;  Gaps  34;
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Qy     58  LLHVAGHGN--VEQMKAQVWLRALETSVSADFY--HRLGPDHFLLLYQKKGQWYEIYDKY   113
            ::.:.: :     :: .:  ::  :.:.:: .    .:.:  :::: . :: :  : :
Db    300  LLLLMPHANYLVKDIAEIILLCANEPLSPKEYLLSVCGSEEFlQMDHSLGS-HKIFQK-   357

Qy    114  QVVVQTLDCLRYKVLHRSPGQIHVVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDE-   172
            : ::  : .::  : :. ::: : :..:    :: :  .::. :.: :   :. ::::
Db    358  ---------------NKSVlQLH-LQKNRDTPGKLSRKSE------DDHSPFHLNQL   392

Qy    173  LEFTRRRLVTPRMAEVAGRDPKLYAMHPWTSKPLPEYLLKKITNNCVFIVIHRST--TS   230
            ::::   :.  :: . :..:::::. : :.:: :::::: :.:.::.:: :.:..   .
Db    393  LEFT------------------HIW-----------KISRQCLSTVMKKYNLHVB   418

Qy    231  QTIKVSADDTPGTIlQSFPTKMAKKKSLMDIPESQNERDFVLRVCG------------   276
            :: ::: ::::: : :::  ::::.:::::   ::::: :: ::
Db    419  HLLKPQKD-----MEEKHLSSMVSGNGHTSQPHVNNVLEEVKNICSVLGCIETKQVSDAV   473

Qy    277  RDEYLVGETPIKNFQWVRQCLKNG--EEIHLVLDTPPDALDEVRKEEWPLVD-----DC   329
            :.:: : ::. :.. ::: :.:.    ::: :::: :.: :.: ::.:::.      :
Db    474  KELNLILQRPSQNFHQNSETSKKGFIERV----------TAELSRSTYQLIDVYCSSFC   522

Qy    330  T--------GVTGYHEQLTIHGKDHESVFTVSLWDCDRKFRVKIRGIDIPVLPRTADLT   380
            :          : : :.::.:   ...:.. :::::::::::::::::  ::  :::.:
```

```
Db    791  LKAGALVIEKCKVMASKKKPlWLEFKCADPTALSNETIGIIFKHGDDLRQDMLILQILRI   850
            ::::::::.::.:.:::::::.:: ::::::::.:::. ::::::::::::::::::::
Db   1044  LLVKGIVPRDCSYPNSNAVPLKLSFQNVDPL---GENIRVIFKCGDDLRQDMLTLQMIRI  1100

Qy    851  MESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTGAFKDEVLSHW   910
            :::::::::::::::::::::::::.::.:::::::: : .::.::.::. :::..:.. :
Db   1101  MSKIWIVQBGLDMRMVIFRCFSTGRGRMVEMIPNAETLRKIQVEH-GVTGSFKDRPLADW  1159

Qy    911  LKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHDNIMISETGNLFHIDFGHLLG   970
            : :.::: .::.:::: :::::::::.::: ::::.:.:::::.: ::::::::: .::.
Db   1160  LQKINPGEDEYEKAVENFIYSCAGCCVATYVLGiCDRHNDNIMLKT*GHMFHIDFGRFLG  1219

Qy    971  NYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKPQDVCVKAYLALRHTNLLIL   1030
            : . ::::.  .::::.   : . :  : .:.:. .  :. . : : : : ::: ::
Db   1220  HAQMFGNIKRDRAPFVFTSDMAYVI-NGDKPSSRFHDFVDLCCQAYNLIRKHTHLFLNL  1278

Qy   1031  FSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGWTVQFNWFHL  1090
            : :::: :.::: ::::::: :::  . :: .. . :. : :. .  :  ::. : .
Db   1279  LGLMLSCGIPELSDLEDLKYVYDALRPQDTEANATTYFTRLIESSLGSVAT-KLNFFIHN  1337

Qy   1091  VLGIK     1095
            ::.:
Db   1338  LAQMK     1342
```

```
RESULT 14
T13801
phosphoinositide 3-kinase (EC 2.7.--.-) - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C;Accession: T13801; T13351
R;MacDougall, L.K.; Domin, J.; Waterfield, M.D.
Curr. Biol. 5, 1404-1415, 1995
A;Title: A family of phosphoinositide 3-kinases in Drosophila identifies a new mediator
A;Reference number: Z17764; MUID:96362138; PMID:8749393
A;Accession: T13801
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1876 <MAC>
A;Cross-references: EMBL:X92892; NID:g2113837; PIDN:CAA63485.1; PID:g2113838
R;Molz, L.M.; Chen, Y.W.; Hirano, M.; Williams, L.T.
J. Biol. Chem. 271, 13892-13899, 1996
A;Title: Cpk is a novel class of Drosophila ptdIns 3-kinase containing a C2 domain.
```

```
A;Reference number: Z17659; MUID:96278830; PMID:8662856
A;Accession: T13351
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-295,'P',297-331,'R',333-576,'T',578-641,'S',643-1876 <MOL>
A;Cross-references: EMBL:U52192; NID:g1272419; PID:g1272420; PIDN:AAC47717.1
C;Genetics:
A;Gene: PI3K 68D; cpk
A;Cross-references: FlyBase:FBgn0015278
A;Map position: 3L
C;Keywords: phosphotransferase

Query Match           15.1%;   Score 873.5;   DB 2;   Length 1876;
Best Local Similarity 32.2%;   Pred. No. 1.2e-50;
Matches  238;   Conservative  129;   Mismatches  298;   Indels  75;   Gaps  22;

Qy  387 IQYGQGQVL------CQRRTSPKPFTEEVLWNVWLEP-SIKIKDLPKGALLNLQIYCGKA 438
            :||       :|:|  ::   | ||    ||:    ::  |||||||::|
Db  878 IVYGTRLLSKPNVLTCSNDTSGGLF-PRLNFSAWLTFDQHPICTLPREARLTFVLY-GKQ 935

Qy  439 PALSGKTSAEMPSPSKGKAQLLYVNLLIDHRFLLRHGEYVLHMW-----QLSGKGED 493
            :|:||     :: :|  |:  :  |    :||:   |
Db  936 AASEGEPNADQ-NGERRQVTTELGWCSIQLFDFKRVMICGPYLLSLWPMTDRMLGPAPA 994

Qy  494 QGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKHRPTDPEGDRVRAEMPNQLRK 553
            :|           : :|   |      :| :
Db  995 RG--------CHPQPDFCPVLSIEVPVGGRIEFPEQEVPKPAPHYDFASLDANLQE 1044

Qy  554 QLEAIIATDPINPLTA-EDKELLWHFRYESLKDPKAYPK-LFSSVKKGQQEIVAKTYQLL 611
         :|   | |    : |      :| | |  :|      : |: :    : |
Db 1045 EL---LDTAELGYTGATERREVFWEKRLYLQSYNALPKVLHAAHSWDYANLI---DLH 1097

Qy  612 AKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYLLQLVQAVKFEP 671
         |       |:  ||  ||| :   |  | ::   :|  ::| | |  ||||||:|
Db 1098 ALLHSW--APISPLQSLELLLPRYPDAKVREKAVEWISKMPNDQLVDFLPQLVQSLKHDT 1155

Qy  672 YHDSALARFLLKRGLRNKRIGHFLFWFL------------RSEIAQSRHY 709
            ::| |||||||:| :| |     || |             || :| ||
Db 1156 YEGASAMARFLLSKCLESPRPAHHMYWLLVHSLPDDPHNSIGAAMVDQEYDESQVTQVRYY 1215

Qy  710 QQRFAVILEAYLRGCGTAMLHDFTQQVQVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQ 769
            :|   |  |:   :       :|  |  || ||:|: |   :|  :| |  :|
Db 1216 -RRNKMMLRALMAICGEKMLQRFMYQHR---MCQKLTTIAESVKEAKESMRQK---SLAA 1268

Qy  770 KLENLQNLNLPQSFRVPYDPGLKAGALVIEKCKVMASKKPLWLEFKCADPTALSNETIG 829
            |  :        | :|  | :|      :  | :   || |        :|| |:
Db 1269 GMDEVHQDLLEQPTCLPLGPELVTGVSVRNCSYFNSNTLPLKINF--VGPDA---ESLP 1323

Qy  830 IIFKHGDDLRQDMLILQLRIMESIWETESLDLCLLPYGCISTGDKIGMEIVKDATTIA 889
         ||| |||| ||| : :|||||      | |||:|:| | ||| :|:||||:| :  |
Db 1324 AIFKCGDDLQQDQDLTIQLIRIMNKMWLAERLDLKMVTFNCVPFTGYKSGMIELVSEAETLR 1383

Qy  890 KIQQSTVGNTGAFKDEVLSHWLKEKCPIEKFQAAVERRVYSCAGYCVATFVLGIGDRHN 949
         |||   |  |:|||  : ::  :  :|  | |:|:| | :||||| |:|:||||:|||||
Db 1384 KIQVE-CGLTGSFKDRPIAEWLGKQNPSPLEYQSAVRNFTLSCAGYSVATYVLGICDRHN 1442

Qy  950 DNIMISETGNLFHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKF 1009
         |||| : :|:|||||||:::|:    :|::|:| ||||:|:   : |  ||  : ||:|
Db 1443 DNIMLKTSGHLFHIDFGKFLGDAQMFGNFKRDRTPFVLTSDMAYVI-NGGDKPSTDFHYF 1501

Qy 1010 QDVCVKAYLALRHHTNLLIILFSMMLMTGMPLQLTSKEDIEYIRDALTVGKSEEDAKKYFL 1069
           |  ::| : : || ::|::: |  |:::|||     :  :|:| | ::  ::|  :|
Db 1502 VDLLCCRAFNIVRKNADLLLHTLAHMATAGMPGVNSNA-VQYVRRALLPSQSNPEAAATFA 1560

Qy 1070 DQIEVCRDKGWTVQFNWFLH 1089
            | :      |:|:||:||||
Db 1561 KMIQSSL-KSWFTQFNFFLH 1579
```

```
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 31-Mar-2003
C;Accession: A59003
R;Zhou, K.; Takegawa, K.; Emr, S.D.; Firtel, R.A.
Mol. Cell. Biol. 15, 5645-5656, 1995
A;Title: A phosphatidylinositol (PI) kinase gene family in Dictyostelium discoideum: bi...
A;Reference number: A59003; MUID:96009592; PMID:7565716
A;Accession: A59003
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-816 <ZHO>
A;Cross-references: GB:U23480; NID:g733529; PIDN:AAA85726.1; PID:g733530
C;Superfamily: phosphatidylinositol 3-kinase Vps34 type
C;Keywords: phosphotransferase

Query Match           12.4%;   Score 720.5;   DB 1;   Length 816;
Best Local Similarity 26.1%;   Pred. No. 8.4e-41;
Matches  216;   Conservative  163;   Mismatches  288;   Indels  161;   Gaps  28;

Qy  340 TIHGKDHE--SVFTVSLWDCDRKFRVKIRGIDIPVLP-----RTADLTVFVEANI-QYGQ 391
           |:| :       |  |:  : :: : :     :|      ||||:||: |:  ||||
Db   25 TLEGKRNKENAPETVDKW-----------IDDPYLKYSSLYRDTTIDLYITCTLYSDGK 72

Qy  392 QVLCQRRTSPKPFTEEVLWNWLEFSIKIKDLPKGALLNLQIYCGKAPALS--GKTSAE 448
         |:|    |: :| | :    :|| :|| |:|| :  |:   :    ||      ||:: :
Db   73 QLSTSEHTSYNPFSVSNKWDETIIFPLKHQDLPFDTMIVITIWDIYSPMKKVPIGGTSFN 132

Qy  449 --MPSPESKGKAQLLYVNLLIDHRFLLRHGE---YVLHNWQLSGKGE-------- 492
             | :  :| ||:|| : ||:     |::  :       :::|
Db  133 IFGMNKIERKGKHKLLIWQD----------REGDGEKETTTPGQIQGKDEQYRLEKLKKK 182

Qy  493 --------DQGSFN-ADKLTSATNPDKENSMSISILLDNYCHPIALPGKHRPTP-- 536
                 |   :|     :|: |      |      :|   |   :   :
Db  183 YDRKLINHCQWLLDKFSLNEIERLSRASESLNKNQIYLTIELPEFELPI-LFKQQNCPLYI 241

Qy  537 --------------DPEGDRVRAEM----------PNQLR-KQLEAIIATDPLNPL 567
                         | :|  :               || |  ::
Db  242 PLSQTQKKSLVLINDIEMDEHPSEQKYHRLNLYDHKDLKPNSTELKQNSDIIKQPPNTKV 301

Qy  568 TAEDKELLWHFRYESLKDPKAYPKLFSSVKKGQQEIVAKTYQLLAKREVWDQSALDVGLT 627
              | |:| |||| ||: :     :  |  | ||::|| :  |||:  |  :
Db  302 TSKEALLIWRFRYYLTMNKKALTKFLRCVEWSESHQKNEALSIMPK---WD--PIDIADS 356

Qy  628 MQLLDCNFSDEN---VRAIAVQKLESLEDDDVLHYLLQLVQAVKFEPY----HDSALARF 680
          :||  :|::|     |: :||||:|:||| :|||||||||| || |      || ||| |
Db  357 LELLSSAFTHKNTIMVRRYAVEILKPADDEELLYYLLQLVQATKYEQFDGNPSDSPLISF 416

Qy  681 LLKRGLRNKRIGHFLEWFLR-SEIAQSRHYQQRFAVILEAYLRGCGTAMLHDFTQQVQVI 739
         | :  : :| | ||  :::  |    :| :   |  :  ::      ::| :: : :|
Db  417 LFERSNKNFILGSHFYWYLTVDSVLKSSIFCSHYKTLQELYFRQLDHTDAQRVNAQNKFI 476

Qy  740 DMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENL----------QNLNLPQSFRVPYDPG 790
          :|:::   :  |  ::          : :::     :|: |  | |:|
Db  477 SRLSLLSVELKAMNITR----------EKKIEKLRIMLAEGEYKDLSDFQPIRLVPNPD 525

Qy  791 LKAGALVIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQDMLIQILRI 850
         :   |:| ||| : | |:|||  :|  :    || |  | ||| ||||||| |: |::
Db  526 IEIIGIVPEKSNIYKSAKSPLGLKLR----TTKGEYGVIFKTNDDLRQDQLIIQLISL 580

Qy  851 MESIWETESLDLCLLPYGCISTGDKIGMEIVKDATTIAKIQQSTVGNTGAFKDEVLSHW 910
          :    : ::||| | ||: :|::| :| |::   | |:    | |: | |||:::
Db  581 MDRLLKKENLDLKLTPYKVLATAEEDGIVEMVNPSEAMASV-------LSKYDGDILKFF 633

Qy  911 LKEKCPIEKFQAA---VERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNLFHIDFGH 967
         :       | :     || :||||||||::|::|||||||||| ||: :|:|||||||
Db  634 KTHNPDADSPYGIAPEVMDTFVKSCAGYCVTTYILGIGDRHLDNLLLTPNGKLFHIDFGY 693

Qy  968 ILGNYKSFLGINKERVPFVLTPDFL----FVMGTSGKKTSLHFQKFQDVCVKAYLALRHH 1023
         ||        :|: :: |: :        ||||:| ||  : |:||:::| ::||:||::
Db  694 ILG-------KDKILPPMKLCKEMVLGMGG-ENSKHYEKFKQLCCEAYNILRKS 741

Qy 1024 TNLILILFSMMLMTGMPLQT--SKEDIEYIRDALTVGKSEEDAKKYFL 1069
         ::||: ||::|:  :||::   |::|  :|  | ::::::::| :: |
Db  742 SHLILNLFALMVDASIPSISDDKEKSILKVQEKLQELTDQEASNSLL 789
```

RESULT 15

A59003

phosphoinositide 3-kinase (EC 2.7.1.-) - slime mold (Dictyostelium discoideum)

C;Species: Dictyostelium discoideum

us-09-974-573-1.rpr

Search completed: February 15, 2004, 02:07:49
Job time : 50 secs

```
OM protein - protein search, using sw model

          Copyright   GenCore version 5.1.6
                       Copyright (c) 1993 - 2004 Compugen Ltd.

Run on:        February 15, 2004, 01:29:38 ; Search time 91 Seconds
                                           (without alignments)
                                           3124.989 Million cell updates/sec

Title:         US-09-974-573-1
Perfect score: 5790
Sequence:      1 MELENYEQPVVLREDNRRRR.........QFNWFLHLVLGIKQGBKHSA 1102

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:      830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters:      830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     SPTREMBL_23:*
               1:  sp_archea:*
               2:  sp_bacteria:*
               3:  sp_fungi:*
               4:  sp_human:*
               5:  sp_invertebrate:*
               6:  sp_mammal:*
               7:  sp_mhc:*
               8:  sp_organelle:*
               9:  sp_phage:*
              10:  sp_plant:*
              11:  sp_rodent:*
              12:  sp_virus:*
              13:  sp_vertebrate:*
              14:  sp_unclassified:*
              15:  sp_rvirus:*
              16:  sp_bacteriap:*
              17:  sp_archeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                              SUMMARIES
```

Result No.	Score	% Query Match	Length	DB	ID	Description	
1	5538	95.6	1102	4	Q8IV23	Q8iv23 homo sapien	
2	5534	95.6	1102	4	Q9BZC8	Q9bzc8 homo sapien	
3	5476.5	94.6	1113	11	Q9EQL1	Q9eql1 mus musculu	
4	1468.5	25.4	1068	13	O42391	O42391 gallus gall	
5	1450.5	25.1	1083	15	O39483	O39483 avian sarco	
6	1363	23.5	1064	11	Q8BTI9	Q8bti9 mus musculu	
7	1339	23.1	1047	11	Q8BS14	Q8bs14 mus musculu	
8	1335	23.1	260	11	Q8C5Q7	Q8c5q7 mus musculu	
9	1329	23.0	1037	11	Q8CI98	Q8ci98 mus musculu	
10	1329	23.0	1043	11	Q8CJ28	Q8cj28 mus musculu	
11	1290	22.3	1068	4	O00334	O00334 homo sapien	
12	1283	22.2	1088	5	P91634	P91634 drosophila	
13	1103.5	19.1	852	13	Q9PTE5	Q9pte5 xenopus lae	
14	1076.5	18.6	1658	11	Q61182	Q61182 mus musculu	
15	1074	18.5	1686	4	O00443	O00443 homo sapien	
16	1040.5	18.0	1509	11	Q61194	Q61194 mus musculu	
17	873.5	15.1	1876	5	Q9VTN5	Q9vtn5 drosophila	
18	820.5	14.2	318	11	Q9CTK7	Q9ctk7 mus musculu	
19	758	13.1	286	4	Q9BTS4	Q9bts4 homo sapien	
20	713.5	12.3	887	11	O88763	O88763 rattus norv	
21	708.5	12.2	887	4	Q8NEB9	Q8neb9 homo sapien	
22	701.5	12.1	1607	5	Q20187	Q20187 caenorhabdi	
23	698.5	12.1	887	4	Q15134	Q15134 homo sapien	
24	683	11.8	847	11	Q8R3S8	Q8r3s8 mus musculu	
25	667	11.5	808	10	Q8GUA6	Q8gua6 medicago tr	
26	660	11.4	813	10	Q8HIS8	Q8his8 brassica na	
27	659.5	11.4	291	11	Q91XL6	Q91xl6 rattus norv	
28	647	11.2	949	5	P91635	P91635 drosophila	
29	645	11.1	949	5	Q9W1M7	Q9w1m7 drosophila	
30	628	10.8	901	5	Q9TXI7	Q9txi7 caenorhabdi	
31	626	10.8	897	5	Q9XZR0	Q9xzr0 caenorhabdi	
32	597	10.3	650	5	Q9TXI6	Q9txi6 caenorhabdi	
33	550.5	9.5	499	10	Q8RXR0	Q8rxr0 arabidopsis	
34	510	8.8	273	5	Q9BLU5	Q9blu5 leishmania	
35	508	8.8	732	10	O04269	O04269 chlamydomon	
36	489	8.4	99	11	Q8C403	Q8c403 mus musculu	
37	472.5	8.2	1016	3	Q9Y8E4	Q9y8e4 pichia angu	
38	435.5	7.5	2028	10	O81129	O81129 arabidopsis	
39	432	7.5	2051	10	Q9SXA1	Q9sxa1 arabidopsis	
40	418.5	7.2	2043	6	O02811	O02811 bos taurus	
41	418	7.2	1889	10	Q94H07	Q94h07 oryza sativ	
42	412.5	7.1	608	10	Q8L5D9	Q8l5d9 oryza sativ	
43	410	7.1	1466	6	Q28925	Q28925 bos taurus	
44	410	7.1	2044	4	Q9UPG2	Q9upg2 homo sapien	
45	409	7.1	1433	5	Q8SQY7	Q8sqy7 encephalito	

```
                              ALIGNMENTS

RESULT 1
Q8IV23
ID   Q8IV23          PRELIMINARY;      PRT;   1102 AA.
AC   Q8IV23;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Phosphoinositide-3-kinase, catalytic, gamma polypeptide.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pancreas;
RA   Strausberg R.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC035683; AAH35683.1; -.
KW   Kinase.
SQ   SEQUENCE   1102 AA;  126453 MW;  EF2B1A0E1CBEF406 CRC64;

Query Match    95.6%;  Score 5538;  DB 4;  Length 1102;
Best Local Similarity 95.3%;  Pred. No. 0;
Matches 1050;  Conservative 20;  Mismatches 32;  Indels 0;  Gaps 0;
```

```
Qy       1 MELENYEQPVVLREDNRRRRRMKPRSTAASLSSMELIPIEFVLPTSQRNTKTPETALLH 60
           |||||||||||||||||:||||||||:||||||||||||||||||||:|||||||||||
Db       1 MELENYKQPVVLREDNCRRRRRMKPRSAAAASLSSMELIPIEFVLPTSQRKCKSPETALLH 60

Qy      61 VAGHGNVEQMKAQVWLRALETSVSADFYHRLGPDHFLLLYQKKGGQWYEIYDKYQVVQTLD 120
           |||||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||
Db      61 VAGHGNVEQMKAQVWLRALETSVAADFYHRLGPHHFLLLYQKKGGQWYEIYDKYQVVQTLD 120

Qy     121 CLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRL 180
           ||||||:|||||||||||||||| ::|||||:||||||||||||||||||||||:||||:|
Db     121 CLRYWKATHRSPGQIHLVQRHPPSESQAFQRQLTALIGYDVTDVSNVHDDELEFTRRGL 180

Qy     181 VTPRMAEVAGRDPKLYAMHPWVTSKPLPEYLLKKITNNCVFIVIHRSTTSQTIKVSADDT 240
           ||||||||||:|||||||||||||||||||||||||||||||||||:|||||||||||:||
```

```
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95506661; PubMed=7624799;
RA   Stoyanov B., Volinia S., Hanck T., Rubio I., Loubtchenkov M.,
RA   Malek D., Stoyanova S., Vanhaesebroeck B., Dhand R., Nurnberg B.,
RA   Gierschik P., Seedorf K., Hsuan J.J., Waterfield M.D., Wetzker R.;
RT   "Cloning and characterization of a G protein-activated human
RT   phosphoinositide-3 kinase.";
RL   Science 269:690-693(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Michalke M., Schaefer M., Stoyanov B., Wetzker R., Nuernberg B.;
RT   "Regulation of a G-protein-activated phosphoinositide-3-kinase.";
RL   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF327656; AAG61115.1; -.
DR   InterPro; IPR001263; PI3Ka.
DR   InterPro; IPR002420; PI3K_C2.
DR   InterPro; IPR000341; PI3K_ras_bind.
DR   InterPro; IPR000403; PI3_PI4_kinase.
DR   Pfam; PF00613; PI3Ka; 1.
DR   Pfam; PF00792; PI3K_C2; 1.
DR   Pfam; PF00794; PI3K_rbd; 1.
DR   Pfam; PF00454; PI3_PI4_kinase; 1.
DR   SMART; SM00145; PI3Ka; 1.
DR   SMART; SM00146; PI3Kc; 1.
DR   SMART; SM00142; PI3K_C2; 1.
DR   SMART; SM00144; PI3K_rbd; 1.
DR   PROSITE; PS00915; PI3_4_KINASE_1; 1.
DR   PROSITE; PS00916; PI3_4_KINASE_2; 1.
DR   PROSITE; PS50290; PI3_4_KINASE_3; 1.
KW   Kinase; Transferase.
SQ   SEQUENCE 1102 AA;  126481 MW;  402BB67E8DD2191A CRC64;

Query Match
Best Local Similarity  95.6%;  Score 5534;  DB 4;  Length 1102;
Matches 1049;  Conservative 21;  Mismatches 32;  Indels 0;  Gaps 0;

Qy    1  MELENYEQPVLREDNRRRRRMKPRSTAASLSSMELIPIEFVLPTSQRNTKTPETALLH   60
         |||||:|||||||| ||||||||||:|||||||||||||||||||||||  ::||||||
Db    1  MELENKQPVLREDNCRRRRRMKPRSAAASLSSMELIPIEFVLPTSQRKCKSPETALLH   60
Qy   61  VAGHGNVEQMKAQVWLRALETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLD  120
         |||||||||||||||||||||||:|||||||||| ||||||||||||||||||||||||
Db   61  VAGHGNVEQMKAQVWLRALETSVAADFYHRLGPHHFLLLYQKKGQWYEIYDKYQVVQTLD  120
Qy  121  CLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRL  180
         ||||| |:|||||||||||||:|||| :||||||.|||||||||||||||||||||||.|
Db  121  CLRYWKATHRSPGQIHVVQRHPPSEESQAFQRQLTALIGYDVTDVSNVHDDELEFTRRGL  180
Qy  181  VTPRMAEVAGRDPKLYAMHPWVTSKPLPEYLWKKIANNCIFIVIHRSTTSQTIKVSADDT  240
         |||||||||:||||||||||||||||||||||||||||||||||||||||||||||.|||
Db  181  VTPRMAEVASRDPKLYAMHPWVTSKPLPEYLWKKIANNCIFIVIHRSTTSQTIKVSPDDT  240
Qy  241  PGTILQSFFTKVAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG  300
         ||:||||||||.||||||||||||||:|:|||||||||||||||||||||||||||:|||
Db  241  PGAILQSFFTKVAKKKSLMDIPESQSEQDFVLRVCGRDEYLVGETPIKNFQWVRHCLKNG  300
Qy  301  EEIHLVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK  360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301  EEIHLVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK  360
Qy  361  FRVKIRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTSPKPFTEEVLWNVWLEFSIKI  420
         ||||||||||||||| .||||||||||:||||||||||||||||||||||||||||||||
Db  361  FRVKIRGIDIPVLPRNTDLTVFVEANIQHGQQVLCQRRTSPKPFTEEVLWNVWLEFSIKI  420
Qy  421  KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGAQLLYYVNLLIDHRFLLRHGEY   480
         |||||||||||||||||||||| :.||:|||..|||| :|||||||||||||||:|||
Db  421  KDLPKGALLNLQIYCGKAPALSSKASAESPSSESKGKVRLLYYVNLLIDHRFLLRRGEY   480
Qy  481  VLHWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKGHRPTPDPEG  540
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(alignment continues, rotated side column)

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Db  181  VTPRMAEVASRDPKLYAMHPWVTSKPLPEYLWKKIANNCIFIVIHRSTTSQTIKVSPDDT  240
Qy  241  PGTILQSFFTKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG  300
Db  241  PGAILQSFFTKMAKKKSLMDIPESQSEQDFVLRVCGRDEYLVGETPIKNFQWVRHCLKNG  300
Qy  301  EEIHLVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK  360
Db  301  EEIHLVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK  360
Qy  361  FRVKIRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTSPKPFTEEVLWNVWLEFSIKI  420
Db  361  FRVKIRGIDIPVLPRNTDLTVFVEANIQHGQQVLCQRRTSPKPFTEEVLWNVWLEFSIKI  420
Qy  421  KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGAQLLYYVNLLIDHRFLLRHGEY   480
Db  421  KDLPKGALLNLQIYCGKAPALSSKASAESPSSESKGKVRLLYYVNLLIDHRFLLRRGEY   480
Qy  481  VLHWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKGHRPTPDPEG  540
Db  481  VLHWQISGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKQPTPDPEG   540
Qy  541  DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQ  600
Db  541  DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKHPKAYPKLFSSVKWGQ  600
Qy  601  QEIVAKTYQLLARKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL  660
Db  601  QEIVAKTYQLLARREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL  660
Qy  661  LQLVQAVKFEPYHDSALARPLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY  720
Db  661  LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY  720
Qy  721  LRGGGTAMLHDFTQQVQVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLP  780
Db  721  LRGGGTAMLHDFTQQVQVIEMLQKVTLDIKSLSAEKYDVSSQVISQLKQKLENLQNSQLP  780
Qy  781  QSFRVPYPDPGLKAGAGALVIBKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKGHGDDLRQ  840
Db  781  ESFRVPYPDPGLKAGALALAIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKGHGDDLRQ  840
Qy  841  DMLIQILRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG   900
Db  841  DMLIQILRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG   900
Qy  901  AFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL  960
Db  901  AFKDEVLNFWLKEKSPTEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMITETGNL  960
Qy  961  FHIDFGHIGLGNYKSFLGINKERVPFLVIPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLAL  1020
Db  961  FHIDFGHIGLGNYKSFLGINKERVPFLVLTPDFLFVMGTSGKKTSPHFQKFQDICVKAYLAL  1020
Qy  1021 RHHTNLLILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW  1080
Db  1021 RHHTNLLILFSMMLMTGMPQLTSKEDIEYIRDALTVGKNEEDAKKYFLDQIEVCRDKGW  1080
Qy  1081 TVQFNWFLHIVLGIKQGEKHSA  1102
Db  1081 TVQFNWFLHIVLGIKQGEKHSA  1102
```

RESULT 2
```
ID   Q9BZC8       PRELIMINARY;      PRT;   1102 AA.
AC   Q9BZC8;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Phosphoinositide-3-kinase gamma catalytic subunit (EC 2.7.1.137).
GN   PI3CG.
OS   Homo sapiens (Human).
```

DR   SMART; SM00145; PI3Ka; 1.
DR   SMART; SM00146; PI3Kc; 1.
DR   SMART; SM00142; PI3K_C2; 1.
DR   SMART; SM00144; PI3K_rbd; 1.
DR   PROSITE; PS00915; PI3_4_KINASE_1; 1.
DR   PROSITE; PS00916; PI3_4_KINASE_2; 1.
DR   PROSITE; PS50290; PI3_4_KINASE_3; 1.
KW   Kinase.
SQ   SEQUENCE   1113 AA; 127538 MW; 6729FE88A5D35691 CRC64;

Query Match   94.6%; Score 5476.5; DB 11; Length 1113;
Best Local Similarity   93.2%; Pred. No. 0;
  Matches 1037; Conservative 31; Mismatches 34; Indels 11; Gaps 1;

Qy   1 MELENYEQPVVLREDNRRRRRMKPRSTAASLSSMELIPIEPVLPTSQRNTKTPETALLH 60
          |||||||||||||||||||||| |||: |:||||||| ||||||:|||:|||||||||
Db   1 MELENYEQPVVLREDNLRRRRRMKPRSAAGSLSSMELIPIEFVLPTSQRISKTPETALLH 60

Qy   61 VAGHGNVEQMKAQVWLRALETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLD 120
          |||||||||||||||||||||| :|| ||||||| ||||||||||||||||:|||||||
Db   61 VAGHGNVEQMKAQVWLRALETSVAAEFYHRLGPDQFLLLYQKKGQWYEIYDRYQVVQTLD 120

Qy   121 CLRYWKVLHRSPGQIHVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEPTRRRL 180
          ||||||| |: |||||||||| ||||||| ||:|||||||||| |||| |||||||||||
Db   121 CLHYWKLMHKSPGQIHVVQRHVPSEETLAFQKQLTSLLGYDVTDISNVHDDELEPTRRRL 180

Qy   181 VTPRMAEVAGRDPKLYAMHPWTSKPLPEYLLKKITNNCVFIVIHRSTTSQTIKVSADDT 240
          ||||||||||| ||||||||||||||||||||||:|||||||||||||||||||||||||
Db   181 VTPRMAEVAGRDAKLYAMHPWTSKPLPDYLSKKIANNCIFIVIHRGTTSQTIKVSADDT 240

Qy   241 PGTILQSFFTKMAKKKSLMDIPSQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNG 300
          |||||||||||||||||||:||| |||:|||||||||||||||||||:||| ||||||||
Db   241 PGTILQSFFTKMAKKKSLMNISESQSEQDFVLRVCGRDEYLVGETPLKNFQWVRQCLKNG 300

Qy   301 EBIHLVLDTPPPDALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK 360
          :|||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db   301 DEIHLVLDTPPPDALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLWDCDRK 360

Qy   361 FRVKIRGIDIPVLPRTADLTVFVEANIQYGGQVLCQRRTSPKPFTEVLWNVWLEFSIKI 420
          |||||||||||||||| ||:||||||||||||||||||||| |||| ||:||||||||||
Db   361 FRVKIRGIDIPVLPRNTDLTVFVEANIQHGGQVLCQRRTSPKPFAEVLWNVWLEFGIKI 420

Qy   421 KDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYYVNLLLIDHRFLLRHGEY 480
          ||||||||||||||| ||| || |: |||| ||| ||||||||||||||||||||||||:
Db   421 KDLPKGALLNLQIYCCKTPSLSSKASAETPGSESKGKAQLLYYVNLLLIDHRFLLRHGDY 480

Qy   481 VLHWQISGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKHRPTPDPEG 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 VLHWQISGKAEBQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKHRPTPDPEG 540

Qy   541 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQ 600
          |||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||
Db   541 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKHPKAYPKLFSSVKWGQ 600

Qy   601 QEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 660
          |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 QEIVAKTYQLLARREIWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 660

Qy   661 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY 720
          |||||||||||||||||||||||||||||||||||||||||||||||:||||||||||||
Db   661 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSXHYQQRFAVILEAY 720

Qy   721 LRGCGTAMLHDFTQQVVQVIDMLQKVTIDIKSLSABKYDVSSQVISQLKQKLENLQNLNLP 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|||
Db   721 LRGCGTAMLQDFTQQVHVIEMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLESLQNSNLP 780

Qy   781 QSFRVPYDPGLKAGALVIEKCKVMASKKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ 840
          :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 ESFRVPYDPGLKAGTLVIEKCKVMASKKKKPLWLEFKCADPTVLSNETIGIIFKHGDDLRQ 840

Qy   841 DMLILQILRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 DMLILQILRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAQIQQSTVGNTG 900

Db   481 VLHWQISGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKHQPTPDPEG 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||:|||||||
Qy   481 VLHWQISGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPIALPKHQPTPDPEG 540

Db   541 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKHPKAYPKLFSSVKWGQ 600
          ||||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||
Qy   541 DRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQ 600

Db   601 QEIVAKTYQLLARREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 660
          |||||||||||| |:|||||||||||||||||||||||||||||||||||||||||||||
Qy   601 QEIVAKTYQLLARRREIWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYL 660

Db   661 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   661 LQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAY 720

Db   721 LRGCGTAMLHDFTQQVVQVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLP 780
          |||||||||||||||| |||||||||||||||:|||||||||||||||||||||||||||
Qy   721 LRGCGTAMLHDFTQQVVIEMLQKVTIDIKSLSLSAEKYDVSSQVISQLKQKLENLQNSQLP 780

Db   781 QSFRVPYDPGLKAGALVIEKCKVMASKKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ 840
          :||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||||
Qy   781 ESFRVPYDPGLKAGALAIEKCKVMASKKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQ 840

Db   841 DMLILQILRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG 900
          |||||||||||||||||||||||||||||||||||||||||||:||:||||||||||||||
Qy   841 DMLILQILRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTG 900

Db   901 AFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL 960
          ||||| ||| |||| |||| ||||||||||||||||||||||||||||||||||:|:||||
Qy   901 AFKDEVLNHWLKEKSPTEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMITETGNL 960

Db   961 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYIAL 1020
          ||||||||||||||||||||||:|:|||||||||||||||||| |||:|||| |||||||
Qy   961 FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSPHFQKFQDICVKAYIAL 1020

Db   1021 RHHTNLLIILFSMNLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGW 1080
          ||||||||||||||:|||||||||||||||||||||||| :|||||||||||||||||||
Qy   1021 RHHTNLLIILFSMMLMTGMPQLTSKEDIEYIRDALTVGKNEEDAKKYFLDQIEVCRDKGW 1080

Db   1081 TVQFNWFLHIVLGIKQGEKHSA 1102
          |||||||||||||||||||||||
Qy   1081 TVQFNWFLHIVLGIKQGEKHSA 1102

RESULT 3
Q9EQL1
ID   Q9EQL1   PRELIMINARY;   PRT;   1113 AA.
AC   Q9EQL1;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Phosphatidylinositol 3-kinase gamma isoform.
GN   PIK3CG.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RA   Chakravarti S., McColl S.R.;
RT   "Cloning of a murine ortholog of PI 3-kinase gamma.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF208345; AAG41122.1; -.
MGD; MGI:1353576; Pik3cg.
DR   InterPro; IPR001263; PI3Ka.
DR   InterPro; IPR002420; PI3K_C2.
DR   InterPro; IPR000341; PI3K_ras_bind.
DR   InterPro; IPR000403; PI3_PI4_kinase.
DR   Pfam; PF00613; PI3Ka; 1.
DR   Pfam; PF00792; PI3K_C2; 1.
DR   Pfam; PF00794; PI3K_rbd; 1.
DR   Pfam; PF00454; PI3_PI4_kinase; 1.

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Qy   901  AFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL  960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901  AFKDEVLNHWLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNL  960

Qy   961  FHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQ---------- 1010
          ||||||||||||||||||||||||||||:||:|||||||:||:|||||::
Db   961  FHIDFGHILGNYKSFLGINKERVPFVLTPDFLVVMGSSGKKTSPHFQKFQDCCVSTLQYY 1020

Qy  1011  -DVCVKAYLALRHHTNLLIILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFL 1069
           ||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021  GDVCVRAYLALRHHTNLLIILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFL 1080

Qy  1070  DQIEVCRDKGWTVQFNWFLHLVLGIKQGEKHSA 1102
          ||||||||||||||||||||||||||||||||
Db  1081  DQIEVCRDKGWTVQFNWFLHLVLGIKQGEKHSA 1113
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RESULT 4
O42391
ID   O42391;        PRELIMINARY;       PRT;   1068 AA.
AC   O42391;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Phosphoinositide 3-kinase catalytic subunit.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=97334438; PubMed=9188528;
RA   Chang H.W., Aoki M., Fruman D., Auger K.R., Bellacosa A.,
RA   Teichlis P.N., Cantley L.C., Roberts T.M., Vogt P.K.;
RT   "Transformation of chicken cells by the gene encoding the catalytic
RT   subunit of PI 3-kinase.";
RL   Science 276:1848-1850(1997).
EMBL; AF001076; AAB62534.1; -.
DR   InterPro; IPR000008; C2.
DR   InterPro; IPR001263; PI3Ka.
DR   InterPro; IPR002420; PI3K_C2.
DR   InterPro; IPR003113; PI3K_p85B.
DR   InterPro; IPR000341; PI3K_ras_bind.
DR   InterPro; IPR000403; PI3_PI4_kinase.
DR   Pfam; PF00613; PI3Ka; 1.
DR   Pfam; PF00792; PI3K_C2; 1.
DR   Pfam; PF02192; PI3K_p85B; 1.
DR   Pfam; PF00794; PI3K_rbd; 1.
DR   Pfam; PF00454; PI3_PI4_kinase; 1.
DR   SMART; SM00239; C2; 1.
DR   SMART; SM00145; PI3Ka; 1.
DR   SMART; SM00146; PI3Kc; 1.
DR   SMART; SM00142; PI3K_C2; 1.
DR   SMART; SM00143; PI3K_p85B; 1.
DR   SMART; SM00144; PI3K_rbd; 1.
DR   PROSITE; PS00915; PI3_4_KINASE_1; 1.
DR   PROSITE; PS00916; PI3_4_KINASE_2; 1.
DR   PROSITE; PS50290; PI3_4_KINASE_3; 1.
KW   Kinase.
SQ   SEQUENCE   1068 AA;   124287 MW;  9912A96B3397735E CRC64;
```

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Query Match          25.4%;   Score 1468.5;   DB 13;   Length 1068;
Best Local Similarity   33.2%;  Pred. No. 5.6e-105;
Matches   380;   Conservative   211;   Mismatches   396;   Indels  157;   Gaps   40;

Qy     23  MKPRSTAASLSSMELIP----IEFVLPTSQRNTKTPETALLHVAGHGNVEQMKAQVWLRA    78
           |:|::::||:|||    |:|||:| :||  :::::::  |  :|||:||:|:::
Db      1  MPPRPSSGELWGIIHLMPPRILVECLLPNGMIVT------LECLREATLLTIKHELFKEA    53

Qy     79  LETSVSADFYHRLGPDHFLLLYQKKGQWYEIYDKYQVVQTLDCLRYWKVLHRSPGQIHVV   138
           :: |
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Qy   1088  LHLIV 1091
            |:
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Db   1059 FHTI 1062

RESULT 5
O39483
ID   O39483          PRELIMINARY;       PRT;   1083 AA.
AC   O39483;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Gag-v-phosphoinositide 3-kinase catalytic subunit fusion protein
DE   (Fragment).
GN   GAG-V-P3K.
OS   Avian sarcoma virus 16.
OC   Viruses; Retroid viruses; Retroviridae; Avian type C retroviruses.
OX   NCBI_TaxID=60029;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97334438; PubMed=9188528;
RA   Chang H.W., Aoki M., Fruman D., Auger K.R., Bellacosa A.,
RA   Tsichlis P.N., Cantley L.C., Roberts T.M., Vogt P.K.;
RT   "Transformation of chicken cells by the gene encoding the catalytic
RT   subunit of PI 3-kinase.";
RL   Science 276:1848-1850(1997).
DR   EMBL; AF001075; AAB62533.1; -.
DR   InterPro; IPR000008; C2.
DR   InterPro; IPR001263; PI3Ka.
DR   InterPro; IPR002420; PI3K_C2.
DR   InterPro; IPR003113; PI3K_p85B.
DR   InterPro; IPR000341; PI3K_ras_bind.
DR   InterPro; IPR000403; PI3_PI4_kinase.
DR   Pfam; PF00613; PI3Ka; 1.
DR   Pfam; PF00792; PI3K_C2; 1.
DR   Pfam; PF02192; PI3K_p85B; 1.
DR   Pfam; PF00794; PI3K_rbd; 1.
DR   Pfam; PF00454; PI3_PI4_kinase; 1.
DR   SMART; SM00239; C2_1.
DR   SMART; SM00145; PI3Ka; 1.
DR   SMART; SM00146; PI3Kc; 1.
DR   SMART; SM00142; PI3K_C2; 1.
DR   SMART; SM00143; PI3K_p85B; 1.
DR   SMART; SM00144; PI3K_rbd; 1.
DR   PROSITE; PS00915; PI3_4_KINASE_1; 1.
DR   PROSITE; PS00916; PI3_4_KINASE_2; 1.
DR   PROSITE; PS50290; PI3_4_KINASE_3; 1.
KW   Kinase.
FT   NON_TER       1      1
SQ   SEQUENCE   1083 AA;  123869 MW;  371EF7055A78ACE8 CRC64;

Query Match         25.1%;  Score 1450.5;  DB 15;  Length 1083;
Best Local Similarity  34.9%;  Pred. No. 1.4e-103;
Matches  359;  Conservative 189;  Mismatches 345;  Indels 135;  Gaps 36;

Qy    135 IHVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRLVTPRMAEVAGRDPK 194
              ||:|| :   :|:  |||| ::| ||||  |||||:  | :  | :: |||
Db    114 LKVIEPVGNREEKI-LNRKIGFAIGMPICEFDMVKDPEVQDFRRNILNVCKEAVDLRDAN 172

Qy    195 -----LYAMHPWTVSKP-LPEYLLKKITNNCVFIVI-----HRSTTSQTIKVSADDTP 241
               ||  ||  ::|| |::|| |:  :|||  |||| ::|| |||
Db    173 APHSRALYVCPPNVESSPELPKHIYNKLDKGQIIVIWIVSPNNDKQKYTLKINHDCVP 232

Qy    242 GTIIQSFFTKQAKKSLMDIPES------QNERDFVLRVCGRDEYLVGETPIKNFQWVRQ 295
               :|   ||:  : |||    :::   :| |||| ::|| |:|:|| |: || ::::
Db    233 EQVIAEAIRK--KTRSMLLSSEQLKLCVLEYQGKYILKVCGCDEYLLEKYPLSQYKYIRS 290

Qy    296 CLKNGEEIHLVLDTPPDPALDEVRKE------EWPLVDDCTGVTGYHEQLT-----IHGKDH 346
              | :|  ::|||  :||    |:|::      || |:  || || |::      || ||
Db    291 CIMLGRMPNLML---------MAKESLYTQLPL--DTFTMPSYSRRISTATPYMNGB-- 336

Qy    347 ESVFTVSLWDCDRKFRVK-------IRGIDIPVLPRTADLTVFVEANIQYGQQVLCQ 396
                ::|   |:  :||   |||         ||  :|   |  | ::::  || :::  ::|
Db    337 --ATAKSLWTINSALRIRILCATYVNVNIRDID-------KIYVRTGIYHGGEPLCD 384
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Qy    397 RRTSPKPFTEEVLWNVWLEFSIKIKDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKG 456
              :  : |  :||: |||:|| ::|||| || || | : ::  : |: ||    :   :|:
Db    385 NVNTQRVPCSNPRWNEWLSYDMYIPDLPRAARLCLSI-C----SVKGRKGA------KE 432

Qy    457 KAQLLYYVNLLLIDHRFLLRHGEYVLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSI 516
              :  :|| : :|:|  :|| :|| |:| |  |   || |  | ::| || :||   ::|
Db    433 EHCPLAWGNINMFDYTDTLVSGKWALNLWAVPHGLED--LLNPIGVT-GSNRNK-GTPCL 488

Qy    517 SILLDNYCHPIALPKHRPTPDPEGDRVRAEM--------------PNQLR----KQLEA 557
              |   | :||   :  ||| :|::|| ::| :              |::|:    :||:|
Db    489 ELEFDWFSNPVKFPDMTVIEBHANWTISRELGFNYSYAGLSNRIARDNELRESDKEQLRA 548

Qy    558 IIATDPLNPLTAEDKELLWHPRYESLKDPKAYPKLFSSVKWGQQEIVAKTYQLLAKREVW 617
              ||  | |||||| ||| ||||| ::||   ||  | | : || :::|:  :|| ::|::
Db    549 ICTRDPLSBITEQBKDPLWSRHYCVKTPEILPKLLLSVKWNSRDEVAQMYCL----VK 603

Qy    618 DQSALDVGLTMQLLDCNFSDENVRAIAVQKLES-LEDDDVLHYLLQLVQAVKFEPYHDSA 676
              |  :| ||| :||  || :  ::|| :|:::|  ||:| :|:|||:||| | ::|   ||
Db    604 DWPPIKPBQAMELLDCNYPDPMVRAFAVRCLEKYLTDDKLSQYLIQLVQVLKYEQYLDNQ 663

Qy    677 LARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAYLRGCGTAMLHDFTQQV 736
              | :|||| | || |  :  |:|:  :||:  |  |: ::|||||: | || ||||| :||
Db    664 LVRFLLKALTNQRIGHFFFWFLKSEM-HNKTVSQRFGLLLESYCRACGMYLKH-LSRQV 721

Qy    737 QVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQN--LNLPQSFRVYPDPGLKA 793
              :   |  ::   |  :| :: |  ||  :||::| ::|   :|:|| |    :||||
Db    722 EAMEKLINLT-DI--LKQEKKDETQKV--QMKFLVEQMRRPFMDALQGFISPLNPAHQL 776

Qy    794 GALVIECKVMASKKKPLWLEFKCADPTALS------NETIGIIFKHGDDLRQDMLILQI 847
              | ::::|  :::  :|:| :  ||  ::          |||||| |||||:|:|||:|:|
Db    777 GNLRLEECRIMSSAKRPLWLNWE---NPDIMSELLFQNNE--IIFKNGDDLRQDMLTLQI 831

Qy    848 LRIMESIWETBSLDLCLLPYGCISTGDKIGMEIVKDATTIAKIQQSTVGNTGA-FKDE 905
              :|||| | :|||| |:||||| || |:|||  |  | | :::::| || || | ||::
Db    832 IRIMENIWQNGGLDLRMLPYGCLSIGDCVGLIEVRSSHTIMQI--QCKGGLKGALQFNSH 890

Qy    906 VLSHWLKEKCPIEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNLFHDF 965
              |:| || :|| ||| ::|  :|| ||||| ||| : |||||| |:::: |:| ||||
Db    891 TLHQWLKDKNK-GEMYDAAIDLFTRSCAGYCVATFIGIGDRHNSNIMVKDDGQLFHIDF 949

Qy    966 GHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKK---TSLHFQKFQDVCVXAYLALRHH 1023
              || ||: :| |:: || |||| || |:|||:::|     |||||  | ::| :||:|: ||
Db    950 GHFLDHKKKKFGYKRERVPFVLTQDLLIVISKGAQECTKTRBFERFQEMCHKAYLAIRQH 1009

Qy   1024 TNLLIILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAXKYFLDQIEVCRDKGWTVQ 1083
              || :|:||:|::||||| |:| |:| |||| :|||:|:  | |||||:|  |: ||||:|
Db   1010 ANLFINLFSMMLGSGMPELQSPDDIAYIRKTLALDKTEQEALEYFMKQMNDAHHGGWTTK 1069

Qy   1084 FNWFLHLV 1091
              | | ::|:
Db   1070 MDWIFHTI 1077
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RESULT 6
Q8BTI9
ID   Q8BTI9          PRELIMINARY;       PRT;   1064 AA.
AC   Q8BTI9;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Phosphatidylinositol 3-kinase catalytic subunit.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Colon;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
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RL   Nature 420:563-573 (2002).
DR   EMBL; AK090116; BAC41102.1; -.
SQ   SEQUENCE   1064 AA;  121753 MW;  3E96729B25C52D1C CRC64;

Query Match             23.5%;  Score 1363;  DB 11;  Length 1064;
Best Local Similarity   32.4%;  Pred. No. 9e-97;
Matches  357;  Conservative 195;  Mismatches 400;  Indels 150;  Gaps 35;

Qy    78 ALETSVSADFYHRLG------PDHFLLLYQKKGQWYEI--YDKYQVVQTLD-----CLR 123
         | :||  ||  ||  |              :||    |      |   |         ||
Db    19 ASDGAISVDFLLPTGIYIQLEVPREATISYIKQMLWKQVHNYPMFNLLMDISYMPACVN 78

Qy   124 YWKVLHRSPGQ-------IHVVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHD 170
         |                :::       :     |  ::
Db    79 QTAVYEELEDETRRLCDVRPFLPVLKLVTRSCDPAEKL--DSKIGVRIGKGLHEFDALKD 136

Qy   171 DEL-EFTR--RRLVTPRMAEVAGRDPKLYAMPWVTSKPLPEY-------LLKKITNNCV 220
         :|      |              |    |              |       ||||||||
Db   137 PEVNEFRRKRMRKKFSEAKIQSLVG----LSWIDWLKHTYPPEBEHPSVLENLEDKLYGGKL 191

Qy   221 FIVIHRSTTSQ-TIKVSADDTPGTILQSFFTKMAKKSLMDIPESQNERDFVLRVCGRD 278
         |:  |   :  |||||||||||||||||||| |  :    | ||||||| ||||| |:
Db   192 VVAVHFENSQDVFSFQVSPNLNPIKINE---LAIQKRLTIRGKEDEASPCDTVLQVSGRV 248

Qy   279 EYLVGETPIKNFQWVRQCLKNGEEIHLVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQ 338
         || :|  || |  |:|                         ::               |:
Db   249 EYVFGDHPLIQFQYIRNCVMNRTLPHFIJ------------VECCKIKKMYEQ 289

Qy   339 --LTIHGKDHESVFTVSL------WDCDRKFRVKIRGIDIPVLPRTADLTVFV 383
           :  |                    :||||||| ||||||||||||||||||
Db   290 EMIALEAAINRNSSNLPLPLPPKKTRVISHIWDNNNPFQITL--VKGNKLNTEETVKHV 347

Qy   384 EANIQYGQOVLCQRRTSPK-PFTEVLMNVWLEFSIKIKDLPKGALLNLQIYCGKAPALS 442
         :| ||| |:||||||||| |||||:||||||||||||||||||||:|||||||||||||
Db   348 RAGLFHGTELLCKTVVSSEISGKNDHIWNEQLEPDINICDLPRMARLCFAVY-AVLDKVK 406

Qy   443 GKTSAEMPSP---ESKGKAQLLYY----VNLLLIDHRFLLRHGEYVLHMWQLSGKGEDQG 495
         ||||||||||                  :|
Db   407 TKKSTKTINPSKYQTIRKAGKVHYPVAWNTMVFDFKGQLRSGDVILHSW---------S 457

Qy   496 SFNADKL--------TSATNPDKENSMSISILL-DNYCHPIALP-------KHRPTPDPE 539
         ||  ::          || |||||||||||||| ||| |||||        |||
Db   458 SF-PDELEEMLNPMGTVQTNPYAENATALHITPENKKQPCYYPPFDKIIEKAAELASGD 516

Qy   540 GDRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKD-PKAYPKLFSSVKW 598
         | ::  :  :||   |  :     ||  | :: :: ||  :    | || |||| |:|||
Db   517 SANVSSRGGKKFLAVLKEILDRDPLSQLCENEMDLIWTLRQDCRENFPQSLPKLLSIKW 576

Qy   599 GQQEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDVLH 658
             ::|  :||   |                 :      |   |||:
Db   577 NKLEDVA--QLQALLQIWPK--LPPREALELLDFNYPDQYVREYAVGCLRQMSDEEISQ 631

Qy   659 YLLQLVQAVKFEPYHDSALARFLLKRGLNKRIGHFLFWFLRSEIAQSRHYQQRFAVILE 718
         ||||||| :|:||  | || |||| | |:|| ||||||:|||| : |  || ||| |||
Db   632 YLLQLVQVLKYEPFPLDCALSRFLLERALDNRR:GQFLFWHLRSEV-HTPAVSVQFGVILE 690

Qy   719 AYLRGCGTAMLHDFTQQVQVIDMLQKVTIDIK----SLSAEKYDVSSQVI---SQLKQKL 771
         || ||  :   |    || ::                :|   |||||  |    ||
Db   691 AYCRG--SVGHMKVLSKQVEALNKLKTLNSLIKLNAVKLSRAKGKEAMTCLKQSAYREAL 749

Qy   772 ENLQNLNLPQSFRVPYDPGLKAGALVIEKCKVNASKKKKPLWLEFKCADPTALSNETIGHI 831
         ::||          |  ||| :|| |:||||:   |    |||:          :   ||:
Db   750 SDLQS--------PLNPCVILSELYVEKCKYMDSKMKPLWLVY---SSRAFGEDSVGVI 797

Qy   832 FKNGDLRQDMLIIQILRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKI 891
         ||||| |||||:||:|| | |:|  | |||| ||||| ||| |:|:|:|  : ||| |:
Db   798 FKNGDDLRQDMLTIQMLRLMDLLWKEAGLDLRMLPYGCLATGDRSGLIEVVSTETIADI 857

Qy   892 Q---QSTVGNTGAFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHN 949
         |    :  ::  ||:|  | ||||: :   : ||||:|| | ||||||| ::||||||||:
Db   858 QLNSSNVAATAAFNKDALLNWLKEYNSGDD-LDRAIEEFTLSCAGYCVASYVLGIGDRHS 916

Qy   950 DNIMISETGNLFHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKF 1009
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Db   917 DNIMVKKTGQLFHIDPGHILGNFKSKFGIKRERVPFILTYDFIHVIQQGKTGNTEKFGRP 976
         |||: : ||:||||| ||||||:||||||:||||||| ||||| ::|| ||||  ||
Qy  1010 QDVCVKAYLALRHHTNLLILFSMMLTMGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFL 1069
         :| ||  || || || | :| :::||:|:| :|:|:|||: |||:|:||::|: ||:|:
Db   977 RQCCEDAYLILRRHGNLFITILFALMLTAGLPELITSVKDIQYLKDSLALGKSEEEALKQFK 1036

Qy  1070 DQIEVCRDKGWTVQFNWFLHLV 1091
         ||: :   : |  |:| |:|:|
Db  1037 QKFDEALRESWTTKVNWMAHTV 1058

RESULT 7
Q8BS14
ID   Q8BS14     PRELIMINARY;     PRT;   1047 AA.
AC   Q8BS14;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Phosphatidylinositol 3-kinase catalytic delta polypeptide.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573 (2002).
DR   EMBL; AK040867; BAC30725.1; -.
SQ   SEQUENCE   1047 AA;  120186 MW;  73654D27449A30B2 CRC64;

Query Match             23.1%;  Score 1339;  DB 11;  Length 1047;
Best Local Similarity   31.9%;  Pred. No. 6.5e-95;
Matches  354;  Conservative 205;  Mismatches 409;  Indels 140;  Gaps 38;

Qy    38 IPIEFVLPTSQRNTKTPETALLH--VAGHGNVEQMKAQVWLRALETSVSADFYHRLG-PD 94
         : : |:|||  :|  | :     |        |   :|  | | ::  :||||||||  |
Db    20 VVVDFLLPTG-------VTLNFVSRNANLSTIKQVLWHRAQYEPL---FHMLSDPE 66

Qy    95 HFLL-LYQKKGQWYEIYDKYQVVQTLDCLRYWKVLHRSPGQIHVVQRHAPSEETLAFQRQ 153
            | |:|:  :   |:|  ::   ||  ||:            :::
Db    67 AYVFTCVNQTAEQQELEDEQR--RLCDIQPFLPVL------RLVAREGDRVKKL-INSQ 116

Qy   154 LNALIGYDVTDVSNVHDDELEFTRRRLVTPRMAEVAGRDPKLYAMHPWVTSKPLPEYL-- 211
         : ::||  : :        :|||:  :           |:
Db   117 ISLLIGKGLHEFDSLRDPEVNDFRTKM--RQPCEEAAAHRQQLGHWVEWL-QYSFPMQLEP 173

Qy   212 ------LKKITNNCVFIVI-HRSTTSQTIKVSADDTPGTILQSFFTKMAK--KKSLM 259
               ||||||||  :|  |||| |:: |:|  :   | :  |: |  ||   ::
Db   174 SARGWRAGLLRVSNRALLVNVKFEGEESFTFQVSTKDMPLALMACALRKKATVFRQPLV 233

Qy   260 DIPESQNERDFVLRVCCRDEXYLVGETPIKNFQWVRQCLKNGEEIHLVL------- 307
         : |                 :|:| |||:       ||| |
Db   234 EQPE------EYALQVNGRHEYLYGNYVPLCHFQYICSCLHSGLTPHLTMVHSSSILAMRDE 288

Qy   308 DTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHESVFTVSLMDCDRKFRVK-IR 366
          : |   :                :|            : :   |: :  ::
Db   289 QSNPAFQVQKPRAKPPP------------IPAKKPSS--VSLWSLEQPFSIELIE 329

Qy   367 GIDIPVLPRTAD--LTVFVERANIQYGQQVLCQRRTSPK-PFTEEVLWNVWLBFSIKIKDL 423
         | ::        |      :    ::| ::  |          :|:::::  |: : : ||
Db   330 GRKV-----NADERMKLJVVQAGLFHGNEMLCKTVSSSEVNVCSEPVWKQRLEFDISVCDL 384

Qy   424 PKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYYVNLLLIDHRFLLRHGEYVLH 483
         |: | |  :   ::    :|::::    :   ::   ::
Db   385 PRMARLCFALYAVVEKAKKARSTKK---KSKKADCPIAWANIMLFDYKDQLKTGERCLY 440

Qy   484 MWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYC-HPIALP-------KHR 533
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Db       :::|     |:  |  ||:    :|  |         ||:          |
Qy  441  MW--PSVPDEKGELLNPAGTVRGNPNTESAAALVIYLPBVAPHPVYFPALEKILELGRH-  497

         ||   :|:   :||||:    |  | || ||    :||  :  |
Db  534  PTPDPEGDRVRAEMPNQLRKQLERIIATDPLNPLTAEDKELLWHFRYESLKD-PKAYPKL  592

              ||:   |  | |||||:|  |:  | | :|: ||:  :: | |  |
Qy  498  ------GERGRITEEQL--QLREILERRGSGELYEHEKDLVNKMRHEVQEHFPEALARL   549

         :|::  ||:|:|  |: | ::|  :: | | |  :| :::|  | |::    |
Db  593  FSSVKWGGQEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLE  652

         :||: |  :||::|  :|||||| |:    :|:  |||:  | :  :||:| | :
Qy  550  LLVTKWNKHEDVAQLSQMIYLLCSWPE--LPVLSALELLDFSFPDCYVGSFAIKSLRKLT  607

         |:|  :|  |:|  || ||| |:|| |||| |:|||| |  |: ||:: ::
Db  653  DDDVLHYILQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQ-  711

         ||: |  |:|||| |:  |:|:|  | |||| ||:|||||||:|:|| |:   |||:|
Qy  608  DDELFQYILLQLVQVLKYBSYLDCELTKFLLGRALANRKIGHFLFWHLRSEM---HVPSV  663

          : |:|   |: |  :|  |::  |: ||: ||: :|  | ||: :|  | ||:|:||
Db  712  --RPAVILBAYLRGCGTAMLHDFTQQVQIDMLQXVT--IDIKSLSAEKYDVSSQVISQL   767

         |::  |:| |::|  |  :|:  |||  | :| |:|| :::| || | ::| | |: |
Qy  664  ALRFGLIMEAYCRG-STHHMKVLMKQGEALSKLKALNDFVKVSSQKTTKPQTKEMMHMCM  722

          :|    |:|  |   |  | |:|||| |  |  :|| | |:::||||||:||
Db  768  KQK--LENLQNLNLPQSFRVPYDPGLKAGALVIEKCKVMASKKKPLWLEFKCADPTALSN  825

         |::::::|  |||    :|:|:|:|||||||||||||||||||||||||||||||||
Qy  723  RQETYMEALSHL-----QSPLDPSTLLBEVCVBQCTFMDSKMKPLWIMYSSEEAGSAGN   776

         ||:|||:|:|||||||||||||:||:|:|||||||||||||||||||||||||||||
Db  826  ETIGIIFKGHDDLRQDMLIQILRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDA  885

         ||:|||:|:|||||||: ||||: |:|||| |||  |  |||||| |||||| ||||||
Qy  777  --VGIIFKNGDDLRQDMTLQMIQLMDVLWKQBGLDLRMTPYGCLPTGDRTGLIEVVLHS  834

         |:||:|| ||||||:||:|:|:|| ||||||||||||||||||||||||||||||||||
Db  886  TTIAKIQ--QSTVGNTGAPKDEVLSHWLKEKCPIEKFQAAVERFVYSCAGYCVATFVLG  943

         |:|:|:  ||:   |::|| ||| |||:| |:| |:||||||||:||||||||||:|||
Qy  835  DTIANIQLNKSNMAATAAFNKDALLNWLKSKNP-GEALDRAIREFTLSCAGYCVATVVLG  893

         ||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  944  IGDRHNDNIMISETGNLFHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTS  1003

         ||||:|||||:|  |||||||||:|||:| ||||:|||||||:|:|||||:|||
Qy  894  IGDRHSDNIMIRESGQLFHIDFGHFLGNFKTKPGINRKRVPFILTYDFVHVIQQGKTNNS  953

         | | |:||||||||||:||||:||||:||||||||||||||||||||||||||||||||
Db  1004 LHFQKFQDVCVKAYLALRHTNLLIILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEED  1063

         |:| |:|| |:||| :|::|||| ||: :|| ||::||| :|||||| :
Qy  954  EKFFRFRGYCERAYTILRRHGLLFLHIFLALMRAAGLFELSCSKDIQYLKDSLALGKTEEE 1013

         |:|| :||||||||||||:||:||
Db  1064 AKKYFLDQIEVCRDKGWTVQFNWFLHLV                                  1091

         |:||:|: ||:|:|::|: ::|
Qy  1014 ALKHFRVKFNEALRESWKTKVNWLAHNV                                  1041
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RESULT 8
Q8C5Q7
ID   Q8C5Q7
AC   Q8C5Q7;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Phosphoinositide-3-kinase.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium;
RA   The RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573 (2002).
DR   EMBL; AK077772; BAC37000.1; -.
FT   NON_TER   1   1
SQ   SEQUENCE   260 AA; 29624 MW; 91C638596663BCC5 CRC64;

Query Match   23.1%; Score 1335; DB 11; Length 260;
Best Local Similarity   97.7%;
Matches 254; Conservative   4; Mismatches   2; Indels   0; Gaps   0;
Pred. No. 1.5e-95;

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Qy  843  LILIQILRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTGAF  902
         ||||||||||||||||||||||||||||||||||||||||||||||||:||||||||||||
Db    1  LILIQILRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAQIQQSTVGNTGAF   60

Qy  903  KDEVLSHWLKEKCPIEBKFQAAVERFVYSCAGYCVATFVLGIGDRENDNIMISETGNLFH  962
         |||||:||||||||||:|||||||||||||||||||||||||||||:|||||||||||||
Db   61  KDEVLNHWLKEKCPIEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNLFH  120

Qy  963  IDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQXFQDVCVKAYLALRH  1022
         |||||||||||||||||||||||||||||||||||:||||||:|| |||| | |||||||
Db  121  IDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGSSGKKTSPHFQKFQDVVVRAYLALRH  180

Qy 1023  HTNLLIILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGWTV  1082
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  HTNLLIILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGWTV  240

Qy 1083  QFNWFLHLVLGIKQGEKGHSA  1102
         |||||||||||||||||||||
Db  241  QFNWFLHLVLGIKQGEKGHSA  260
```

RESULT 9
Q8CI98
ID   Q8CI98
AC   Q8CI98;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Phosphatidylinositol 3-kinase catalytic delta polypeptide.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Salivary gland;
RA   Strausberg R.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC035203; AAH35203.1; -.
KW   Kinase.
SQ   SEQUENCE   1037 AA; 119130 MW; 4446B78B5F37A0E2 CRC64;

Query Match   23.0%; Score 1329; DB 11; Length 1037;
Best Local Similarity   32.1%; Pred. No. 3.8e-94;
Matches 356; Conservative 203; Mismatches 407; Indels 142; Gaps 40;

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Qy   38  IPIBEFVLPTSQRNTKTPETALLH--VAGHGNVEQMKAQVWLRALETSVSADFYHRLG-PD   94
         :|::||:||| ::    |  ||||          :| :  |  |:         :|: | |:
Db   12  VVVDFLLPTG--------VVINFPVSRNANLSTIKQVLWHRAQYEPL---FHMLSDPE   58

Qy   95  HFPLL-LYQKGQWYEIYDKYQVVQTLDCLRYWKVLHRSPGQIHVVQRHAPSEETLAFORQ  153
            |:  | ::  |:|  ::  :: | |    ::|:  :  |||        ::   : :|
Db   59  AYVFTCVNQTAEQQEIEDEQR--RLCDIQPFLPVL------RLVAREGDRVKKL-INSQ  108

Qy  154  LNALIGYDVTDVSNVHDDELEFTRRLVTPRMAEVAGRDPKLYAMHPWT-SKPLP-----  208
         :  ||| ::  : :  ||  :|  |:      |           ||:| |||:
Db  109  ISLLIGKGLHEFDSLRDPEVNDFRTKM--RQFCEEAAAHRQQLGWEWLQYSFPLQLEPS  166

Qy  209  ---EVILLKKITNNCVFIVI--HRSTTSQTIKVSADDTPGTILQSFFTKMAK--KKSLMD  260
             | :|   :  |:  :|   |||::  :||||:|  | ::  |:| |:||    :
Db  167  ARGWRAGLLRVSNRALLVNVKFEGSSEESFTFQVSTKDMPLALMACALRKKATVRPQPLVE  226

Qy  261  IPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNGBEIHIVL---------D  308
         :||   :   :  |  |:|::  |  |||  :  || |        :|
Db  227  QPE------EYALQVNGRHEVYLYGNYPLCHFQYICSCLHSGLTPHLTMVHSSSILAMRDEQ  281

Qy  309  TPPDALDEVRKEEWPLVDDCTGVTGYHEQLTIHGKDHSSVFTVSLWDCDRKFRVK-IRG  367
         : |    :||    ||  |  | ||::|||  |||| ||||||||| |||| |||| |:|
Db  282  SNPAPQVQKPRAKPPP-----------------IPAKKPSS---VSLWSLEQPFSIELIEG  322

Qy  368  IDIPVLPRTAD--LTVFVEANIQYGQQVLCQRRTSPK-PFTBEVLWNVWLEFSIKIKDLP  424
         :::|:| ::|   ||:||: |||||:|||||||:|||  ||:|||||:|||| ||||:|||
Db  323  RKV-----NADERMKLVVQAGLFHGNEMLCKTVSSSEVNVCSEPVWKQRLEFDISVCDLP  377
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OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97133288; PubMed=8978685;
RA   Leevers S.J., Weinkove D., MacDougall L.K., Hafen E., Waterfield M.D.;
RT   "The Drosophila phosphoinositide 3-kinase Dp110 promotes cell
RT   growth.";
RL   EMBO J. 15:6584-6594(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BERKELEY;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
CC   -!- CATALYTIC ACTIVITY: ATP + 1-PHOSPHATIDYL-1D-MYO-INOSITOL = ADP +
CC       1-PHOSPHATIDYL-1D-MYO-INOSITOL 3-PHOSPHATE.
DR   EMBL; Y09070; CAA70291.1; -.
DR   EMBL; AE003731; AAF55792.1; -.
DR   FlyBase; FBgn0015279; PI3K92E.
DR   InterPro; IPR011263; PI3Ka.
DR   InterPro; IPR002420; PI3K_C2.
DR   InterPro; IPR003113; PI3K_p85B.
DR   InterPro; IPR000341; PI3_PI4_kinase.
DR   InterPro; IPR000403; PI3_PI4_kinase.
DR   Pfam; PF00613; PI3Ka; 1.
DR   Pfam; PF00792; PI3K_C2; 1.
DR   Pfam; PF02192; PI3K_p85B; 1.
DR   Pfam; PF00794; PI3K_rbd; 1.
DR   Pfam; PF00454; PI3_PI4_kinase; 1.
DR   SMART; SM00145; PI3Ka; 1.
DR   SMART; SM00146; PI3Kc; 1.
DR   SMART; SM00142; PI3K_C2; 1.
DR   SMART; SM00143; PI3K_p85B; 1.
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DR   SMART; SM00144; PI3K_rbd; 1.
DR   PROSITE; PS00915; PI3_4_KINASE_1; 1.
DR   PROSITE; PS00916; PI3_4_KINASE_2; 1.
DR   PROSITE; PS50290; PI3_4_KINASE_3; 1.
KW   Kinase; Transferase.
SQ   SEQUENCE   1088 AA;   127005 MW;  ABDEF07902AAB81C CRC64;

Query Match             22.2%;  Score 1283;  DB 5;  Length 1088;
Best Local Similarity   33.1%;  Pred. No. 1.6e-90;
Matches  315;  Conservative 189;  Mismatches 333;  Indels 114;  Gaps 28;

Qy    194 KLYAMHP--WVTSKPLPEYLLKKITNNCVPIVIHRSTTSQ--TIKVSADDTPGTILQSF 248
Db    189 RLLYEHPLRLANSTKMPE-LIRERHPTRTFLIVVKNENDQSTFLSVNEQDTPFSLTEST 247

Qy    249 FTKMAKKKSLMDIPESQNER--DFVLRVCGRDEYLVGETPIKNFQWVRQCLKNGEEIHLV 306
Db    248 LQKMNRSQMKM------NDRTSDYILKVSGRDEYLLGDYPLIQFLYIQEMLSD-------- 294

Qy    307 LDTPPDALDEVRKEWPLVDDCTGVTGYHEQL------TIHGKDHESVFTVSLW 355
Db    295 -SAVPNVVLQSVYRLE------SYINHHNEQAMVTKRPLPKKRTVH--LHKSI--SSLW 342

Qy    356 DCDRKFRVKIRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTSPKP--FTEBVLWNV 412
Db    343 DMGNYFQLTLHSISNVNFDKTRALKVGVHVCLYHGDKKLCAQRSTSPNGNFDTFLFNDL 402

Qy    413 WLEFSIKIKDLPKGALLNLQIYCGKAPALSGKTS----AEMPSPESKGKAQLLYVNLL 467
Db    403 VMDFDIQMRNLPRMTRLCIVIFEVTKMSRSKKSSNNKDIALKDVPYNKNP---LAWNTT 459

Qy    468 LIDHRFLLRHGEYLHMWQLSGKGEDQGSFNADKLTSA------TNPDKENSMSIS 517
Db    460 IFDHKDILRTGRHTLYTWTY-------ADDIQSVEVFHPLGTIEPNPRKEECALVD 508

Qy    518 I-LLDNYCHPIALPKHRPTDPEGDRVRAEMPNQLR---------KQLEAIIAT--D 562
Db    509 LTFLSSGTGTVRYPSEEVVLQYAADR--EQVNRLQRQLAGPEKPIKELKELMANYTGLD 565

Qy    563 PLNPLTABDKELLWHFRYESLKD-PKAYPKLFSSVKWGGQEIVAKTYQLLIAKREVWDQSA 621
Db    566 KIYEMVDQDRNAIWERRNDIRELEPELSILHCVVWKERDDVADMWYLIKQ---W--PL 620

Qy    622 LDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYLLQLVQAVKFPPYHDSALARFL 681
Db    621 ISIERSLELLDYAYPDPAVRRFAIRCLHFLKDEDILLYLLQLVQLVQAIKHESYLESDLVVFL 680

Qy    682 LKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAYLRGCGTAMLHDFTQQVQVIDM 741
Db    681 LERALRNQRIGHYFFWHLRSEM-QTPSMQTRFGLLLEVYLKGC-KHHVAPLRKQLHVLEK 738

Qy    742 LQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLPQSFRVPYDPGLKAGALVIEKC 801
Db    739 LKQGSLIAKKGSKEK------VKTMLQDFLRDQRNSAVFQNIQNPLNPSPRCSGVTPDRC 792

Qy    802 KVMASKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQDMLILQILRIMESIWETESLD 861
Db    793 KVMDSKMRPLWVVFENADVNA---SDVHIIFKNGDDLRQDMLTLQMLRVMDQLWKRDGMD 849

Qy    862 LCLLPYGCISTGDKIGMIEIVKDATTIAKIQ--QSTVGNTGAFKDEVLSHWLKEKCPIEE 919
Db    850 FRMNIYNCISMEKSLGMIEVVRHAETIANIQKEKGMFSATSPFKKGSLLSWLKEHNKPAD 909

Qy    920 KFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNLFHIDFGHILGNYKSFLGIN 979
Db    910 KLNKAINEFTLSCAGYCVATVLGVADRHSDNIMVKRNGQLFHIDFGHILGNFHFKEKLGVR 969

Qy    980 KERVPFVLTPDFLFVNGTS-GKKTSLHFQKFQDVCVKAYLALRHHTNLLILFSNMLMTG 1038
Db    970 RERVPFVLTHDFVYVINKGFNDRESKEFCHFQELCERAFLVLRKHGCLILSLFSMMISTG 1029

Qy   1039 MPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGWTVQFNWFLH 1089
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Db  1030  LPELSSEKDLDYIRETIVLDYTEEKAREHFRAKFSEALANSWKTSLNWASH  1080
```

```
RESULT 13
Q9PTE5
ID   Q9PTE5              PRELIMINARY;    PRT;   852 AA.
AC   Q9PTE5;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Phosphoinositide 3 kinase catalytic subunit (Fragment).
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Distal nephron;
RA   AL-Khalili O.K., Tran T., Eaton D.C.;
RT   "Molecular cloning of Xenopus laevis phosphoinositide 3 kinase
RT   catalytic subunit mRNA.";
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Distal nephron;
RA   Al-Khalili O.K., Eaton D.C.;
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF204924; AAF15300.1; -.
DR   InterPro; IPR000008; C2.
DR   InterPro; IPR001263; PI3Ka.
DR   InterPro; IPR002420; PI3K_C2.
DR   InterPro; IPR003113; PI3K_p85B.
DR   InterPro; IPR000341; PI3K_ras_bind.
DR   InterPro; IPR000403; PI3_PI4_kinase.
DR   Pfam; PF00613; PI3Ka; 1.
DR   Pfam; PF00792; PI3K_C2; 1.
DR   Pfam; PF02192; PI3K_p85B; 1.
DR   Pfam; PF00794; PI3K_rbd; 1.
DR   Pfam; PF00454; PI3_PI4_kinase; 1.
DR   SMART; SM00239; C2; 1.
DR   SMART; SM00145; PI3Ka; 1.
DR   SMART; SM00146; PI3Kc; 1.
DR   SMART; SM00142; PI3K_C2; 1.
DR   SMART; SM00144; PI3K_rbd; 1.
DR   PROSITE; PS00915; PI3_4_KINASE_1; 1.
DR   PROSITE; PS00916; PI3_4_KINASE_2; 1.
DR   PROSITE; PS50290; PI3_4_KINASE_3; 1.
KW   Kinase.
FT   NON_TER       1      1
FT   NON_TER     852    852
SQ   SEQUENCE   852 AA;  98705 MW;  15C1F3CCDDE28884 CRC64;

Query Match             19.1%;  Score 1103.5;  DB 13;  Length 852;
Best Local Similarity   33.1%;  Pred. No. 1e-76;
Matches  298;  Conservative 162;  Mismatches 310;  Indels 129;  Gaps  34;
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Qy  135  IHVQRHAPSEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRLVTPRMAEVAGRDPK  194
              |:||  :      ::    :|    :  : :::
Db   16  LKVVBPVGNREEKI-LNREIGFAIGMPVCEFDMVKDSEVQDFRRNVLNVCKDSVELRDAN  74

Qy  195  ------LYAMHPWV-TSKFLPEYLLKKITNNCVIVI------HRSTTSQTIKVSADDTP  241
                 :: : :|    ||: :|  :::|:|:          ::|:::   ||::::
Db   75  GPISRALYVYPPNVESSSELPKHIESKLDKGQIIVWIWIVSPNNEKQKYSLKINHDCVP  134

Qy  242  GTILQSFFTKMAKKKSLMDIPES------QNERDPVLRVCGRDEYLVGETPIKNFQWVRQ  295
              ::  :|     :: :|   :::        ||:: ||||| |||:| :|  :::|::
Db  135  EHVIAEAIRK--KPRSMLLSTEQLKLCVLEYQGKYILKVCGCDEYLLEKYPLSQYKYIRS  192

Qy  296  CLKNGEEIHVLDTPPDPALDEVRKEEWPLVDDCTGVTGYHEQLT-----IHGKDHESVF  350
             : :|   :|    :  ::     ||:   :::  : : :|:      |:|:|:|: :
Db  193  CIMLGRMPNLML------MAKESLYNQIPV--DIFTMPSYSRRISTAAPYMNGETSAK--  242
```

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Qy  351  TVSLWDCDRKPRVK--------IRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTS  400
              |||         :|  :  ||:  .|.|||.:||:.|:  .  :|  ::|
Db  243  --SLWAINSTLRIKILWATYVNVTIRDID---------KIYVRTGIYHGVEPLCDNVNT  290

Qy  401  PKPFTEVLWNVWLEFSIKIKDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQL  460
         ||||      |||  ::|:||||||||  ::|                 :     |:||
Db  291  QRVPCSNPRWNEWLLYDMFIPDLPRAARVCLSI-C----SVKGRKGA---------KEEHCP  338

Qy  461  LYYVNLLIDHRPLLRHGEYVLHMWQLSGKGEDQ----GSFNADKLTSATNPDKENSMSI  516
              ||:::  :|: ||||||:|:|||| |||  :        ::||::     ::  :
Db  339  LAWGNINLFDYTDTLVSGKWALNLWPVPHGLEDLLNPIG------VSGSNPNKB-TPCL  390

Qy  517  SILLDNYCHPIALPKHRPTPDPEGDRVRAEM------PNQLR---KQLEA  557
            :::    |   |:     :|:  :||   ::        :|::::   ::||
Db  391  ELEFDCFSSPVKFPPDMTAIEDHANKVLERELGYNYSHSGLSNRIVRENEVRENDKEQLRA  450

Qy  558  IIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQQEIVAKTYQLLAKREVW  617
          |::|||::|| |:|:|:|||:|||:||:||  ||||||:|||:: ||:::| ||:::| |
Db  451  ISNRDPlSEITEQEKFLWSHRLYCRNIPEVLSKLLSVKWNCRDDVSQMYCLLKE---W  507

Qy  618  DQSALDVGLTMQLLDCNFSDENVRAIAVQKLES-LEDDVLHYLLQLVQAVKFPEYHDSA  676
              |  ::||:||:|:|:||  ||:|:|| |||:|:  |  ::|:|:|||||:||:::|
Db  508  --PAIRPEQAMELLDFNYPDRIVRSFAVSCLEKYLTDDKLSQFLIQLVQVMKEYQYLDNH  565

Qy  677  LARFLLKRGLERNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAYLRGCGTAMLHDFTQQV  736
          |.|||||| :.|:||||||:|||:|:||:|  |:|||| |:|||::|:||  :|: :::|:
Db  566  LVRFLLKRALVNQRIGHFFFWHLKSEM-HNKTVSQRFGLLLESYCRACGMYLKH-LSKQV  623

Qy  737  QVIDMLQKVTIDIKSLsAEKYDVSSQVISQLKQKLENLQN--LNLPQSFRVPYDPGLKA  793
          : ::||:||| |||::| :|| |::||:  |::|:::  : | ::  |||:|||: ||:
Db  624  EAMEKLJNLT-DI--LKQEKKDETQKV--QMKFLFEQMKRPDFMDALQGFTSPLNPAHQL  678

Qy  794  GALVIEKCKVMASKKKPLWLEFKCADPTA---LSNETIGIIPKHGDDLRQDMLIIQILR  849
          | | :|:| ::|::|:|||:: :|:|:     |||::|||::|:|||||||||:||||:
Db  679  GNLRLEECRIMSSAKRPLWILSWENPDIMSEMLFLNNE---IIFKNGDDLRQDMLTIQIIR  735

Qy  850  IMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTGA--FKDEVL  907
          ||::||::: |||::|||||:|:||::|::|:|| |  ::::|:| :::: | |  :::|:
Db  736  IMENIWQNQGLDLRMLPYGCLSIGDCVGLIIVVRCSHTIMQI-QCKGGLKGALQFNSHTL  794

Qy  908  SHWLKEKCPIEKFQAAVERPVYSCAGYCVATFVLGIGDRHNDNIMISETGNLFHIDFG  966
           :||:::| :|::  |:| |:| ||||||||||:||||||||:|||:  ::|||||||
Db  795  HQWLKDRNK-GETYDAAIDLFTRSCAGYCVATFILGIGDRHNSNIMVKDSGQLFHIDFG  852
```

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RESULT 14
Q61182
ID   Q61182              PRELIMINARY;    PRT;   1658 AA.
AC   Q61182;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Phosphoinositide 3-kinase.
GN   PIK3C2A OR CPK-M.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=balb c;
RX   MEDLINE=96278830; PubMed=8662856;
RA   Molz L., Chen Y.W., Hirano M., Williams L.T.;
RT   "Cpk is a novel class of Drosophila Ptdins 3-kinase containing a C2
RT   domain.";
RL   J. Biol. Chem. 271:13892-13899(1996).
CC   -!- SIMILARITY: CONTAINS 1 C2 DOMAIN.
DR   EMBL; U52193; AAC52604.1; -.
DR   HSSP; P21707; 1BYN.
DR   MGD; MGI:1203729; Pik3c2a.
DR   InterPro; IPR000008; C2.
DR   InterPro; IPR001263; PI3Ka.
DR   InterPro; IPR002420; PI3K_C2.
```

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Db   867  LWENRYYCLKHPNCLPKILASAPNWKWAN---LAKTYSLLHQ---W--PPICPLAALELL  918
Qy   632  DCNFSDENVRAIAVQKLESLEDDDVLHYLLQLVQAVKFEPYHDSALARPLLKRGLRNKRI  691
Db   919  DAKFADQGVRSLAVSWMEAISDDELADLLPQFVQALKYEIYLNSSLVRPLLSRALGNIQI  978
Qy   692  GHFLFWFLRSEIAQSRHYQQRFAVILEAYLRGCGTAMLHDFTQQVQVIDMLQKVTIDIKS  751
Db   979  AHSIYWLLKDAL-HDTHFGSRYEHVLGALLSVGGKGLREELSKQMKLVQLLGGVAEKVRQ 1037
Qy   752  LSAEKYDVSSQVISQLKQKLENLQNLNLPQSFRVPYPDGLKAGALVIEKCKVMASKKKPL  811
Db  1038  ASGS----TRQVV--LQKSMERVQSFFLRNKCRLPLKPSLVAKELNIKSCSFFSSNAMPL 1091
Qy   812  WLEFKCADPTALSNETIGIIFKHGDDLRQDMLIIQILRIMESIWETESLDLCLLPYGCIS  871
Db  1092  KVTMVNADPL---GEEINVMFKVGEDLRQDMLALQMIKIMDKIWLKEGLDLRMVIFRCLS 1148
Qy   872  TGDKIGMIEIVKDATTIAKIQQSTVGNTGAFKDEVLSHWLKEKCPIEEKFQAAVERFVYS  931
Db  1149  TGRDRGMVELVPASDTLRKIQVE-YGVTGSFRDKPLAEWLRKYNPSEEYEKASENFIYS  1207
Qy   932  CAGYCVATFVLGIGDRHNDNIMISETGNLFHIDFGHILGNYKSFLGINKERVPFVLTPDF  991
Db  1208  CAGCCVATVVLGICDRHNDNIMLRSTGHMFHIDFGKFLGHAQMFGSFKRDRAPPVLTSDM 1267
Qy   992  LFVMGTSGKKTSLHFQKFQDVCVKAYLALRHHTNLLILFSMMLMTGMPQLTSKEDIEYI  1051
Db  1268  AYVI-NGGEKPTIRFQLFVDLCCQAYNLIRKQTNLFLNLFLNLLSMIPSGLPELTSIQDLKYV 1326
Qy  1052  RDALTVGKSEEDAKKYFLDQIEVCRDKGWTVQPNWFLH  1089
Db  1327  RDAIQPQTTDAEAIFFTLRIESSLGSIAT-KPNFFIH  1363

RESULT 15
O00443
ID   O00443      PRELIMINARY;      PRT;   1686 AA.
AC   O00443;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Phosphoinositide 3-kinase.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97479209; PubMed=9337861;
RA   Domin J., Pages F., Volinia S., Rittenhouse S.E., Zvelebil M.J.,
RA   Stein R.C., Waterfield M.D.;
RT   "Cloning of a human phosphoinositide 3-kinase with a C2 domain which
RT   displays reduced sensitivity to the inhibitor wortmannin.";
RL   Biochem. J. 326:139-147(1997).
CC   -!- SIMILARITY: CONTAINS 1 C2 DOMAIN.
DR   EMBL; Y13367; CAA73797.1; -.
DR   HSSP; P21707; 1BYN.
DR   Genew; HGNC:8971; PIK3C2A.
DR   InterPro; IPR000008; C2.
DR   InterPro; IPR001263; PI3Ka.
DR   InterPro; IPR002420; PI3K_C2.
DR   InterPro; IPR000341; PI3K_ras_bind.
DR   InterPro; IPR000403; PI3_PI4_Kinase.
DR   InterPro; IPR001683; PX.
DR   Pfam; PF00168; C2; 1.
DR   Pfam; PF00613; PI3Ka; 1.
DR   Pfam; PF00792; PI3K_C2; 1.
DR   Pfam; PF00794; PI3K_rbd; 1.
DR   Pfam; PF00454; PI3_PI4_kinase; 1.
DR   Pfam; PF00787; PX; 1.
DR   SMART; SM00239; C2; 1.
DR   SMART; SM00145; PI3Ka; 1.
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DR   InterPro; IPR000341; PI3K_ras_bind.
DR   InterPro; IPR000403; PI3_PI4_Kinase.
DR   InterPro; IPR001683; PX.
DR   Pfam; PF00168; C2; 1.
DR   Pfam; PF00613; PI3Ka; 1.
DR   Pfam; PF00792; PI3K_C2; 1.
DR   Pfam; PF00794; PI3K_rbd; 1.
DR   Pfam; PF00454; PI3_PI4_kinase; 1.
DR   Pfam; PF00787; PX; 1.
DR   SMART; SM00239; C2; 1.
DR   SMART; SM00145; PI3Ka; 1.
DR   SMART; SM00146; PI3Kc; 1.
DR   SMART; SM00142; PI3K_C2; 1.
DR   SMART; SM00144; PI3K_rbd; 1.
DR   SMART; SM00312; PX; 1.
DR   PROSITE; PS50004; C2_DOMAIN_2; 1.
DR   PROSITE; PS00915; PI3_4_KINASE_1; 1.
DR   PROSITE; PS00916; PI3_4_KINASE_2; 1.
DR   PROSITE; PS50290; PI3_4_KINASE_3; 1.
DR   PROSITE; PS50195; PX; 1.
KW   Kinase.
SQ   SEQUENCE  1658 AA;  187439 MW;  B8CC8E581DB20F20 CRC64;

Query Match            18.6%;  Score 1076.5;  DB 11;  Length 1658;
Best Local Similarity  28.0%;  Pred. No. 3.6e-74;
Matches  330;  Conservative 198;  Mismatches 381;  Indels 269;  Gaps  39;

Qy   108  EIYDKKYQVVQTLDCLRYWKVLHRSPGQIHVVQRHAPSEETLAPRQLN--ALIGYDVTDV  165
Db   259  QISPKSEDINKPD---W--LDLDPWDAVLLEERSPS---CHLERKVNGKSLSGATVTRS   309
Qy   166  SNVHDDELEFTRRRLVTPRMAEVAGRDP------------------------K        194
Db   310  QSLIIRTAQFTKAQ------GQVSQKDPNGTSSLPTGSSLLQEFVQNDEVAAFCQSIMK   363
Qy   195  LYAMHPWTSKPLPEYLLKKIT---NNCVFIVIHRSTTSQTIKVSADDTPGTILQSFFT-   250
Db   364  LKTKFPYTDHCTNPGYLLSPVTVQRNMC--------GENASVKVSI-EIEGLQLPVTFTC  414
Qy   251  -KMAKKKSLMDIPESQNERD---FVLRVCGRDEYLVGETPIKNFQWVRQCLKNGE      301
Db   415  DVSSTVEIIIMQALCWVHDDLNQVDVGSYILKVCGQEEVLQNNHCLGSHEHIQNCRKWDT  474
Qy   302  EIHLVLDT------------PPDALDEVRKE-----EWPLVDDCTG-----VTGYHEQL   339
Db   475  EIKLQLLTLSAMCQNLARTAEDDEAPVDLNKYLYQIEKPYKEVWTRHPVEELLDSYHYQV  534
Qy   340  TI---HGKDHESVFFTVSLWDCCDRKFPVKIRGIDIPV-----------LPR--TADLT-  380
Db   535  ELALQTENQHRAVDQVI--KAVRKICSALDGVETPSVTEAVKKLKRAVNLPRNKSADVTS  592
Qy   381  ---------------VFVEANIQYGQQVL--------------CQRRT-----        399
Db   593  LSGSDTRKNSTKGSLNPENPVQVSMDHLTTAIYDLLRLHANSSRCSTGCPRGSRNIKEAW  652
Qy   400  --------------------------------SPKPFTEEVL                  409
Db   653  TATEQLQFTVYAAHGISSNWVSNYEKYYLICSLSHNGKDLFKPIQSKKVGTYKNFFYLIK  712
Qy   410  WNVWLEFSIKIKDLPKGALLNLQIY--CGKAPALSGKTSAEMPSPESKGKAQLLYYVNLL  467
Db   713  WDELIIFPIQISQLPLESVLHLTLFGVLNQSSGSSPDSNKQRKGPEALGX------VSLT  766
Qy   468  LIDHRFPLLRHGEYVLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDNYCHPI 527
Db   767  LFDFKRFLTCGTKLLYLWTSSHTNSIPGAI-------PKKSYVMERIVLQVDF---      812
Qy   528  ALPKIRPTP------DPEGDR--VRAE---MPNQLRKQLEAIIATPDLNPLTAEDKEL    574
Db   813  ------PSPAFDIIYTSPQIDRNIIQQDKLETLESDIKGKLLDIIHRDSSFGLSKEDKVF  866
Qy   575  LWHFRYESLKDPKAYPKLFSSV---KWGQQEIVAKTYQLLAKREVWDQSALDVGLTMQLL  631
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DR   SMART; SM00146; PI3Kc; 1.
DR   SMART; SM00142; PI3K_C2; 1.
DR   SMART; SM00144; PI3K_rbd; 1.
DR   SMART; SM00312; PX; 1.
DR   PROSITE; PS50004; C2_DOMAIN_2; 1.
DR   PROSITE; PS00915; PI3_4_KINASE_1; 1.
DR   PROSITE; PS00916; PI3_4_KINASE_2; 1.
DR   PROSITE; PS50290; PI3_4_KINASE_3; 1.
DR   PROSITE; PS50195; PX; 1.
KW   Kinase.
SQ   SEQUENCE   1686 AA;  190736 MW;  E9311C803025C96F CRC64;

Query Match          18.5%;  Score 1074;  DB 4;  Length 1686;
Best Local Similarity   28.9%;  Pred. No. 5.8e-74;
Matches 309;  Conservative 178;  Mismatches 343;  Indels 238;  Gaps 32;

Qy   194  KLYAMHPWVTSKPLPEYLLKKIT--NNCVFIVIHRSTTSQTIKVSADDTPGTILQSFFT  250
Db   390  KLKTKFPYTNHRTNPGYLLSPVTAQRNIC--------GENASVKVSI-DIEGFQLPVTFT  440

Qy   251  ------KMAKKKSLMDIPESQNERD---FVLRVCGRDEYLVGETPIKNFQWVRQCLKNG  300
Db   441  CDVSSTVEIIIMQALCWVHDDLNQVDVGSYVLKVCGQEEVLQNNHCLGSHEHIQNCRKWD  500

Qy   301  EEIHLVL-----------------DTPPDPALDEVRKEEWPLVDDCTG---------VT  333
Db   501  TEIRLQLLTPSAMCQNLARTAEDDETPVD-----LNKHLYQIEKPCKEAMTRHPVEELID  555

Qy   334  GYHEQ----LTIHGKDH--------ESVFTVSLWDCDRKFRVKIRGIDIPVL  373
Db   556  SYHNQVELALQIENCHRAVDQVIKAVRKICSALDGVETLAITESVKKLK---RAVNLP-R  611

Qy   374  PRTADLTVFV----------EANIQYGQQVLCQRRT-----------SP-----  401
Db   612  SKTADVTSLFGGEDTSRSSTRGSLNPENPVQVSINQLTAAIYDLLRLHANSGRSPTDCAQ  671

Qy   402  --------------------------------------------  401
Db   672  SSKSVKEAWTTEQLQFTIFAAHGISSNWVSNYEKYYLICSLSHNGKDLFKPIQSKKVGT  731

Qy   402  -KPFTEEVLMNVWLEFSIKIKDLPKGALLNLQIY--CGKAPALSGKTSAEMPSPESKGKA  458
Db   732  YKNFPYLIKWDELIIFPIQISQLPLESVLHLTLFGILNQSSGSSPDSNKQRKGPEALGK-  790

Qy   459  QLLYVNLLLIDHRPLLRHGEYVLHMWQLSGKGEDQGSFNADKLTSATNPDKRNSMSISI  518
Db   791  -----VSLPLCDFRRPLTCGTKLLYLWTSS-------------------HTNSVPGTV  824

Qy   519  LLDNY-CHPIALPKHRPTP---------DPEGDRVRAE----MPNQLRKQLEAIIATDPL  564
Db   825  TKKGYVMERIVLQVDFPSPAFDIIYTTPQVDRSIIQQHNLETLENDIKGKLLDILHKDSS  884

Qy   565  NPLTAEDKELLWHFPRYESLKDPKAYPKLFSSV---KWGQQEIVAKTYQLLAKREVWDQSA  621
Db   885  LGLSKEDKAFLWEKRYYCFXHPNCLPXIILASAPNWKWGN---LAKTYSLLHQ---W--PA  936

Qy   622  LDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYLLQLVQAVKFEPYHDSALARPL  681
Db   937  LYPLLALELLDSKFADQEVRSLAVTWIEAISDDELTDLLPQFVQALKYEIYLNSSLVQFL  996

Qy   682  LKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAYLRGCGTAMLHDFTQQVQVIDM  741
Db   997  LSRALGNIQIAHNLYWLLKDAL-HDVQFSTRYEHVLGALLSVGGKRLRELLKQTKLVQL  1055

Qy   742  LQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLPQSFRVPYDPGLKAGALVIEKC  801
Db  1056  LGGVAEKVRQASGS---ARQVV--LQRSMERVQSFFQKNKCRLPLKPSIVAKELNIKSC  1109

Qy   802  KVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQDMLIIQILRIMESIWETESLD  861
Db  1110  SFFSSNAVPLKVTMVNADPL---GEEINVMFKVGEDLRQDMLALQMIKIMDKIWLKEGLD  1166

Qy   862  LCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTGAFKDEVLSHWLKEKCPIEBKF  921

Db  1167  LRMVIFKCLSTGRDRGWVELVPASDTLRKIQVE-YGVTGSFKDKPLAEWLRKYNPSEBEY  1225

Qy   922  QAAVERFYSCAGYCVATFVLGIGDRHNDNIMISETGNLFHIDFGHILGNYKSFLGINKE  981
Db  1226  EKASENFIYSCAGCCVATYVLGICDRHNDNIMLRSTGHMFHIDFGKFLGHAQMFGSFKRD  1285

Qy   982  RVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLALRHHTNLLILFSMMLMTGMPQ  1041
Db  1286  RAPFVLTSDMAYVI-NGGEKPTIRFQLFVDLCCQAYNLIRKQTNLFLNLLSLMIPSGLPE  1344

Qy  1042  LTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGWTVQFNWFLH  1089
Db  1345  LTSIQDLKYVRDALQPQTTDAEATIFFTRLIESSLGSIAT-KPNFFIH  1391

Search completed: February 15, 2004, 02:06:56
Job time : 104 secs
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OM protein - nucleic search, using frame_plus_p2n model

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GenCore version 5.1.6

Run on: February 15, 2004, 02:10:12 ; Search time 5171 Seconds
(without alignments)
5179.565 Million cell updates/sec

```
Title:           US-09-974-573-1
Perfect score:   5790
Sequence:        1 MELENYEQPVVLREDNRRRR.........QFNWFLHLVLGIKQGEKHSA 1102

Scoring table:   BLOSUM62
                 Xgapop  10.0 , Xgapext  0.5
                 Ygapop  10.0 , Ygapext  0.5
                 Fgapop   6.0 , Fgapext  7.0
                 Delop    6.0 , Delext   7.0

Searched:        22781392 seqs, 1215223056 residues

Total number of hits satisfying chosen parameters:        45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO.spool/US0974573/runat_11022004_180014_18105/app_query.fasta_1.1287
-DB=EST _QFMT=fastp -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09974573_@CGN_1_3909 @runat_11022004_180014_18105 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=30 -TIMEOUT=0.5 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :       EST:*
     1:   em_estba.*
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     7:   em_estro.*
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     9:   gb_est1:*
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    11:   gb_htc:*
    12:   gb_est3:*
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    14:   gb_est5:*
    15:   em_estfun:*
    16:   em_eston:*
    17:   em_gss_hum.:*
    18:   em_gss_inv:*
    19:   em_gss_pln:*
    20:   em_gss_vrt:*
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    23:   em_gss_mus:*
    24:   em_gss_pro:*
    25:   em_gss_rod:*
    26:   em_gss_phg:*
    27:   em_gss_vrl:*
    28:   gb_gss1:*
    29:   gb_gss2:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5484	94.7	4805	11	AK040543	AK040543 Mus muscu
2	1429	24.7	3866	11	AK051885	AK051885 Mus muscu
3	1363	23.5	4731	11	AK090116	AK090116 Mus muscu
4	1361	23.5	880	14	CD171634	CD171634 AGENCOURT
5	1347.5	23.3	4996	11	AK081350	AK081350 Mus muscu
6	1339	23.1	4852	11	AK040867	AK040867 Mus muscu
7	1335	23.1	1937	11	AK077772	AK077772 Mus muscu
8	1286.5	22.2	915	10	BB619812	BB619812 BB619812
9	1268.5	21.9	1127	10	BG389556	BG389556 602414255
10	1244	21.5	861	13	BU517397	BU517397 AGENCOURT
11	1181.5	20.4	1043	13	BQ072706	BQ072706 AGENCOURT
12	2170	20.2	976	14	CA966024	CA966024 CcLL03a12
13	1163.5	20.1	761	10	BG615507	BG615507 602642812
14	1106	19.1	896	14	CA471197	CA471197 AGENCOURT
15	1036.5	17.9	852	13	BQ232683	BQ232683 AGENCOURT
16	1032	17.8	649	9	AJ450490	AJ450490 AJ450490
17	1029	17.8	1170	12	BM920113	BM920113 AGENCOURT
18	977.5	16.9	695	14	CA376640	CA376640 655052 NC
19	953	16.5	542	9	AW786623	AW786623 119902 MA
20	951	16.4	581	14	CA579737	CA579737 K0741F09-
21	951	16.4	583	14	CA577647	CA577647 K0712D03-
22	928	16.0	558	12	BI775259	BI775259 467670 MA
23	921	15.9	665	12	BM935801	BM935801 UI-M-BH3-
24 c	919	15.9	575	2	HSM062224	Bx504620 Homo sapi
25	917.5	15.8	806	13	BU598381	BU598381 AGENCOURT
26	889	15.4	547	10	BG019410	BG019410 dab08e12.
27 c	886	15.3	769	29	BX185016	BX185016 Danio rer
28	851	14.7	577	12	BM878584	BM878584 if42b10.Y
29	820.5	14.2	1627	11	AK003230	AK003230 Mus muscu
30	816	14.1	664	10	BB613870	BB613870 BB613870
31	814	14.1	509	12	BI326875	BI326875 AR07OH08i
32	782	13.5	499	9	AW761865	AW761865 uq26f05.Y
33	771	13.3	576	9	AW491415	AW491415 UI-M-BH3-
34	743.5	12.8	759	12	BI459766	BI459766 60320O816
35	738	12.7	861	14	CA472545	CA472545 AGENCOURT
36	729	12.6	617	14	CA352614	CA352614 623926 NC
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38	719.5	12.4	661	13	BW037945	BW037945 BW037945
39	719	12.4	630	14	CA346520	CA346520 677427 NC
40	714.5	12.3	644	10	BB629321	BB629321 BB629321
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42	699	12.1	441	9	AA464765	AA464765 zx83e07.r
43	698.5	12.1	3099	11	AK044997	AK044997 Mus muscu
44	684.5	11.8	3211	11	BC027029	BC027029 Mus muscu
45	669.5	11.6	669	13	BX310281	BX310281 BX310281

ALIGNMENTS

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RESULT 1
AK040543
LOCUS        AK040543    4805 bp    mRNA    linear    HTC 05-DEC-2002
DEFINITION   Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched
             library, clone:A430105015 product:phosphoinositide-3-kinase,
             catalytic, gamma polypeptide, full insert sequence.
ACCESSION    AK040543
VERSION      AK040543.1  GI:26087918
KEYWORDS     HTC; CAP trapper.
SOURCE       Mus musculus (house mouse)
  ORGANISM   Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
```

```
REFERENCE    1
AUTHORS      Carninci,P. and Hayashizaki,Y.
TITLE        High-efficiency full-length cDNA cloning
JOURNAL      Meth. Enzymol. 303, 19-44 (1999)
PUBMED       10349636
REFERENCE    2
AUTHORS      Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
             Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE        Normalization and subtraction of cap-trapper-selected cDNAs to
             prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL      Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE      20499374
PUBMED       11042159
REFERENCE    3
AUTHORS      Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
             Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
             Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
             Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
             Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
             Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
             Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE        RIKEN integrated sequence analysis (RISA) system--384-format
             sequencing pipeline with 384 multicapillary sequencer
JOURNAL      Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE      20530913
PUBMED       11076861
REFERENCE    4
AUTHORS      Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
             Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
             Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
             Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
             Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
             Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
             Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J.,
             Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
             Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
             Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
             Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
             Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
             Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
             Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
             Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
             Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
             Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
             Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
             and Hayashizaki,Y.
TITLE        Functional annotation of a full-length mouse cDNA collection
JOURNAL      Nature 409 (6821), 685-690 (2001)
MEDLINE      21085660
PUBMED       11217851
REFERENCE    5
AUTHORS      The FANTOM Consortium and the RIKEN Genome Exploration Research
             Group Phase I & II Team.
TITLE        Analysis of the mouse transcriptome based on functional annotation
             of 60,770 full-length cDNAs
JOURNAL      Nature 420, 563-573 (2002)
REFERENCE    6
             (bases 1 to 4805)
AUTHORS      Adachi,J., Akimura,T., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
             Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,T.,
             Hayashida,K., Hayatsu,N., Hiramoto,K., Hiracka,T., Hirozane,T.,
             Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
             Katoh,H., Kawai,J., Kojima,Y., Kondo,Y., Konno,H., Kouda,M.,
             Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
             Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
             Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
             Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
             Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
             Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
             Muramatsu,M. and Hayashizaki,Y.
TITLE        Direct Submission
JOURNAL      Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
             Physical and Chemical Research (RIKEN), Laboratory for Genome
             Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
             RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
             Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
             URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
             Fax:81-45-503-9216)
COMMENT      cDNA library was prepared and sequenced in Mouse Genome
             Encyclopedia Project of Genome Exploration Research Group in Riken
             Genomic Sciences Center and Genome Science Laboratory in RIKEN.
             Division of Experimental Animal Research in Riken contributed to
             prepare mouse tissues.
             Please visit our web site for further details.
             URL:http://genome.gsc.riken.go.jp/
             URL:http://fantom.gsc.riken.go.jp/.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /strain="C57BL/6J"
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                     /clone="A430105O15"
                     /tissue_type="thymus"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="0 day neonate"
     misc_feature    106..3415
                     /note="Phosphoinositide-3-kinase, catalytic, gamma
                     polypeptide (MGD|MGI:1353576, GB|NM_020272, evidence:
                     BLASTN, 99%, match=3776)"
                     putative"
BASE COUNT     1261 a   1215 c   1149 g   1180 t
ORIGIN

Alignment Scores:
Pred. No.:                    0                    Length:        4805
Score:                     5484.00                 Matches:       1038
Percent Similarity:         96.92%                 Conservative:    31
Best Local Similarity:      94.11%                 Mismatches:      33
Query Match:                94.72%                 Indels:           1
DB:                            11                  Gaps:             0

US-09-974-573-1 (1-1102) x AK040543 (1-4805)

Qy     1 MetGluGluAsnTyrGluGlnProValValArgGluAspAsnArgArgArgArg  20
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Db   106 ATGGAGGTGGAGAACTATGAACAACCGGTGGTTCAAGAGAGGACAACCTCCGCGCCGGCGC 165

Qy    21 ArgArgMetLysProArgSerThrAlaAlaSerLeuSerMetGluLeuIleProIle  40
           ||||||||||||||||| |||: ||||||||||||||||||||||||||||||||||
Db   166 CGGAGGATGAAGCCACGGAGCCCAGCGGCAGGCAGCCTGGTCTTCCATGGAGCTCATCCCCATT 225

Qy    41 GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeuLeuHis  60
           |||||||||||||||||||||||||||  :::||||||||||||||||||||||||
Db   226 GAGTTCGTACTCCCCACCAGCCAGCGCATCAGCAGACTCCAGAAACAGCGCTGCTGCAT 285

Qy    61 ValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnIleValTrpLeuArgAlaLeuGlu  80
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Db   286 GTGGCTGGCCATGGCAATGTGGAACAGATGAAAGCTCAGTTGGTGTGGCGCCACTGGAG 345

Qy    81 ThrSer-ValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTy 100
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Db   346 ACCAGCGTGGGCTGCGGAGTTCTACCACCGGTTGGGCCCGGACCAATTCCTCCTGCTCTA 405

Qy   100 rGlnLysLysGlyGlnTrpTyrGlnIleTyrAspTyrArgLeuGlnValValGlnThrLeuAs 120
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Db   406 CCAGAAGAAAGGACAATGGTATGAGATCTATGACAGTGACAGTGACACCAAGTGGTGCAGACCCTAGA 465

Qy   120 pCysLeuArgTyrTrpLysValLeuHisArgSerProGlyGlnIleIleHisValValGlnAr 140
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Db   466 CTGCCTGCATTACTGGAAGTTGATGCACAAGAGCCCTGGCCAGATCCACGTGGTCAGACGG 525

Qy   140 gHisAlaProSerGluGluThrLeuAlaPheGlnArgGlnLeuAsnAlaAlaLeuIleGlyTyT 160
           ::|||||||:||:||||||||||||||||:  ::|||||||||||||||||:||||||
Db   526 ACACGTACCTTCTGAGGAGGACCTTGGCTTTCCAGAAGCAGCTCAACTTCCCGATTGGCTA 585
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Db   2746  GATTGTAAAGGATGCCACAACGATCGCTCAAATTCAGCAAGCAAAGCACAGTGGGTAACACGGG  2805
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Qy    900  yAlaPheValAspGluValLeuSerHisTrpLeuLysGluLysCysProIleGluGluLuLy   920
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Db   2866  GTTTCAGGCGCCGCAGTGGAAAGGTTGTTTACTCCGTGCAGGCTACTGTGCGCCACATT  2925
Qy    940  eValLeuGlyIleGlyLYsAspArgHisAsnAspAsnIleMetIleSerGluThrGlyAsnLe  960
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Db   2926  TGTTCTTGGATCGGTGCAGAGCGACAACGACACATTATGATCTCAGAGACAGGAAACCT  2985
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Qy   1000  sLysThrSerLeuHisPheGlnLysAspGlnLYsAspValCysValValAlaTyrLeuAlaLe  1020
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Db   3106  AAAGACAAGTCACCAACTTCCAGAAATTCCAGGATGTCTGTGTTAGAGCTTACCTTACCTAGCTCT  3165
Qy   1020  uArgHisHisThrAsnLeuLeuIleIleLeuPheSerMetMetLeuMetThrGlyMetPr  1040
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Qy   1060  rGluGluLeuAspAlaLysLysTyrPheLeuAspGlnIleGluValCysArgAspLysGlyTr  1080
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Db   3286  CGAGGAGGACGCGTAAGAAATATTTCCTTGATCAGATCGAAGTCGCGAGACAAAGGATG  3345
Qy   1080  pThrValGlnPheAsnTrpPheLeuHisLeuValLeuGlyIleLeuLysGlnGlyGluLysHi  1100
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Qy   1100  sSerAla  1102
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Db   3406  CTCCGCT  3412
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RESULT 2
AK051885
LOCUS       AK051885              3866 bp    mRNA        linear   HTC 05-DEC-2002
DEFINITION  Mus musculus 12 days embryo eyeball cDNA, RIKEN full-length
            enriched library, clone:D230015E05 product:phosphatidylinositol
            3-kinase, catalytic, alpha polypeptide, full insert sequence.
ACCESSION   AK051885
VERSION     AK051885.1  GI:26094824
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
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   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,S., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
            Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
            Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
            Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
            Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
            Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
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            Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
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            Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
            Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
            Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
            and Hayashizaki,Y.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409 (6821), 685-690 (2001)
  MEDLINE   21085660
   PUBMED   11217851
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 3866)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
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            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,T., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.go.jp/
            URL:http://fantom.gsc.riken.go.jp/.
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ORIGIN

Alignment Scores:
Pred. No.:              3.63e-154            Length:          3866
Score:                  1429.00             Matches:         356
Percent Similarity:     53.19%              Conservative:    177
Best Local Similarity:  35.53%              Mismatches:      343
Query Match:            24.68%              Indels:          126
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US-09-974-573-1 (1-1102) x AK051885 (1-3866)
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Db 226 CACATCTACACAGTTAGATAAAGGACAAAATCATAGTGGTGATTTGGGTAAAATGTCTCT 285

Qy 225 ---HisArgSerThrThrSerGlnThrLeuThrProIleLysAsnPheGlnTrpValArgGlnCysLeu 243
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Db 286 CCAAACAACGACAAGCAGAGTACACTCTGAAGATCAATCATGACTGTGTGCCAGAGCAA 345

Qy 244 IleLeuGlnSerPhePheThrLysMetAlaLysLysSerLeuMetAspIleProGlu 263
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DEFINITION   Mus musculus embryo RCB-0549 Cle-H3 cDNA, RIKEN full-length
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VERSION      AK090116.1  GI:26354950
KEYWORDS     HTC; CAP trapper.
SOURCE       Mus musculus (house mouse)
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             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE    1
  AUTHORS    Carninci,P. and Hayashizaki,Y.
  TITLE      High-efficiency full-length cDNA cloning
  JOURNAL    Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE    99279253
   PUBMED    10349636
REFERENCE    2
  AUTHORS    Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
             Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE      Normalization and subtraction of cap-trapper-selected cDNAs to
             prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL    Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE    20499374
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REFERENCE    3
  AUTHORS    Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
             Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
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             Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE      RIKEN integrated sequence analysis (RISA) system-384-format
             sequencing pipeline with 384 multicapillary sequencer
  JOURNAL    Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE    20530913
   PUBMED    11076861
REFERENCE    4
  AUTHORS    The RIKEN Genome Exploration Research Group Phase II Team and the
             FANTOM Consortium.
  TITLE      Functional annotation of a full-length mouse cDNA collection
  JOURNAL    Nature 409, 685-690 (2001)
REFERENCE    5
  AUTHORS    The FANTOM Consortium and the RIKEN Genome Exploration Research
             Group Phase I & II Team.
  TITLE      Analysis of the mouse transcriptome based on functional annotation
             of 60,770 full-length cDNAs
  JOURNAL    Nature 420, 563-573 (2002)
REFERENCE    6 (bases 1 to 4731)
  AUTHORS    Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
             Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
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Db   2689 CTTTTTTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAAATCTTTGATGACATTGCA 2748
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TITLE   Direct Submission
JOURNAL   Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT   cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.go.jp/
            URL:http://fantom.gsc.riken.go.jp/.
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     CDS   226..3420
                     /note="unnamed protein product; PHOSPHATIDYLINOSITOL
                     3-KINASE CATALYTIC SUBUNIT, BETA ISOFORM (EC 2.7.1.137)
                     (PI3-KINASE P110 SUBUNIT BETA) (PTDINS-3-KINASE P110)
                     (PI3K) (PI3KBETA) homolog [Rattus norvegicus]
                     (SWISSPROT|Q9Z1L0, evidence: FASTY, 98.1%ID, 100%length,
                     match=3210)
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                     SWIDWLKHTYPPEHEPSVLENLEDKLYGGKLVVAVHFENSQDVFSFQVSPNLNPIKIN
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                     NKLNTEETVKVHVRAGLPHGTELLCKTVVSSEISGKNDHIWNEQLEPDINICDLPRMA
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                     VILHSWSSFPDELEBMLNPMGTVQTNPYAENATALHITFPENKKQPCYPPFPKIIEK
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                     SDEELSQYLLQLVQVLKYEPFLDCALSRFLLERALDNRRIGQFLWHLRSEVTPAVS
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                     KQSAYREALSDLQSPLNPCVILSELYVEKCKVMDSKMKPLMLVYSSRAFGEDSVVIF
                     KNGDDLRQDMLTLQMLRLMDLLWKEAGLDLRMLPYGCLATGDRSGLIEVVSSETIAD
                     IQLNSSNVAATAAFNKDALLNWLKEYNSGDDLDRAIEEFTLSCAGYCVASYLLGIGDR
                     HSDNIMVKKTGQLFHIDFGHILGNFKSKFGIKRERVPFILTYDFIHVIQQGKTGNTEK
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     polyA_signal   4703..4708
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                     /note="putative"
BASE COUNT 1290 a   1014 c   1128 g   1299 t
ORIGIN

Alignment Scores:
Pred. No.:   2.57e-146   Length: 4731
Score: 1363.00   Matches: 357
Percent Similarity: 50.09%   Conservative: 195

Best Local Similarity: 32.40%   Mismatches: 400
Query Match: 23.54%   Indels: 150
DB: 11   Gaps: 35

US-09-974-573-1 (1-1102) x AK090116 (1-4731)

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Qy      78 AlaLeuGluThrSerValSerAlaAspPheTyrHisArgLeuGly------------------------ 92
              ||| ::: ||| | ||||:| ::::|||  |||||
Db     280 GCATCCGATGGCGGCCATATCCGTCGATTTCCTTCGCCACCGGGATTATATCCAGTTG 339

Qy      93 -----ProAspHisPheLeuLeuTyrGlnLysLysGlyGlnTrpTyrGluIle----- 109
                 ------  ::|:: :|:|::: ||||::| | :|::|
Db     340 GAAGTACCTCGGAAGCTACCATTCTTTATATATAAACAGATGTTATGAAGCAAGTTCAC 399

Qy     110 ---TyrAspLysTyrGlnValValGlnThrLeuAsp------------------CysLeuArg 123
              ::| ::  :::::  ||:||
Db     400 AACTACCCGATGTTTAACCTCCTCATGGACATTGACTCGTATATGTTTGCATGTGTGAAT 459

Qy     124 TyrTrpLysValLeuHisArgSerProGlyGln----- 134
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Db     460 CAAACTGCTGTATATGAGGAACTGGAAGACGAAACACGAAGACTTTGTGATGTCAGACCT 519

Qy     135 ------------IleHisValValGlnArgHisAlaProSerGluGlnThrLeuAlaPhe 150
                       ::|| :::
Db     520 TTTCTTCCAGTTCTCAAACTAGTGACTAGGAAGGTGTGACCCCGCAGAAAAATTG------ 573

Qy     151 GlnArgGlnLeuAsnAlaLeuIleGlyTyrAspValThrAspValSerAsnValHisAsp 170
              :::::: | :|: ||| :|| |||
Db     574 GACTCAAAAATTGGGGTTCGTATAGGAAAAGGTCTTCATGAGTTGATGCCTTGAAGGAT 633

Qy     171 AspGluLeu--GluPheThrArg-----ArgArgLeuValThrProArgMetAlaGlu 187
              |||::::: | | ||:|||:  || ||||:::
Db     634 CCCGAAGTGAATGAATTTAGAAGAAAAATGCGCAAATTCAGTGAGGCCAAGATTCAGTCT 693

Qy     188 ValAlaGlyTyrAspProLysLeuTyrAlaMetHisProValThrSerLysProLeu 207
              :::  |||
Db     694 TTGTCTTGGATCGACTGGCTAAAGCACACGTATCCG 738

Qy     208 ProGluTyr------------------------------LeuLeuLysIleThrAsnAsnCysVal 220
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Db     739 CCTGAGCACCAGCCGTCCGTCCTCGGAGAACTTGGAAGATAAACTTTATGGAGGAAAGCTG 798

Qy     221 PheIleValIleHisArgSerThrThrSerGln---------ThrIleLysValSerAlaAsp 238
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Db     799 GTTGTGGCTGTGCACTTTGAAAATAGCCAGGATGTATTAGTTTCAAGTGTCTCCCAAT 858

Qy     239 AspThrProGlyThrIleLeuGlnSerPheThrLysMetAlaLysLysSerLeu 258
              :::|: ::: ||: :::
Db     859 TTGAATCCTATAAAATAAATGAA------------------TTGGCAATCCAGAAACGCCTCACTATT 909

Qy     259 MetAspIleProGluSerGlnAsnGluArgAspPheValLeuArgValCysGlyArgAsp 278
              ||||:::|||:: ||:::::: | :::
Db     910 CCGTGGAAAGGAAGATGAAGCTAGCCCCTGTGACTATGTTACAGGTGCACGTGGGAGAGTG 969

Qy     279 GluTyrLeuValGlyTyrLeuThrProIleLysAsnPheGlnThrValArgGlnCysLeuLys 298
              |||||||||:: :::
Db     970 GAGTATGTGTTTGGCGATCATCCACTACTCAGTTCAGTACATCCGAATTGTGTGATG 1029

Qy     299 AsnGlyGluGluIleHisLeuValLeuAspThrProProAspAlaLeuAspGluVal 318
              ||||:::
Db    1030 AATAGAACCCTGCCCACTTCATCCTT----------------- 1056

Qy     319 ArgLysGluGluTrpProLeuValAspAspCysThrGlyValThrGlyTyrHisGluGln 338
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Db    1057 ------------GTGGAATGTGTAAGATCAAGAAAATGATGAACAA 1092

Qy     339 ------------LeuThrIleHisGlyLysAspHisGluSerValPheThrValSerLeu--- 354
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Db    1093 GAAATGATTGCCATAGAGGCTGCCATCAACCGAACTCTCCCCTTTA 1152

Qy     355 TrpAspCysAspArgLysPheArgVal 363
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Db    1153 CCACCAAAGAAAACGCGAGTTATTTCTCATATCTGGGACAACACACCCTTTCCAAATT 1212
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```
Qy   364 LysIleArgGlyIleLeuProValLeuProArgThrAlaAspLeuThrValPheVal 383
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Db  1213 ACCTTG------GTTAAAGGAAAATAAGCTTAATACAGAGAAGAAACTGTGAAAGTTCATGTC 1266

Qy   384 GluAlaAsnLeuGlnTyrGlyGlnValLeuCysGlnArgArgThrSerProLys--- 402
              ||||||||        ||||||                :::
Db  1267 CGAGCTGGGCTTTTCACGGAACCGAGCTCCGTGTAAAACCGTCGTAAGCTCAGAGATA 1326

Qy   403 ProPheThrGluGluValLeuTrpAsnValTrpProLeuGluPheSerIleLysIleLysAsp 422
              :::|||                       ||||||
Db  1327 TCAGGAAAGAACGACCATATTTGGAATGAACAACTGGAATTTGATATTAATATTTGTGAC 1386

Qy   423 LeuProLysGlyAlaLeuLeuAsnLeuGlnIleLeuTyrCysGlyLysLeuAlaProAlaLeuSer 442
              |||          :::|||            :::
Db  1387 TTACCAAGAGATGGGCTCGATTATGTTTGCTGTTTAT---GCAGTTTGATAAAGTAAAA 1443

Qy   443 GlyLysThrSerAlaGluMetProSerPro---------GluSerLysGlyLysAlaGln 459
              |||                       :::|||
Db  1444 ACGAAGAAAATCAACAAAGACTATTAATCCCTCAAGTATCAGACCATCAGGAAAGCCCGGG 1503

Qy   460 LeuLeuTyrTyr---------ValAsnLeuLeuLeuIleAspHisArgPheLeuLeu 475
              |||       :::|||
Db  1504 AAAGTGCATTATCCTGTCGCCATGGGTAAATACCATGGTTTTTGACTTCAAGGACAGCTG 1563

Qy   476 ArgHisGlyGluTyrValLeuHisMetTrpGlnLeuSerGlyLysGlyGlnGlyGly 495
              :::||||||       |||       :::
Db  1564 AGGTCTGGAGACGTCATATTGCATAGCTGG---------------------TCT 1596

Qy   496 SerPheAsnAlaAspLysLeu----------ThrAlaThrAsn 507
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Db  1597 TCGTTT---CCTGATGAGCTGGAAGAAATGCTGAATCCATGGGGACCTGTGCAGACGAAC 1653

Qy   508 ProAspLysGluAsnSerMetSerIleSerIleLeuLeu---AspAsnTyrCysHisPro 526
              |||       :::|||       :::|||
Db  1654 CCATATGCTGAGAAGCGCCACCGCCTTGCACATTACGTTCCCAGAGAATAAGAGCAGCCG 1713

Qy   527 IleAlaAlaLeuPro----------------LysHisArgProThrProAspProGlu 539
              |||                       :::
Db  1714 TGTTATTATCCCCCTTCGATAAGATCATTGAGGAGGCCAGCTGAGCTTGCCAGCGGACAC 1773

Qy   540 GlyAspArgValArgAlaGluMetProAsnGlnLeuArgLysGlnLeuGlnLeuAlaIleIle 559
              |||       :::          ||||||
Db  1774 AGTGCTAATGTGTCAAGTCGTGGTGTGGTGAAAAAATTCTTGCTGTGCTGAAAGAAATCTTG 1833

Qy   560 AlaThrAspProLeuAsnProLeuThrAlaGluLysLysAspLysGluLeuTrpHisPheArg 579
              |||       :::|||
Db  1834 GACAGGGACGACCCCTGTCCAGCTGTGTGAGAACGAAATGGACCTTATTTGGACTCTACGG 1893

Qy   580 TyrGluSerLeuLysAsp---ProLysAlaTyrProLysPheSerSerValLysTrp 598
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Db  1894 CAAGACTGCCGAGAAAATTTCCCTAGTCACTGCCAAAACTACTCTTGTCAATCAAGTGG 1953

Qy   599 GlyGlnGlnLeuValIleValAlaAlaLysThrTyrGlnLeuLeuAlaLysArgGluValTrpAsp 618
              :::|||                :::|||
Db  1954 AATAAAACTTGAAGATTTGCT-----------CAGCTTCAGGCGCTCCTGCAGATATGGGCCC 2004

Qy   619 GlnSerAlaLeuAspValGlyLeuThrMetGlnLeuLeuAspCysAsnPheSerAspGlu 638
              :::          |||       :::|||
Db  2005 AAA------CTGCCCCCCAGGGAACGCCTGGAACTCCTGGAACTTCAACATCCAGACCAG 2058

Qy   639 AsnValArgAlaIleAlaAlaValGlnLeuLysGluSerLeuGluAspAspAspValLeuHis 658
              |||       :::|||
Db  2059 TATGTCCGGGAATACGCTGTAGGCGTGCCTCGACAGATGAGTGAAGGAAGAACTCCTCTCAG 2118

Qy   659 TyrLeuLeuGlnLeuValGlnAlaIleAlaValLysPheGluProTyrHisAspSerAlaLeuAla 678
              |||       :::|||
Db  2119 TATCTTTTACAATTGGTGCAAGTTTGAAATATGAAGCCTTTTCTCGATTGTGCCCTCTCC 2178

Qy   679 ArgPheLeuLeuGlyArgGlyLeuArgLysAsnLysArgIleGlyHisPheLeuPheTrpPhe 698
              :::|||       |||
Db  2179 AGATTCCTATTAGAAAGAGCACTTGATAATCGGAGAATTGGGCAGTTTCTGTTTTGGCAT 2238
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Qy   699 LeuArgSerGluIleAlaGlnSerArgHisTyrGlnArgPheAlaValIleLeuGlu 718
              ||||||                   :::          |||
Db  2239 CTTAGGTCAGAGGTG------CACACTCCTGCTGTCCGTACAGTTGGTGTCATCCTGGAA 2295

Qy   719 AlaTyrLeuArgGlyCysGlyThrAlaMetLeuHisAspPheThrGlnValGlnVal 738
              |||       :::|||
Db  2296 GCATACTGTCGAGGA---AGCCTGGGCACATGAAAGTGCTTCCAAACAGTGGAAGCA 2352

Qy   739 IleAspMetLeuGlnLysValThrIleAspIle------------SerLeuSerAla 754
              :::|||       |||
Db  2353 CTCAATAAGTTAAAACTTAAATAGCTTAATCAAACTGAATGCGGTGAGCTGAGCAGA 2412

Qy   755 GluLysTyrAspValSerSerGlnValIle--------SerGlnLeuLysGlnLysLeu 771
              |||       :::
Db  2413 GCTAAGGAAGGAGGCCATGGCACACGTGCCTGCTGCTTACCGGGGAGGCGCTC 2472

Qy   772 GluAsnLeuGlnAsnLeuAsnLeuProGlnSerPheArgValProTyrAspProGlyLeu 791
              |||                       :::
Db  2473 TCTGACCTGCAGTCG---------------------------CCGCTGAACCCCTGCGTC 2505

Qy   792 LysAlaGlyAlaLeuValIleLeuLysCysLysValMetAlaSerLysLysLysProLeu 811
              |||       :::|||
Db  2506 ATCCTCTCAGAGTCTATGTTGAAAAGTGCAAATACATGGACTCCAAGATGAAGCCCCTG 2565

Qy   812 TrpLeuPheLysCysAlaAspProThrAlaLeuSerAsnGluThrIleGlyIleIle 831
              |||       :::
Db  2566 TGGCTGGTCTAC---------AGCAGCAGCCTTTGAGGAGCTCGTTGGAGTGATC 2616

Qy   832 PheLysHisGlyAspAspLeuArgGlnMetMetLeuIleLeuLeuGlnIleLeuLeuArgIleMet 851
              |||       :::|||
Db  2617 TTTAAAAATGGTGACGATTTGCGGCAGATGCTGCATCGCTGCAGATGTTGCGCCTGATG 2676

Qy   852 GluSerIleTrpGluThrGluSerLeuAspLeuCysLeuLeuProTyrGlyCysIleSer 871
              :::|||       |||
Db  2677 GATCTGCTTGGAAAGAAGCTGGCTTGGCACCTGTGCGGGATGCTCCCCATGGGCTGCTAGCA 2736

Qy   872 ThrGlyAspLysTyrIleGlyMetIleGluIleLeuValLysAspAlaThrThrIleAlaLysIle 891
              |||       :::
Db  2737 ACAGGAGATCGCTCGGCCTCATTGGAGTTGTGAGCAACTGCTGACAATT 2796

Qy   892 Gln------------GlnSerThrValGlyAsnThrGlyValAlaPheLysLysAspGluValLeuSerHis 909
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Db  2797 CAGCTGAACAGTAGTAACGTGCCACGGCAGCCTTCAACAAAGACGCACTCCTGAAC 2856

Qy   910 TrpLeuLysGluLysCysProIleGluGlnLeuLysPheGlnAlaIleAlaValGluArgPheVal 929
              |||       :::|||
Db  2857 TGGCTCAAGGAGTACAACTCTGGGATGAC---CTGGACCGAGCGATTGAGGAGTTACC 2913

Qy   930 TyrSerCysAlaGlyTyrCysValAlaAlaThrPheValLeuIleLeuGlyTyrIleGlyArgArgHisAsn 949
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Db  2914 TTGTCCGTGCTGGCTACTGTGGCTACTGTGTAGCCTCTTATGTCCTCGGCATTGTGAGCCACAGT 2973

Qy   950 AspAsnIleMetIleSerGluThrGlyTyrAsnLeuPheHisIleAspPheValProPheValLeu 969
              |||       :::|||
Db  2974 GACAACATCATGGTGAAGAAAACCGGCCCAGCTCCTTCCACATAGATTTTGGGCATATTCTT 3033

Qy   970 GlyAsnTyrLysPheAsnLeuGlyIleAsnLysGluLysValProPheValProThrPro 989
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Db  3034 GGAAATTTCAAAATCTAAAATTCGCATTAAAAGGAGGCCAGTACCTTTATTCTTACTTAT 3093

Qy   990 AspPheLeuPheValMetGlyThrSerGlyLysLysThrSerLeuHisPheGlnLysPhe 1009
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Db  3094 GACTTCATTCATGATCATTCAACAAGGAAAACACTGAAAAAATTTGGCAGATTC 3153

Qy  1010 GlnAspValCysValLeuAlaTyrLeuAlaLeuArgHisThrAsnLeuLeuIleIle 1029
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Db  3154 CGCCAGTGCTGTGAAGATGCGTATCTGATTTTACGGGCCATGGAATCTCCATCACC 3213

Qy  1030 LeuPheSerMetMetLeuMetThrGlyMetProGlnLeuThrSerGluLysAspIleGlu 1049
              |||       :::|||
Db  3214 CTGTTTGCCCTGATGTTGACTGGACGGGCTGCCTGAGCTCACATCGGCTCAAGATATACAG 3273

Qy  1050 TyrIleArgAspAlaLeuThrValGlyLysSerGluGluAspAlaLysLysTyrPheLeu 1069
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Db    3274 |||||:::|||    :::|||||||||||||||::::|||    ||| 3333
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Qy    1070 AspGlnIleGluValCysArgAspArgLysGlyTrpThrValGlnPheAsnTrpPheLeuHis 1089
Db    3334 |||    :::    :::    :::|    |||    ::|||||||||| 3393
           CAGAAGTTTGACGAGGCCCTCAGGGAAAGCTGGACTACTAAAGTGAACTGGATGGCTCAC

Qy    1090 LeuVal 1091
Db    3394 |||
           ACAGTA 3399
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RESULT 4

CD171634
LOCUS   CD171634   880 bp   mRNA   linear   EST 19-MAY-2003
DEFINITION AGENCOURT_14065893 NIH_MGC_180 Homo sapiens cDNA clone
            IMAGE:30378933 5', mRNA sequence.
ACCESSION   CD171634
VERSION   CD171634.1   GI:30852375
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 880)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Michael Brownstein
            cDNA Library Preparation: Invitrogen Corp
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDAM445 row: i column: 22
            High quality sequence start: 20
            High quality sequence stop: 719.
FEATURES   Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:30378933"
                     /lab_host="DH10B-Ton A (T1 and T5 phage resistances)"
                     /clone_lib="NIH_MGC_180"
                     /note="Organ: Testis; Vector: pCMV-SPORT6.1; Site_1: NotI;
                     Site_2: EcoRV (destroyed); Library is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed upon cloning
). Average insert size 1.68 kb. Library was constructed by
                     (Invitrogen). Note: this is a NIH_MGC Library."
BASE COUNT   229 a   254 c   224 g   173 t
ORIGIN

Alignment Scores:
Pred. No.:   2.58e-147
Score: 1361.00
Percent Similarity: 94.81%   Matches: 880
Best Local Similarity: 92.39%   Conservative: 267
Query Match: 23.51%   Mismatches: 7
DB: 14   Indels: 11
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US-09-974-573-1 (1-1102) x CD171634 (1-880)

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Qy     293 ValArgGlnCysLeuLysAsnGlyGluIleHisLeuValLeuAspThrProP-Asp 312
Db      21 |||    ||||||||||||||||||||||||||||||    |:|||||||||| 79
           CTCCGGATCGTCCTCAAGAACGGAGAAGATATTCC-GTGGTACTGGACACGCCTCCAGAC

Qy     313 ProAlaLeuAspGluValArgGluLysGluGluValTrpProLeuValAspAspCysThrGlyVal 332
Db      80 |||    :|||    |||||||||||||    ||||||    |||:||||||||||| 139
           CCGGCCCTAGACGACGAGGTGAGGGAAGAAGAGTGGCCGCTGGTGACGACTGCCACGGGAGTC
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RESULT 5
AK081350
LOCUS   AK081350   4996 bp   mRNA   linear   HTC 05-DEC-2002
DEFINITION Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched
            library, clone:C130009D19 product:PHOSPHATIDYLINOSITOL 3-KINASE
            CATALYTIC SUBUNIT, BETA ISOFORM (EC 2.7.1.137) (PI3-KINASE P110
            SUBUNIT BETA) (PTDINS-3-KINASE P110) (PI3K) (PI3KBETA) homolog
            [Rattus norvegicus], full insert sequence.
ACCESSION   AK081350
VERSION   AK081350.1   GI:26099860
KEYWORDS   HTC; CAP trapper.
SOURCE   Mus musculus (house mouse)
  ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE   High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
  PUBMED   10349636
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Qy     333 ThrGlyTyrHisGluGlnLeuThrIleHisGlyLysAspHisGluSerValPheThrVal 352
Db     140 ||||    ||||    ||||||||||||||||||||||||||    |:|||||| 199
           ACCGGCTACCATGAGCAGCTTACCATCCACGGCAAGGACCACGAGAGTGTGTTCACCGTG

Qy     353 SerLeuTrpAspCysAspArgLysGlyPheArgValLysIleArgGlyIleAspIleProVal 372
Db     200 ||||    :::    :::||||    :::    :|||||||||||||||| 259
           TCCCTGTGGGACTGCGACCGCAAGTTCAGGGTCAAGATCAGAGGCATTGATATCCCGTC

Qy     373 LeuProArgThrAlaAspLeuValPheValGlnAsnIleGlnTyrGlyGlnGln 392
Db     260 |||    :::||||    :::    :::|||||||||| 319
           CTGCCTCCGGAACACCGACCTCACAGTTTTGTGAGAGGCAAACATCCAGCATGGGCAACAA

Qy     393 ValLeuCysGlnArgArgThrSerProLysProGluThrProPheGluValTrpAsnVal 412
Db     320 ||||    :::||||    :::    :::|||    ||||||||||||| 379
           GTCCTTTGCCAAAGGAGGAACCACAGCCCCAAACCCTTCACAGAGGAGGTGCTGTGGAATGTG

Qy     413 TrpLeuGluPheSerIleLysAspLeuProLysGlyAlaLeuLeuAsnLeuGln 432
Db     380 |||    :::    :::    :::    ::||||||||||||||| 439
           TGGCTTGAGTTCAGTATCAAAATCAAAGACTTGCCCAAAGGGGCTCACTGAACCTCCAG

Qy     433 IleTyrCysGlyLysAlaProAlaLeuSerGlyLysThrSerAlaGluMetProSerPro 452
Db     440 ||||    :::    :::    :::||||||||||||| 499
           ATCTACTGCGGTAAAGCTCCAGCACTGTCAGGCAAGACCTCTGCAGAGTCCCCCAGTTCT

Qy     453 GluSerLysGlyLysAlaGlnLeuLeuTyrValValAsnLeuLeuLeuAspHisArg 472
Db     500 ||||    :::    :::||||||||||||||||||| 559
           GAGTCCAAGGGCAAAGTTCAGCTTCTCTATATGTGAACCTGCTGCTGATAGACCACCGT

Qy     473 PheLeuLeuArgHisGlyGluTyrValLeuHisMetTrpGlnLeuSerGlyGlyGlu 492
Db     560 ||||    :::    :::||||||||||||||||||| 619
           TTCCTCCTGCGGCCGTGGAGAATACGTCCTCCACATGTGGCAGATATCTGGGAAGGGAGAA

Qy     493 AspGlnGlySerPheAsnAlaAspLysGluThrSerAlaThrAsnProAspLysGluGluAsn 512
Db     620 ||||    :::    :::    :::|||||||||| 679
           GACCAAGGAAGTTCAATGCTCAATGCTGACAAACTCACGTCTCGAACTAACCCAGACAAGGAGAAC

Qy     513 SerMetSerIleSerIleLeuLeuAspAsnTyrCysHisProIleAlaLeuProLysHis 532
Db     680 ||||    :::||||    :::||||||||||||||| 739
           TCAATGTCCATCTCCATTCTTCTGGACAATTACTGCCACCCGATAGCCCTGCCTAAGCAT

Qy     533 ArgProThrProAspPro-GluGlyAspArgValArgAlaGluMetProAsnGlnLeuAr 552
Db     740 ::|||    :::    :::::::||||    ||||||||| 799
           CAGCCCACCCCTGACCCGGAGGGACCGGGTTCAGCAGAAATGCCAACCAGCTTCG

Qy     552 gLysGlnLeuGluAlaIleIleAlaThrAspProLeu-AsnProLeuThrAlaGlu-Asp 571
Db     800 ||||    :::    :::|||||||||||||||| 859
           CAAGCAATTGGAGGCGATCATAGCCACTGATCCACTTTAACCCTCTCACAGCAGAAGGAC

Qy     572 -LysGluLeuLeuTrpHis 577
Db     860 |||    ::|||
           CAAAGATTTGCTCTGGCAT 878
```

REFERENCE 2
AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
          Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE   Normalization and subtraction of cap-trapper-selected cDNAs to
          prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE   20499374
PUBMED   11042159
REFERENCE 3
AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
          Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
          Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
          Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
          Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
          Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
          Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE   RIKEN integrated sequence analysis (RISA) system--384-format
          sequencing pipeline with 384 multicapillary sequencer
JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE   20530913
PUBMED   11076861
REFERENCE 4
AUTHORS   Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
          Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
          Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
          Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
          Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
          Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
          Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
          Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
          Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
          Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
          Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
          Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
          Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
          Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
          Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
          Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
          Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
          Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
          and Hayashizaki,Y.
TITLE   Functional annotation of a full-length mouse cDNA collection
JOURNAL   Nature 409 (6821), 685-690 (2001)
MEDLINE   21085560
PUBMED   11217851
REFERENCE 5
AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
          Group Phase I & II Team.
TITLE   Analysis of the mouse transcriptome based on functional annotation
          of 60,770 full-length cDNAs
JOURNAL   Nature 420, 563-573 (2002)
REFERENCE 6   (bases 1 to 4996)
AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
          Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
          Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
          Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
          Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
          Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
          Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
          Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
          Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
          Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
          Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
          Muramatsu,M. and Hayashizaki,Y.
TITLE   Direct Submission
JOURNAL   Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
          Physical and Chemical Research (RIKEN), Laboratory for Genome
          Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
          RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
          Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp;
          URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
          Fax:81-45-503-9216)
COMMENT   cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.

FEATURES   Location/Qualifiers
     source   1..4996
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                     /mol_type="mRNA"
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                     /db_xref="FANTOM_DB:C130009D19"
                     /db_xref="taxon:10090"
                     /clone="C130009D19"
                     /tissue_type="head"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="16 days embryo"
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                     /note="PHOSPHATIDYLINOSITOL 3-KINASE CATALYTIC SUBUNIT,
                     BETA ISOFORM (EC 2.7.1.137) (PI3-KINASE P110 SUBUNIT BETA)
                     (PTDINS-3-KINASE P110) (PI3K) (PI3KBETA) homolog [Rattus
                     norvegicus] (SWISSPROT:Q9Z1L0, evidence: FASTY, 98.1%ID,
                     100%length, match=3210)
                     putative"
     polyA_signal   4975..4980
                     /note="putative"
     polyA_site   4996
                     /note="putative"
BASE COUNT   1326 a   1113 c   1222 g   1335 t
ORIGIN

Alignment Scores:
Pred. No.:   1
Score: 1.81e-144
Percent Similarity: 50.27%
Best Local Similarity: 32.61%
Query Match: 23.27%
DB: 11

Length: 4996
Matches: 1347.50
Conservative: 360
Mismatches: 195
Indels: 395
Gaps: 155
            37

US-09-974-573-1 (1-1102) x AK081350 (1-4996)

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Db   598 GCATCCGATGGCGCCATACCGTCGATTTCCTTCTGCCCACCGGGATTTATATCCAGTTG 657

Qy    93 --------ProAspHisPheLeuLeuLeuTyrGlnLysGlyGlnTrpTyrGlnGlu--------- 109
Db   658 GAAGTACCTCGGGAGCTACCATTTCTTATATTAAACAGATGTTATGGAAGCAAGTTCAC 717

Qy   110 ---TyrAspLysTyrGlnValValGlnThrLeuAsp------------CysLeuArg 123
          :::            ::: :::::|||||||::|:|
Db   718 AACTACCCGATGTTAACCTCCTATCGACATTGACTCGTGTATATGTTTGCATGTGGAAT 777

Qy   124 TyrTrpLysValLeuHisArgSerProGlyGln------------------------------ 134
Db   778 CAAACTGCTGTATATGAGGAGACTGGAAGACCGAAACACGAGAGACTTTGTGATGTCAGACCT 837

Qy   135 ------------IleHisValGlnArgHisAlaProSerGluGlnThrLeuAlaPhe 150
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Db   838 TTTCTCCAGTTCTCAAACTAGTGACTAGACGTGACCCCGCAGAAAAATTG-------- 891

Qy   151 GlnArgGlnLeuAsnAlaLeuLeuGlyTyrAspValSerAsnValHisAsp 170
          :::::            |||||
Db   892 GACTCAAAAATGGGGTTCTTATAGGAAAAGTTCTCATGAGTTTGATGCCTTGAAGGAT 951

Qy   171 AspGluLeu----GluPheThrArg------ArgArgLeuValThrProArgMetAlaGlu 187
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Db   952 CCCGAAGTGAATGAATTAGAAGAAAAATCGCAAATTCAGTGAGGCCAAGATTCAGTCT 1011

Qy   188 ValAlaGlyArgAspProLysLeuTyrAlaMetHisProTrpValThrSerLysProLeu 207
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Qy   547 MetProAsnGlnLeuArg---------------------------LysGlnLeuGluIleIleAla 560
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Db  2092 AGTGCTAATGT-AGTCGTGGTGGTGAAAAAATTTCTGTCGTGTCGTGAAAGAAATCTTCGAC 2150

Qy   561 ThrAspProLeuAsnProLeuThrAlaGluAspLysGluLeuLeuTrpHisPheArgTyr 580
         |||||||||||||||||||||||||||||||||     ::::::
Db  2151 AGGGACCCCCTGTCTCAGCTGTGTGAGAACGAAATGGACTTTATTTGACTCTACGGCAA 2210

Qy   581 GluSerLeuLysAsp---ProLysGluLeuPheSerSerValLysTrpGly 599
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Db  2211 GACTGCCGGAAGATGAAGCTAGCCCCTGTCCCCAGTCACTGCCAAAACTACTCCTGTCAATCAGTGGAAT 2270

Qy   600 GlnGlnGluIleValAlaLysThrTyrGlnLeuLeuAlaLysArgGluValTrpAspGln 619
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Db  2271 CAGCTTCAGGCGCTCCTGACGATATGGCCCAAA 2321

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Qy   700 ArgSerGluIleAlaGlnSerArgHisTyrGlnArgPheAlaValIleLeuGluAla 719
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Qy   720 TyrLeuArgGlyCysGlyThrAlaMetLeuHisAspPheThrGlnValGlnValIle 739
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Qy   833 LysHisGlyAspAspLeuArgGlnAspMetLeuIleLeuGlnLeuLeuArgIleMetGlu 852
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Db  2934 AAAAATGGTACGATTTGCGGCAGCAATGCTCGACGTGCCTGATGGAT 2993

Qy   853 SerIleTrpGluThrGluSerLeuAspLeuCysLeuLeuProTyrGlyCysIleSerThr 872
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Qy   208 ProGluTyr-----------------LeuLeuLysLysIleThrAsnAsnCysVal 220
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Qy   221 PheIleValIleHisArgSerThrThrSerGln------ThrIleLysValSerAlaAsp 238
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Db   3054  GGAGATCGGCTCTGCCTCATTGAGGTTGTGAGCACCTGAGCAATCGCTGACATTCAG   3113
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Db   3174  CTCAAGGAGTACAACTCTGGGGATGAC---CTGGACCGAGCGATTGAGGAGTTTACCTTG   3230
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Db   3411  TTCATTCATGTCATT------CAAGCAAGGAAAAACCGGGAAACACTGAAAAATTTGGCAG   3464
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Db   3705  TCACACAGTA   3714
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RESULT 6
AK040867

LOCUS   AK040867   4852 bp   mRNA   linear   HTC 05-DEC-2002
DEFINITION   Mus musculus adult male aorta and vein cDNA, RIKEN full-length
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             3-kinase catalytic delta polypeptide, full insert sequence.
ACCESSION   AK040867
VERSION   AK040867.1 GI:26334014
KEYWORDS   HTC; CAP trapper.
SOURCE   Mus musculus (house mouse)
ORGANISM   Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE   1
AUTHORS   Carninci,P. and Hayashizaki,Y.
TITLE   High-efficiency full-length cDNA cloning
JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
MEDLINE   99279253
PUBMED   10349636

REFERENCE   2
AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
             Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE   Normalization and subtraction of cap-trapper-selected cDNAs to
             prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE   20499374
PUBMED   11042159

REFERENCE   3
AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
             Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
             Sumi,N., Ishii,Y., Nakamura,S., Hazama,A., Nishine,T., Harada,A.,
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             Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
             Yoneda,Y., Ishikawa,T., Ozawa,Y., Tanaka,T., Matsuura,S., Kawai,J.,
             Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE   RIKEN integrated sequence analysis (RISA) system--384-format
             sequencing pipeline with 384 multicapillary sequencer
JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE   20530913
PUBMED   11076861

REFERENCE   4
AUTHORS   Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
             Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
             Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
             Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
             Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
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             Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
             Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
             Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
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             Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
             Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
             Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
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             Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
             Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
             Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
             Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
             and Hayashizaki,Y.
TITLE   Functional annotation of a full-length mouse cDNA collection
JOURNAL   Nature 409 (6821), 685-690 (2001)
MEDLINE   21085660
PUBMED   11217851

REFERENCE   5
AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
             Group Phase I & II Team.
TITLE   Analysis of the mouse transcriptome based on functional annotation
             of 60,770 full-length cDNAs
JOURNAL   Nature 420, 563-573 (2002)

REFERENCE   6 (bases 1 to 4852)
AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
             Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
             Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,Y., Hirozane,T.,
             Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
             Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
             Koya,S., Kurihara,C., Matsuyama,Y., Miyazaki,A., Murata,M.,
             Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
             Okazaki,Y., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
             Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
             Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
             Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
             Muramatsu,M. and Hayashizaki,Y.
TITLE   Direct Submission
JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
             Physical and Chemical Research (RIKEN), Laboratory for Genome
             Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
             RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
             Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
             URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
             Fax:81-45-503-9216)

COMMENT   cDNA library was prepared and sequenced in Mouse Genome
             Encyclopedia Project of Genome Exploration Research Group in Riken
             Genomic Sciences Center and Genome Science Laboratory in RIKEN.
             Division of Experimental Animal Research in Riken contributed to
             prepare mouse tissues.
             Please visit our web site for further details.
             URL:http://genome.gsc.riken.go.jp/
             URL:http://fantom.gsc.riken.go.jp/.

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RESULT 7

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REFERENCE    1
AUTHORS      Carninci,P. and Hayashizaki,Y.
TITLE        High-efficiency full-length cDNA cloning
JOURNAL      Meth. Enzymol. 303, 19-44 (1999)
MEDLINE      99279253
PUBMED       10049636
REFERENCE    2
AUTHORS      Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
             Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE        Normalization and subtraction of cap-trapper-selected cDNAs to
             prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL      Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE      20530913
PUBMED       11042159
REFERENCE    3
AUTHORS      Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
             Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
             Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
             Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
             Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
             Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
             Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE        RIKEN integrated sequence analysis (RISA) system-384-format
             sequencing pipeline with 384 multicapillary sequencer
JOURNAL      Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE      20530913
PUBMED       11076861
REFERENCE    4
AUTHORS      Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
             Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
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             Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
             Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
             Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
             Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
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             Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
             Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
             Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
             and Hayashizaki,Y.
TITLE        Functional annotation of a full-length mouse cDNA collection
JOURNAL      Nature 409 (6821), 685-690 (2001)
MEDLINE      21085660
PUBMED       11217851
REFERENCE    5
AUTHORS      The FANTOM Consortium and the RIKEN Genome Exploration Research
             Group Phase I & II Team.
TITLE        Analysis of the mouse transcriptome based on functional annotation
             of 60,770 full-length cDNAs
JOURNAL      Nature 420, 563-573 (2002)
REFERENCE    6  (bases 1 to 1937)
AUTHORS      Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A.,
             Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y.,
             Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K.,
             Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M.,
             Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M.,
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             Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T.,
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             Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE        Direct Submission
JOURNAL      Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
             Physical and Chemical Research (RIKEN), Laboratory for Genome
             Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
             RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
             Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
             URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
             Fax:81-45-503-9216)
COMMENT      cDNA library was prepared and sequenced in Mouse Genome
             Encyclopedia Project of Genome Exploration Research Group in RIKEN
             Genomic Sciences Center and Genome Science Laboratory in RIKEN.
             Division of Experimental Animal Research in Riken contributed to
             prepare mouse tissues.
             Please visit our web site for further details.
             URL:http://genome.gsc.riken.go.jp/
             URL:http://fantom.gsc.riken.go.jp/.
FEATURES             Location/Qualifiers
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                     /sex="male"
                     /tissue_type="thymus"
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                     /dev_stage="adult"
     CDS             <1..785
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                     GB|NM_020272, evidence: BLASTN, 99%, match=3776]
                     putative"
                     /codon_start=3
                     /protein_id="BAC37000.1"
                     /db_xref="GI:26346703"
                     /db_xref="MGI:1923289"
                     /translation="LIIQILRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDAT
                     TIAQIQSTVGNTGAFKDEVLNHWLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGI
                     GDRHNDNIMISETGNLFHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGSGKKT
                     SPHFQKFQDVYVRAYLALRHTNLLILFSMMLMTGMPQLTSKEDIEYIRDALTVGKS
                     EEDAKKYFLDQIEVCRDKGWTVQFNWFLHLVLGIKQGEKHSA"
BASE COUNT      546 a    423 c    407 g    561 t
ORIGIN
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Alignment Scores:
Pred. No.:                    1937
Score:                     1335.00
Percent Similarity:         99.23%
Best Local Similarity:      97.69%
Query Match:                23.06%

Length:                     1937
Matches:                     254
Conservative:                  4
Mismatches:                    2
Indels:                        0
Gaps:                          0
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US-09-974-573-1 (1-1102) x AK077772 (1-1937)

Qy     843 LeuIleLeuGlnIleLeuArgIleMetGluSerIleTrpGluThrGluSerLeuAspLeu 862
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3 TTGATCTGCAGATTCTACGCATCATGGAGTCCATTTGGGAGACTGAATCTCTGGACCTG 62

Qy     863 CysLeuLeuProTyrGlyCysIleSerThrGlyAspLysIleGlyMetIleGluIleVal 882
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      63 TGCCTTCTGCCTTACGGTTGCATCTCAACTGGTGACAAAATAGGAATGATCGAGATTGTA 122

Qy     883 LysAspAlaThrThrIleAlaGlnIleGlnSerThrValGlyAsnThrGlyAlaPhe 902
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     123 AAGGATGCCACAACGATCGCTCAAATTCAGCAAAGCACAGTGGTAACACGGGGGCATTC 182

Qy     903 LysAspGluValLeuSerHisTrpLeuLysGluLysCysProIleGluGluLysPheGln 922
                |||||||||||||::|::::||||:|||||||||||||||||||||||||||||||||
Db     183 AAAGATGAAGTCCTGAATCACTGGCTCAAGGAAAAATGTCCTATTGAAGAAAAGTTTCAG 242

Qy     923 AlaAlaValGluArgPheValTyrSerCysAlaGlyTyrCysValAlaThrPheValLeu 942
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     243 GCCGCAGTGGAAAGGTTTGTTTACTCCTGTGCAGGCTACTGTGTGGCCACATTTGTTCTT 302
```

RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa
,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
Hayashizaki,Y.
Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
e mouse tissues.

```
FEATURES             Location/Qualifiers
     source          1..915
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="5830428L06"
                     /sex="male"
                     /tissue_type="thymus"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="RIKEN full-length enriched, adult male thymus"
                     /note="Site 1: SalI; Site 2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. cDNA went through one round of normalization
                     to Rot = 10.0 and subtraction to Rot = 100.0. Second
                     strand cDNA was prepared with the primer adapter of
                     sequence [5' GAGAGAGAATTCCGAGTTAATTAATAATCCCCCCCCCCCCCC
                     3']. cDNA was cloned into the XhoI and BamHI sites.
                     Vector: a modified pBluescript KS(+) after bulk excision
                     from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end:
                     BamHI."
BASE COUNT    259 a    206 c    212 g    238 t
ORIGIN

Alignment Scores:
Pred. No.:
Score:                   1.36e-138    Length:          915
Percent Similarity:      1286.50      Matches:         248
Best Local Similarity:   98.44%       Conservative:      4
Query Match:             96.88%       Mismatches:        4
DB:                      22.22%       Indels:            1
                         10           Gaps:              0

US-09-974-573-1 (1-1102) x BB619812 (1-915)

Qy   843 LeuIleLeuGlnIleLeuArgIleMetGluSerIleTrpGluThrGluSerLeuAspLeu 862
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3 TTGATCTTGCAGATTCTCACGCATCATGGAGTCGATCCATTGGGAGACTGAATCTCTGGACCTG 62

Qy   863 CysLeuLeuProTyrGlyCysIleSerThrGlyAspLysIleGlyMetIleGluIleVal 882
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    63 TGCCTTCTGCCTTACGGTTGCATCTCAACTGGTGACAAATAGGAATGATCGAGATTGTA 122

Qy   883 LysAspAlaThrIleAlaLysIleGlnGlnSerThrValGlyAsnThrGlyAlaPhe 902
         ||||||||||||||||||||||||||:::|||||||||||||||||||||||||
Db   123 AAGGATGCCACAACGATCGCTCAAATTCAGCAGAAGACAGTGGGTAACACCGGGGCATTC 182

Qy   903 LysAspGluValLeuSerHisTrpLeuLysGluLysProIleGluLeuLysPheGln 922
         ||||||||||||||:::||||||||||||||||||||||||||||||||||
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Qy   943 GlyIleGlyAspArgHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeuPheHis 962
Db   303 GGGATCGGTGACAGGCCACAACGACAACATTATGATGATCTCAGAGAGACAGACAGACAGA 362

Qy   963 IleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIleAsnLysGluArg 982
Db   363 ATAGACTTCGGACACATTCTTGGGAATTACAAGAGTTTCTGGGCATCAATAAAGAGAGA 422

Qy   983 ValProPheValLeuThrProAspPheLeuPheValMetGlyThrSerGlyLysLysLysThr 1002
Db   423 GTGCCCTTGCCTCCTAACCCCAGACTTCTTGTTTGTGATGGGACTTTCTGGAAAAAAGACA 482

Qy 1003 SerLeuHisPheGlnLysPheGlnAsnAspValCysValLysAlaTyrLeuAlaLeuArgHis 1022
Db   483 AGTCCACACTTCCAGAAATTCCAGGATGTCTATGTTACCTAGCTCTTCGCCAT 542

Qy 1023 HisThrAsnLeuLeuIleIleLeuPheSerMetMetLeuMetThrGlyMetProGlnLeu 1042
Db   543 CACACAAACCTGTTGATCATCTTGTTCTCCATGATGCTGATGACAGGAATGCCCCAGCTG 602

Qy 1043 ThrSerLysGluArgIleGluTyrIleArgAspAlaLeuThrValGlyLysSerGluGlu 1062
Db   603 ACAAGCAAAGAGGACATTGAATATATCCGGGATGCCCTCACCGTGGGAAAAAGCGAGGAG 662

Qy 1063 AspAlaLysIleTyrPheLeuAspGlnIleGluValCysArgAspLysGlyTrpThrVal 1082
Db   663 GACGCTAAGAAATATTTCCTTGATCAGATCGAAGTCTGCAGAGACAAAGGATGGACTGTG 722

Qy 1083 GlnPheAsnTrpPheLeuHisLeuValLeuGlyIleLeuLysGlnGlyGluLysHisSerAla 1102
Db   723 CAGTTTAACTGGTTCCTACATCTTGTTCTTGGCATCAAACAAGGAGAAAAGCACTCCGCT 782

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RESULT 8
BB619812

LOCUS       BB619812    915 bp    mRNA    linear    EST    26-OCT-2001
DEFINITION  BB619812 RIKEN full-length enriched, adult male thymus Mus musculus
            cDNA clone 5830428L06 5', mRNA sequence.
ACCESSION   BB619812
VERSION     BB619812.1    GI:16459063
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 915)
  AUTHORS   Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.
            , Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
            ,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
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            ,D., Shibata,K., Shinagawa,A., Shiraki,F., Sogabe,Y., Suzuki,H.,
            Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
  JOURNAL   Unpublished
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.go.jp
            URL:http://genome.gsc.riken.go.jp/
            Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
            ,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
            Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. 10 (10), 1617-1630 (2000)
            wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
            Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
            ,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
            Hayashizaki,Y.
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Site 2: SalI; Cloned unidirectionally; oligo-dT-primed;
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

BASE COUNT     381 a    252 c    251 g    243 t
ORIGIN

Alignment Scores:
Pred. No.:                        1127
Score:              2.44e-136
Percent Similarity:  1268.50   Matches:         1127
Best Local Similarity: 89.14%  Conservative:     265
Query Match:         84.66%    Mismatches:        14
                     21.91%    Indels:            28
DB:                  10        Gaps:               6
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US-09-974-573-1 (1-1102) x BG389556 (1-1127)

Qy      642 AlaIleAlaValGln-LysLeuGluSerLeuGluAspAspValLeuHisTyrLeuLe 661
            ||||||||||||||   |:: ||||||||  |||  |||||||||||||::||||
Db        2 GCCATTGCAGTTCAGAAACTGGAGAGCTTGGAGGACGATGATGTTCTGCATTACCTTCT 61

Qy      661 uGlnLeuValGlnAlaValLysPheGluProTyrHisAspSerAlaLeuAlaArgPheLe 681
            |||||||:||||| ||||||||||  ||||::||||||||||||::||||||||||
Db       62 ACAATTGGTCAGGCTGTGAAATTTGAACCATACCATGATGTGCCTTGCCCAGATTTCT 121

Qy      681 uLeuLysArgGlyLeuArgAsnLysArgIleGlyHisPheLeuPheTrpPheLeuArgSe 701
            |  |||| |||| || |||||  ||||||| ||||||||||||||||||||||
Db      122 GCTGGAGCGTGGTTTAAGAACAAAAGAATTGGTCACTTTTTGTTTTGGTTCTTGAGAAG 181

Qy      701 rGluIleAlaGlnSerArgHisTyrGlnGlnArgPheAlaValIleLeuGluAlaTyrLe 721
            |  || ||| || ||||||||||||||||||||||  ||||||||||||||
Db      182 TGAGATAGCCCAGTCCAGACACTATCAGCAGAGGTTCGCTGTGATTCTGGAGCCTATCT 241

Qy      721 uArgGlyCysGlyThrAlaMetLeuHisAspPheThrGlnGlnValGlnValIleAspMe 741
            |||||  |||||||||||  ||||  ||||| |||||||||||||||||||
Db      242 GAGGGGCGTGTGGCACAGCCATGCTGCACGACTTTACCCAACAAGTCCAAGTAATCGAGAT 301

Qy      741 tLeuGlnLysValThrIleAspIleLysSerLeuSerAlaGluLysTyrAspValSerSe 761
            |||||||||||  |:|| ||:||||||||||||||| ||| ||| |
Db      302 GTTACAAAAGTCACCCTTGATATTAAATCGCTCTCTGCTGAAAAGTATGACGTCAGTTC 361

Qy      761 rGlnValIleSerGlnLeuLysGlnLysLeuGluAsnLeuGlnAsnLeuLysLeuProGl 781
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Db      362 CCAAGTTATTTCACAACTTAAACAAAGCTTGAAAACCTGCAGAATTCTCAACTCCCCGA 421

Qy      781 nSerPheArgValProTyrAspProGlyLeuLysLysAlaGlyAlaLeuValIleGluLysCy 801
            ||| ||| ||||||||||  |||  |||||||||:||||||||||||  |||||||
Db      422 AAGCTTTAGAGTTCCATATGATCCTGGACTGAAAGCAGGAGGCGCTGGCAATTGAAAAATG 481

Qy      801 sLysValMetAlaSerLysLysProLeuTrpLysGluPheLysCysAlaAspProTh 821
            ||||| |||||  ||||||||||||  ||| || |||||  |||  ||||||
Db      482 TAAAGTAATGGCTCAAGAAAAAACCACTATGGCTTGAGTTAAATGTCCGATCCTAC 541

Qy      821 rAlaLeuSerAsnGluThrIleGlyThrIleIleGlyPheLysHisGlyAspAspLysArgGlnAs 841
            ||||| ||||| |||| ||||||||||||||||||| ||:|||||||||||||
Db      542 AGCCCTATCCAATGAACAATTGGAATTATCTTTAAACATGGTGATGAGATCTGCGCCAAGA 601

Qy      841 pMetLeuIleLeuGlnIleLeuArgIleMetGluSerIleTrpGluSer-LeuA 861
            ||||:||||||:||||||||| ||||:| |||||  ||  |||||  |||
Db      602 CATGCTTATTTTACAGATTCTCACGAATCATGATGGTGGAGACTGAATCTTTTGG 661

Qy      861 spLeuCysLeuLeuProTyrGlyCysIleSerThrGlyCysIleGlyMetIleGl 880
            ||| ||  ||||  ||||:|  |||||||  ||||:|  ||||||  |||
Db      662 ATCTTATGCCTCCTCTGCACATGGTTGCATTTCAGTGACAAAATTGGAATGATCGA 721

Qy      880 uIleValLysAspAlaThrThrIleAlaLysIleGlnSerThrValGlyAsnThrGl 900
            |||||  |||||| |||||||::|||:||||||||||||||||| |||
Db      722 GATTGGTGAAAGACGGCACGAAAATTCGCAAAATTCGAAAAATTCGCAAAGGGGCAACACGG 781

Qy      900 lyAlaPheLysAspGluValLeuSerHisTrpLeuLysGluLysCysProIleGluGluL 920
            ||| |||:
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Db      183 AAAGATGAAGTCCTGAATCACTGGCTCAAGGAAAAATGTCCTATTGAAGAAAAGTTTCAG 242

Qy      923 AlaAlaValGluArgPheValTyrSerCysValGlyTyrCysValAlaThrPheValLeu 942
            || ||||| |||  ||||:|  |||||| ||| |  ||||||||||||||||||
Db      243 GCCCGAGTGGAAAGTTTGTTTACTTCCTGTGCAGGCTACTGCGTGTGCCACATTTGTTCTT 302

Qy      943 GlyIleGlyAspArgHisAsnAspAsnIleMetIleSerGluThrGlyAsnLeuPheHis 962
            ||:|| ||||  ||| ||||||  |||||| |  ||| ||||||  ||||||||:
Db      303 GGGATCGGTGACAGCACGACAACATTATGATCTCAGAGACAGGAAACCTATTCAT 362

Qy      963 IleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheGlyIleLeuAsnLysGluArg 982
            ||||||||||| ||  ||||:| |||  ||::| |  |||| ||||||||  ||:
Db      363 ATAGACTTCGGACACATTCTTGGGAATTACAAGAGTTTCCTGGCATCAATAAAGAGAGA 422

Qy      983 ValProPheValThrProAspPheValLeuPheValMetGlyThrSerGlyLysLysThr 1002
            |||||| ||  ||||||||||||||:||||||||||||| |  ||||||:||  ||||
Db      423 GTGCCCTTCGTCCTTAACCCCAGACTTCTTGTTTGTGATGGGATCTTCTGGAGAAAAAGACA 482

Qy     1003 SerLeuHisPheGlnLysPheGlnIleAspValCysValLysAlaTyrLeuAlaLeuArgHis 1022
            ||||| || ||||||||| |||:   ||| || ||:| |   || ||:||:
Db      483 AGTCCACACTTCCAGAAATTCCAGGATGTGTCTATGTTAGAGCTTACCTAGCTCTTCGGCCAT 542

Qy     1023 HisThrAsnLeuLeuIleIleLeuPheSerMetMetLeuMetThrGlyMetProGlnLeu 1042
            |||  ||:| |:|||||:|| ||||||||| |||||:|||||||||||:|
Db      543 CACACAAACCTGTTGATCATCTTGTTCTCCATGATGCTGATGACAGGAATGCCCCAGCTG 602

Qy     1043 ThrSerLysGluAspIleGluTyrIleArgAspAlaLeuThrValGlyLysSerGluGlu 1062
            |||:|||| ||:|||:| ||:||||| |:|| ||| ||:|||||||:|||| |  |
Db      603 ACAAGCAAAGAGGACATTGAAATATATCCGGGATGCCCCTACCGTTGGGAAAAAGCGAGAG 662

Qy     1063 AspAlaLysTyrPheLeuAspGlnIleGluGluValCysValCysArgAspLysGlyTyrThrVal 1082
            ||| |||||:|||| ||||| ||  |||||||||||  ||:| |||||||||||||
Db      663 GACGCTAAGAAAATATTTTCTTGATCAGATAGAAGTCTGCAGAGACAAGGATGGGACTGTG 722

Qy     1083 GlnPheAsnTrpPheLeuHisLeuValLeuValLeuGlyIleLeuGlyIleLeuLysLysGlnGlnGlyGlu 1098
            ||  |  ||| || |||:| |||||::|| |  ||||||||||:|
Db      723 CAGTCTAACTGGTTCCTACATCTTGTTCTGTTGGCATCAA-CAAGGAGAA 769

RESULT 9
BG389556
LOCUS      BG389556                1127 bp    mRNA       linear    EST  12-MAR-2001
DEFINITION 6024142SF1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4522932 5',
           mRNA sequence.
ACCESSION  BG389556
VERSION    BG389556.1  GI:13282991
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1  (bases 1 to 1127)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished
COMMENT    Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: ATCC
           cDNA Library Preparation: Life Technologies, Inc.
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLAM10424  row: m  column: 13
           High quality sequence stop: 725.
FEATURES             Location/Qualifiers
     source          1..1127
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Qy   41 GluPheValLeuProThrSerGlnArgAsnThrLysThrProGluThrAlaLeuLeuHis   60
         |||||||||||||||||||||||||||||||| ::|||||||||||||||||||||||||
Db 180 GAGTTCGTACTGCCCACCAGCCAGGGCATCGAACAGCCTCCAGAAACAGCGCTGCTGCAT 239

Qy   61 ValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnValTrpLeuArgAlaLeuGlu   80
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 240 GTGGCTGGCCATGGCAATGTGGAACAGATGAAAGCTCAGGTGTGGCTGCGCGCACTGGAG 299

Qy   81 ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTyr 100
         ::||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 300 ACCAGTGTGGCTGCGGAGTTCTACCACCGGTTGGGCCCGGACCAATTCCTCCTGCTCTAC 359

Qy 101 GlnLysGlyGlnTyrTrpTyrGluIleTyrGluLysTyrAspLysTyrGlnValGlnThrLeuAsp 120
         ||||||||||| |||||||||||||||||||||||| :::||||||||||||||||||
Db 360 CAGAAGAAAGGACAATGGATATTGAGATCTATGAGAAGTATGACAAGTACCAAGTGCAGACCCTAGAC 419

Qy 121 CysLeuArgTyrTrpLysValLeuHisArgSerProGlyGlnIleHisValValGlnArg 140
         ||||||||||||||||||||||||||||||||||| :|:|||||||||||||||||||||
Db 420 TGCCTGCATTACTGGAAGGTTGATGCACAAGAGCCCTGGCCAGATCCACGTGGTACAGCGA 479

Qy 141 HisAlaProSerGluGluThrLeuAlaPheGlnArgGlnLeuAsnAlaLeuIleGlyTyr 160
         |||| :::||||||||||||||||||||||||||||| ||||||||||||||||||||
Db 480 CACGTACCTTCTGAGGAGACCTTGGCTTTCCAGAGGCAGCTCAACTCCTATGCAGTTGGCTAT 539

Qy 161 AspValThrProLysHisAspSerAsnValHisAspAspGluGlnLeuGluPheThrArgArgLeu 180
         ||||||||||||||||:::::|||:::::|||||||||||||||||||||||||||||||
Db 540 GACGTCACTGACATCAGCAATGTGCACGATGATGAGCAGCTAGAGTTCACTCGGCGCGTCTG 599

Qy 181 ValThrProArgMetAlaGluValAlaGlyTyrArgAspProLysLeuTyrArgAlaMetHisPro 200
         |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db 600 GTTACGCCCCGCATGGCTGAAGTGGCCGGCTATCGCGATCCCAAACTCTATCGTGCTATGCACCCT 659

Qy 201 TrpValThrSerLysProLeuProGluTyrLeuLeuLysLysIleThrAsnAsnCysVal 220
         |||||||||||||||||||||||||||||:::||:|||||:::||||||||||||||||
Db 660 TGGGTAACGTCCAAACTCTCCAGACTACCTGTCAAAAAAAGATTGCCAACAACTGCATC 719

Qy 221 PheIleValIleHisArgSerThrThrSerGlnThrIleLysValSerArgAlaAspThr 240
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Db 720 TTCATCGTCATCCACCGCAGTACCACCAGCCAAACCATCAAGGTCTCCGCAGATGATACT 779

Qy 241 ProGlyThrIleLeuGlnSerProPheThrLysMetAlaLysLysLysSer--LeuMetAs 260
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Db 780 CCTGGTACCATCCTCCAGAGCTTCTTCACCAAGATGGCCAAGAAGAAGTCCCCTAATGAA 839

Qy 260 pIleProGlu 263
         ||| |||
Db 840 TATCTCAGAA 849

RESULT 11
BQ072706
LOCUS   BQ072706   1043 bp   mRNA   linear   EST 02-APR-2002
DEFINITION AGENCOURT_6763227 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5756177
            5', mRNA sequence.
ACCESSION   BQ072706
VERSION   BQ072706.1 GI:19901752
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1043)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov

```
Qy   201  TrpValThrSerLysProLeuPro-GluTyrLeuLeuLysLysIleThrAsnAsnCysVa  220
          ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db   684  TGGGTGACGTCCCAGCCCCTCCGGNAGTACCTGTGGAAGAAGATTGCCAACAACTGCAT  743

Qy   220  lPheIleValIleHisArgSerThrThrSerGlnThrIleLysValSerAlaAspAspTh  240
          |||||||||||||||||||||||| ||| ||||||||||||||  ||||||| |||||||
Db   744  CTTCATCGTCATTCACCGAGCNACACCAGCCAGAACATTAAGGTCTCACCCGACGACAC  803

Qy   240  rProGlyThrIleLeuGlnSerPhe-PheThrLysMetAlaLysLysLysSer-LeuMet  259
          ||||||||||||||||||||||||| |||||||||||||||| ||||| ||||| ||||
Db   804  CCCCGGCGCCATCTTGCAGAGCTTCCTTCACCAAGATGCCCANAAGAAAATCTCCGGATG  863

Qy   260  AspIle---ProGluSerGlnAsnGlu--ArgAspPhe--ValLeuArgValCysGlyA  277
          ||||     |||||||||||||| ||   ||| |||  |||||||||||||||
Db   864  GATATTTCCCCGAAAGCCCAAGCGAACAGGGATTTTGTGGCCCGCCGGTTCTGGGGG  923

Qy   277  rgAspGluTyrLeu----------ValGlyGluThrPro---IleLysAsnPhe---G  291
                               :::            :::
Db   924  CCCGGGATAAAATAAACCCCGGGGGGGGGAAAACCCCCATCCAAAAAACTTTTCCC  983

Qy   291  lnTrp-Val--ArgGlnCys-----LeuLysAsnGlyGluGlu  302
          ||| ||| || |||  |||
Db   984  AGTGGGGTGGAAAGGCACTGTCCCCTCCTAAAAAAGGGGGAAAA  1028
```

```
RESULT 12
CA966024
LOCUS       CA966024        976 bp    mRNA    linear    EST  03-JAN-2003
DEFINITION  CcLL03a12h19f2 Carp liver library 3 Cyprinus carpio cDNA clone
            12h19 5', mRNA sequence.
ACCESSION   CA966024
VERSION     CA966024.1  GI:27492581
KEYWORDS    EST.
SOURCE      Cyprinus carpio (common carp)
  ORGANISM  Cyprinus carpio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
            ; Cyprinidae; Cyprinus.
REFERENCE   1  (bases 1 to 976)
  AUTHORS   Gracey,A.Y., Fraser,E., Li,W. and Cossins,A.R.
  TITLE     Microarray and EST analysis of the carp (Cyprinus carpio)
            transcriptome during environmental stress
  JOURNAL   Unpublished
  COMMENT   Contact: Andrew R. Cossins
            Laboratory for Environmental Gene Regulation
            University of Liverpool
            School of Biological Sciences, The Biosciences Building, Crown
            Street, Liverpool, United Kingdom, L69 7ZB
            Tel: +44(0)151-795-4510
            Fax: +44(0)151-795-4431
            Email: cossins@liv.ac.uk
            Vector has been trimmed from this EST.
            Plate: 12 row: h column: 19
            Seq primer: TriplEx 5' LD (5'-CTCCGGGAAGCCGCCATTGTGTTGGT-3')
            High quality sequence start: 80
            High quality sequence stop: 676.
FEATURES             Location/Qualifiers
     source          1..976
                     /organism="Cyprinus carpio"
                     /mol_type="mRNA"
                     /db_xref="taxon:7962"
                     /clone="12h19"
                     /sex="Male & female"
                     /tissue_type="Liver"
                     /dev_stage="Adult"
                     /lab_host="E.coli Electromax DH10B"
                     /clone_lib="Carp liver library 3"
                     /note="Vector: pTriplEx2; Site_1: Sfil GGCCATTACGGCC;
                     Site_2: Sfil GGCCGCCTCGGCC; Normalized and serially
                     subtracted cDNA library prepared from liver of warm, cold
                     and hypoxia challenged animals"
BASE COUNT    263 a    220 c    243 g    247 t    3 others
ORIGIN
```

```
Plate: LLAM12796 row: f column: 18
High quality sequence stop: 691.
FEATURES             Location/Qualifiers
     source          1..1043
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5756177"
                     /tissue_type="leukocyte"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_118"
                     /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
                     (destroyed); RNA source leukocytes from anonymous pool of
                     non-activated adult donors. Library is oligo-dT primed
                     and directionally cloned (EcoRV site is destroyed upon
                     cloning). Average insert size 1.7 kb, insert size range
                     1.2-3.3 kb. Library is normalized and enriched for
                     full-length clones and was constructed by C. Gruber
                     (Invitrogen). Research Genetics tracking code 027. Note:
                     this is a NIH MGC Library."
BASE COUNT    244 a    323 c    293 g    180 t    3 others
ORIGIN

Alignment Scores:
Pred. No.:                             1043
Score:              3.04e-126    Length:        1043
Percent Similarity: 1181.50     Matches:        253
Best Local Similarity: 83.70%   Conservative:   14
Query Match:        79.31%      Mismatches:     35
DB:                 13          Indels:         17
                                Gaps:           7
```

```
US-09-974-573-1 (1-1102) x BQ072706 (1-1043)

Qy     1  MetGluLeuGluAsnTyrGlyLeuGlnProValLeuArgGluAspAsnArgArgArgArg   20
          |||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||:
Db    84  ATGGAGCTGGAGAACTATAAACAGCCCGTGCTGCGTGAGGAGGACAACTGCCAAGGCGGC  143

Qy    21  ArgArgMetLysProArgSerThrAlaAlaSerLeuSerMetGluLeuIleProIle     40
          |||||||:|||||||||||||||||:||||||||||||||||||||||||||||||||||
Db   144  CGGAGGATGAAGCCCCGCAGTGCTGCGGCCAGCCTGTCCTCCATGGAGCTCATCCCCATC  203

Qy    41  GluPheValLeuProThrSerGlnIleArgAsnThrLysThrProGluThrAlaLeuLeuHis  60
          |||||||||:|||||:||||||||||||||:||||||||||||||||||:||||||||||
Db   204  GAGTTCGTGCTGCCCCACAGCCAGATCAGAAATGCAAGAGCCCGAAACGGCGCCTGCTGCAC  263

Qy    61  ValAlaGlyHisGlyAsnValGluGlnMetLysAlaGlnInValTrpLeuArgAlaLeuGlu   80
          ||||||||||:|||||||||||||:||||||||||||||||||||||:||||||||||||
Db   264  GTGGCCGGCCACGGCAACGTGGAGCAGATGAAGGCCCAGGTGTGGCTGCGAGCGCTGGAG  323

Qy    81  ThrSerValSerAlaAspPheTyrHisArgGluGlyProAspHisPheLeuLeuLeuTyr  100
          |||:||:|||:||||:|||||||||||||||:||||||||||||||:|||||:||||||
Db   324  ACCAGCGTGGCCGGCGACTTCTACCACCGGGCTGGACCCGACCATCACTTCCTCCTGCTCTAT  383

Qy   101  GlnLysGlyGlnIleTrpTyrAspTyrGluLeuTyrValValGlnIleHisThrLeuAsp  120
          |||||||||:|||||||||||||:|||||||||||||:|||:|||||||||:|||||||:
Db   384  CAGAAGAGAGGGCAGTCAGTGTACGACCTCTACACACAAGTGGTGCAGACTCTGGAC  443

Qy   121  CysLeuArgTyrTrpLysValLeuHisArgSerProGlyGlnIleHisValValGlnArg  140
          |||:||||||||||||||||||||||||||:||||||||:||:|||||||:||:||||||
Db   444  TGCCTGGCTACTGCGAAGGCCCACGACCGGAGCCCCGGAGATCCACCGTGGTGCAGCGG  503

Qy   141  HisAlaProSerGluGluThrLeuAlaPheGlnArgGlnLeuAsnAlaLeuIleGlyTyr  160
          |||:||||||||:|||:|||||:|||||||||||||||||||:||||||||||:||||||
Db   504  CACCCCGCCTCCGAGGAGTCCCAAGCCTTCCAGCGGCAGCTTCAGGCGCTGATTGGCTAT  563

Qy   161  AspValThrArgAspValSerAsnValHisSerAspAspLeuGluGlnPheThrArgArgLeu  180
          ||||||||:||||||||||||||||||:|||||:||||:|||||||||:|||||||||||
Db   564  GACGTCACTCGAGCTCAGCGACGTCAGCAACGTGCAGGACGATAGCTGAGTTCACCCGCCGTGGCTTG  623

Qy   181  ValThrProArgMetAlaGluValAlaGlyLeuTyrArgAspProLysLeuTyrAlaMetHisPro  200
          ||||||||||:||||||||||||||||||||:|||||||||||||||||:||:||||||
Db   624  GTGACCCCGCGGATGGCGGAGGTGGCCAGCCGGCTGTACCGCGACCCCAAGCTTCACGCCCATGCACCCG  683
```

```
Alignment Scores:
Pred. No.:              976
Score:          1170.00
Percent Similarity:  88.97%        Length:             976
Best Local Similarity: 80.00%      Matches:            232
Query Match:                       Conservative:        26
DB:                                Mismatches:          32
                                   Indels:               2
                                   Gaps:                 0

US-09-974-573-1 (1-1102) x CA966024 (1-976)

Qy  792 LysAlaGlyAlaLeuValIleGluLysCysLysValMetAlaSerLysLysProLeu 811
            ::: |||||||||||||||::||:::|||||||||||||||||||||
Db   29 CGTCGAGGGGTCGGAGTGATTGAACAATGCAGATGCATCCAAAAAGAACCCTTTG 88

Qy  812 TrpLeuGluPheLysCysAlaAspProThrAlaLeuSerAsnGluThrIleGlyIleIle 831
            |||||||||||||||::|| ::|||||||||||||||| :::||||||||
Db   89 TGGCTGCAGTTCAAACAGCAGCCCCACAACCTTGCCAGTGACACGATTGGGATCATC 148

Qy  832 PheLysHisGlyAspAspAspMetGlnLeuMetIleLeuLeuArgIleMet 851
            |||||||| |||||||||| |::|||||||| ||::||||||
Db  149 TTTAAAGAGGCGGGGATGACCTTGCTCAGGAGCATGCATGACTGATATTACAGATTTTACTGATAATG 208

Qy  852 GluSerIleTrpGluThrGlySerLeuAspLeuCysLeuLeuProTyrGlyTyrCysIleSer 871
            |||||||||||||||||| |||||| ::|||||||::::||||||||||||||
Db  209 GAGTCTATCTGGGAACTGGGAGTCTTTGGATCTTTCCTTGTTACCATATGGATGTATTTCC 268

Qy  872 ThrGlyAspIleGlyMetIleGluIleLysValLysAspAlaThrArgIleAlaLysIle 891
            ::||||::||||:::||||||||||::::|||||||||::||||:::|||
Db  269 ACTGGAAAATAAAATTGGAATGATTGAAATAGTAGGAAGATGCCACTACTATTGCTAACATT 328

Qy  892 GlnGlnSerThrValGlyTyrAsnThrGlyAlaPheLysLysAspGluValLeuSerHisTrpLeu 911
            |||||||||||||| ||||||||| |||||||:::||||||||||||||||
Db  329 CAACAAAGTACTGTGGGACACCGGAGCTTTTAAAGATGAAAATCCTCAGTCAGTGGCTT 388

Qy  912 LysGluLysCysProIleGluGluLysPheGlnIleAlaAlaValAlaValGluArgPheValTyrSer 931
            ::||||||||||||||||||||||||||||::|||| :::||||||||||
Db  389 CGTGAAAAGTGTGTGGAATAGGACAAGCACCAGCGGCTGTTGAACGGTTTGTGTTCTCC 448

Qy  932 CysAlaGlyTyrCysValAlaThrPheValLeuGlyTyrIleGlyLysAspArgHisAsnAspAsn 951
            |||||||||||| ||||||||::::|||||||:::||||::::|||||::::||
Db  449 TGTGGAGGGTATTGTGTGGCAACTTATGTCCTGGGCATCGTCACAATGACAAC 508

Qy  952 IleMetIleSerGluThrGlyLysAsnLeuPheHisIleLeuAspGlyHisGlyLeuGlyAsn 971
            |||| ::||||||||||| ::|||||||||||||||||||||::::|||:::||
Db  509 ATAATGCATTACAGACAGGCAACCTATTCCACATTGATTTCGGTCACATACTTGGAAAC 568

Qy  972 TyrLysSerProLeuGlyIleGluAsnLysGluArgValProPheValLeuThrProAspPhe 991
            ||||||||||||||||||||||||||||||||||| :::|||||||||::
Db  569 TACAAGAGTTTCATGGGGATCAGCAAGGAGCGAGTTCCTTTGTCTGACTCCTGATTTC 628

Qy  992 LeuPheValMetGlyThrSerGlyLysLysThrSerLeuHisPheGlnLysPheGlnIleAsp 1011
            |::||||:::||||||||||||||||||||::||||||||||| :::|||||
Db  629 CTCTATGTGATGAGCACCAGCACGGGGAAAAAAACCAGCCCATTTCCTTCAGTTTCAGAAC 688

Qy 1012 ValCysValLysAlaThrTyrLeuAlaLeuArgHisHisThrAsnLeuIleLeuIleLeuLeuPhe 1031
            |||||||||| ::::||||||||||| |:::|||||||||| :::|||||:::|||
Db  689 GTTTGCCTAAGGCCTCGAAGGCCTACCTGGCTCTGAGACC-CACACTAACCTGCTGATCATCCTGTTC 747

Qy 1032 SerMetMetLeuMetThrGlyIleGluThrProGlnLeuThrSerLysGluLysIleGluTyrIle 1051
            ||||::||||||||||||::||||||||| :::||||||| :::||||||||||
Db  748 TCCATGATGCTGATGACCGGCCATGCTCAGCTGACCAGCAAGAGAGGACATCAGTACATA 807

Qy 1052 ArgAspAlaLeuThrValGlyLysSerGluGluAspAlaLysSerTyrPheLeuGlnGln 1071
            ||||||||||||||||| :::||::::|| ::|||||||||:::|||||||||
Db  808 CGGGAACCGCCTACCGTCGGATGCTCGGAAGACAGCACCAGGCCAACCA-CACTTTTTGGAACAA 866

Qy 1072 IleGluValCysArgAspLysGlyTyrTrpThr 1081
            |||||:::|||||||| |::|||||||||
Db  867 ATCGAGATCTGCCGGGACAAGGGGTGGGACG 896


RESULT 13
BG615507       761 bp    mRNA      linear    EST 18-APR-2001
LOCUS       BG615507
DEFINITION  6O2&42812F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4773914 5',
            mRNA sequence.
ACCESSION   BG615507
VERSION     BG615507.1    GI:13666878
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 761)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: CLONETECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1646 row: g  column: 03
            High quality sequence stop: 758.
FEATURES             Location/Qualifiers
     source          1..761
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4773914"
                     /tissue_type="embryonal carcinoma"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_61"
                     /note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
                     Sfil (ggccattatggcc); Site_2: Sfil (ggccattggcc).
                     Double-stranded cDNA was prepared from cell line RNA. 5'
                     and 3' adaptors were used in cloning as follows: 5'
                     adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor
                     sequence: 5'-ATTCTAGAGGCGGAGGCGGCCGACATG-dT(30)BN-3'
                     (where B = A, C, or G and N = A, C, G, or T).  Average
                     insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
                     contained inserts by PCR. This library was enriched for
                     full-length clones and was constructed by Clontech
                     Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
                     Library."
BASE COUNT    239 a   157 c   161 g   203 t    1 others
ORIGIN

Alignment Scores:
Pred. No.:                761
Score:          2.25e-124
Percent Similarity:  93.00%        Length:             761
Best Local Similarity: 91.44%      Matches:            235
Query Match:                       Conservative:         4
DB:                                Mismatches:          12
                                   Indels:               6
                                   Gaps:                 1

US-09-974-573-1 (1-1102) x BG615507 (1-761)

Qy  781 GlnSerPheArgValProTyrAspProGlyLeuProLysAlaAlaLeuAlaLeuValIleGluLys 800
            :|| |||||||||||||||||||||||||||||||||||||||||||||
Db    1 GAAAGCTTTAGAGTTCCATATGATCCTGGACTGAAAGCAGGAGCGCGGCCATTGAAAAA 60

Qy  801 CysLysValMetAlaSerLysLysProLeuTrpLeuGluPheLysCysAlaAspPro 820
            ||||||||||||||||||||||||||||||||||||||||||::::|||||
Db   61 TGTAAAGTAATGGCCTCCAAGAAAAAACCACTATGGCTTGAGTTTAAATGTGCCGATCCT 120

Qy  821 ThrAlaLeuSerAsnGluThrIleGlyIleIlePheLysHisGlyAspAspAspLeuArgGln 840
            ||||||||||||||||||||||||||||||||||::::|||||||| ::|||
Db  121 ACAGCCCTATCAAATGAAACAATTGGAATTATCTTTAAACATGGTGATGATCTGCGCCAA 180

Qy  841 AspMetLeuIleLeuGlnIleLeuArgIleMetGluSerIleTrpGluThrGlySerLeu 860
            |::||::||||||||||:::|||||||::::|||||||||||||:::||
Db  181 GACATGCTTATTTTACAGATTCTACGAATCATGGAGTCTATTTGGGAGACTGAATCTTTG 240
```

```
/note="Organ: kidney; Vector: pCMV-SPORT6.ccdb; Site_1:
EcoRV; Site_2: NotI; Cloned unidirectional; Primer:
Oligo dT. Average insert size 1.8 kb. Constructed by J.
Wang (Research Genetics, Invitrogen Corp) from tissue
donated by L. Zon (Harvard Univerity). Note: this is a
NCI_CGAP Library."
```

BASE COUNT   250 a   210 c   215 g   221 t
ORIGIN

Alignment Scores:
Pred. No.:
Score: 1.52e-117   Length: 896
Percent Similarity: 82.72%   Matches: 214
Best Local Similarity: 71.10%   Conservative: 35
Query Match: 19.10%   Mismatches: 44
DB: Indels: 8
                                             Gaps: 1

US-09-974-573-1 (1-1102) x CA471197 (1-896)

```
Qy  423 LeuProLysGlyAlaLeuLeuAsnLeuGlnIleTyrCysGlyLysAlaProAlaLeuSer 442
            :: ||||||||:::||||:||:|||:
Db    1 TTACCCAAAGGTGCCCGACTTAGCCTGCCAGTGTGCTGTGAAAGGCACAGACACAAACA  60

Qy  443 GlyLysThrSerAlaGluMetProSerProGluSerLysGlyLysAlaGlnLeuLeuTyr 462
            :::
Db   61 TCAAAGGAAACT----------------------GAAATGTAAAAACAAGTCTCGGCTTACTCTAC 102

Qy  463 TyrValAsnLeuLeuIleAspHisArgHisGlyGluTyrValLeu 482
            |||||||:||||:|||||
Db  103 TATGTCAACCTGTTATTAGTTGATCACCGTCCCTACTTAGACAAGGTGAGTTCATCTTG 162

Qy  483 HisMetTrpLeuSerGlyLysGlyAspGlySerPheAsnAlaAspLysLeu 502
            |:||||:|:|||
Db  163 CACATCTGGAAGATGCCTGAGAGATGCTGAAGACAACAGCAGTGTAAATGCAGATAAGCTT 222

Qy  503 ThrSerAlaThrAsnProAspLysGluAsnSerMetSerIleSerIleLeuLeuAspAsn 522
Db  223 ACATCCGCACCAACCCAGACAAGAACAACTCAATGGCTGTTGCTATTCTCCTGGACAAG 282

Qy  523 TyrCysHisProIleAlaLeuProLysHisArgProThrProAspProGluGlyAspArg 542
            |||:||||::|||:|:|:::||||
Db  283 TACTGTCACCCTGGCCTCTTCCCAAGAGCAAAGATTCCTGATATTGAAGGCGAAAGA 342

Qy  543 ValArgAlaGluMetProAsnGlnLeuArgLysGlnLeuGluLysIleIleAlaThrAsp 562
Db  343 GGGCAGAGAGATGCCAACATCTCACCGCAAACAATTTGAGCAGATTATTGCTACAGAC 402

Qy  563 ProLeuAsnProLeuThrAlaGluValAspLysGluLeuLeuTrpHisSerTyrGluSer 582
            ||||||:::
Db  403 CCTTTGCACCCGCTCACCTGCCGAAGATAAAGAGTTGCTCTGGCACTTCCGGAGGAGTGC 462

Qy  583 LeuLysAspProLysAlaTyrProLysLeuPheSerSerValLysTrpGlyGlnGlnGlu 602
            ||:||:|||||||:::|||||
Db  463 ATGAAGGATCCGAAAGCATCCGAAGTTCTTCCTCCTCGTTAAGTGGGGCAACAAGAG 522

Qy  603 IleValAlaLysThrTyrGlnLeuLeuAlaLysArgGluValLeuValTrpAspGlnSerAlaLeu 622
            :::|||||:|||||
Db  523 GCTGTGGCCATAACGCATTATCTTCTGGAAAGGAGCACCATATGGGAGCCGAAGCGTGCTT 582

Qy  623 AspValGlyLeuThrMetGlnAsnCysAsnPheSerAspCysAsnValArgAla 642
            :::|||||||:::||||
Db  583 GATGTGGGTTTGGTCTTACAATTACTGGACTGCAATGTTTCTGATGAAAACGTGCGCACT 642

Qy  643 IleAlaValGlnLysLeuGluSerLeuGluAspAspAspValLeuHisTyrLeuLeuGln 662
Db  643 ATAGCTGTCCGGAAGTTGGAGACTTTGGGAGATGAATGTCCTGCGGTATCTTCTGCAA 702

Qy  663 LeuValGlnAlaValLysPheGluProTyrHisAspSerAlaLeuArgPheLeuLeu 682
Db  703 CTTGTCCAGGCTGTAAAATTGAACCATACCATGACAGCCGCACTTGCAAGGTTCCTTCTG 762

Qy  683 LysArgGlyLeuArgAsnLysArgIleGlyHisPheTrpPheLeuArgSerGlu 702
            |||||||:::|||||
```

```
Qy  861 AspLeuCysLeuLeuProTyrGlyCysIleSerThrGlyAspLysIleGlyMetIleGlu 880
            ||||||||||
Db  241 GATCTATGCCTCCTGCCATATGGTTGCATTTCAACTGGTGACAAAATAGGAATGATCGAG 300

Qy  881 IleValLysAspAlaThrThrIleAlaLysIleAlaLysGlnSerThrValGlyAsnThrGly 900
            |||||||
Db  301 ATTGTGAAAGACGCCACGACAATTGCCAAAATTGCAAAGCAAGTGGGCAACACGGGA 360

Qy  901 AlaPheLysAspGluValValLeuSerHisTrpLeuLysGluLysCysProIleGluGlnLys 920
            |||||||||
Db  361 GCATTAAAGATGAAGTCCTGAATCACTGGCTCAAAGAGAAAATCCCCTACTGAAGAAAAG 420

Qy  921 PheGlnAlaAlaAlaGluArgPheValTyrSerCysAlaGlyTyrCysValAlaThrPhe 940
            ||||||:|||||
Db  421 TTTCAGGCAGCAGTGGAGAGATTTGTTTATTCCTGCGCAGGCTACTGTGTGGCAACCTTT 480

Qy  941 ValLeuGlyIleIleGlyAspArgHisAsnAspAsnIleMetIleSer-GluThrGlyAsnIle 960
            ||||||:::||||||
Db  481 GTTCTTGGAAATAGGCGACAGACAGACCATGATCAGATGATCACCCCGAGACAGGAAACCT 540

Qy  960 uPheHisIleAspPheGlyHisIleLeuGlyAsnTyrLysSerPheLeuGlyIle-AsnL 980
            |||||:::||||||
Db  541 ATTTCATATTGACTTCGGGCACATTCTTGGGAATTACAAAGTTTCCTGGGCATTTAATA 600

Qy  980 ys-GluArgValProPheValGluThrProAspPheLeuProPheValMetGlyThrSerGly 999
            ||||||:::
Db  601 AACGAGGAGAGTGCCATTTGTGCTAACCCCTGACTTCCTCTTTGTGATGGAACTTCTGGA 660

Qy 1000 LysLysThrSerLeuHis---PheGlnLysPheGlnAspValCysValValLysAla-TyrLe 1018
            |||||||:::
Db  661 ACAGCAAGACAAGCCCAACAACTTCCAGAAATCTCAGGACAATCTGTGTTAAGGCTTTATCT 720

Qy 1018 uAla-LeuArgHisHisThrAsnLeuLeuIleLeuLeuPhe 1031
            |||||||:::
Db  721 AGCCNTTTCGTCATCACAAAAAACTAACTGACATCATCCTGTTC 761
```

```
RESULT 14
CA471197
LOCUS       CA471197         896 bp    mRNA    linear    EST 12-NOV-2002
DEFINITION  AGENCOURT_10698181 NCI_CGAP_ZKid1 Danio rerio cDNA clone
            IMAGE:6791058 5', mRNA sequence.
ACCESSION   CA471197
VERSION     CA471197.1  GI:24927549
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
ORGANISM    Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
            ; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 896)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Leonard I. Zon, M.D.
            cDNA Library Preparation: Invitrogen Corp
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM14294 row: b column: 17
            High quality sequence stop: 757.
FEATURES             Location/Qualifiers
     source          1..896
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /db_xref="taxon:7955"
                     /clone="IMAGE:6791058"
                     /lab_host="DH10B (T1-resistant)"
                     /clone_lib="NCI_CGAP_ZKid1"
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Db    763 AAACGTGCACTCAGAAGCAAGCCGATCGGCCATTTCTTGTTCTCGGTTTTTAGAAGTGAA 822              Db    273 GTGGCCCGGCCACGGCAACGTCGAGCAGATGAAGGCCCAGGTGTGCGCTGCGAGCGCTGGAG 332
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||                         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    703 IleAlaGlnSerArgHisTyrGlnGlnArgPheAla-ValIleLeu-GluAlaTyrLeu 721             Qy     81 ThrSerValSerAlaAspPheTyrHisArgLeuGlyProAspHisPheLeuLeuLeuTyr 100
          ||||||||||||||||||||||||||:::||                                                        ||||||||||||||||||::::||::|||||||||
Db    823 AATTGCCCAATCCATCGCACTATCAGCAGAGGTATGCTTGTAATACTGGGAAGCGTATCTC 881            Db    333 ACCAGCGTGGCGGCGGACTTCTACCACCGGCTGGGACCCGCCATCACTTCCTCCTGCTCTAT 392

RESULT 15                                                                          Qy    101 GlnLysLysGlyGlnTrpTyrGluIleTyrAspLysTyrGluValValGlnThrLeuAsp 120
BQ232683                                                                                    |||||||||||||||||||||||||||||||||||||||||||||||||||
LOCUS       BQ232683             852 bp    mRNA    linear   EST 02-MAY-2002        Db    393 CAGAAGAAGGGGCAGTGGTACGAGATCTACGACAAGTACGAGGTGGTGCAGACTCTGGAC 452
DEFINITION  AGENCOURT_7558824 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:6045373
            5', mRNA sequence.                                                      Qy    121 CysLeuArgTyrTrpLysValLeuHisArgSerProGlyGlnIleHisValValGlnArg 140
ACCESSION   BQ232683                                                                        |||||||||||||||||||||||||||||||:::|
VERSION     BQ232683.1   GI:20414083                                              Db    453 TGCCTGCGCTACTGGAAGGCCACGCACCAGATCCACCTGGTGCAGCGG 512
KEYWORDS    EST.
SOURCE      Homo sapiens (human)                                                   Qy    141 HisAlaProSerGluGluThrLeuAlaPheGlnArgGlnLeuAsnAlaLeuIleGlyTyr 160
  ORGANISM  Homo sapiens                                                                    |||  |||||||||||||:::::||
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;     Db    513 CACCCGCCCTCCGAGGAGTCCCAGCCTTCCAGCGGCAGCTCACGGCGCTGATTGGCTAT 572
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 852)                                                    Qy    161 AspValThrArgMetAlaGluValHisAspAspValHisGluPheThrArgArgLeu 180
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.                                                 ||||||||||||||||||||||||||||||||||||||||||||||||
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)        Db    573 GACGTCACTCGACGTCAGCAACGTGCACGACGATGAGCTGGAGTTCACGCGCCGTGGCTTG 632
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.                                      Qy    181 ValThrProArgMetAlaGluValAlaGlyArgAspProLysLeuTyrArgAlaMetHisPro 200
            Email: cgapbs-r@mail.nih.gov                                                     |||||||||||||||||||||||||||||||||||
            Tissue Procurement: ATCC                                               Db    633 GTGACCCCGCGCATGGCGGAAGTGGCCAGCCGGACACCCCAAGCTCTACCGCCATGCACCCG 692
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)              Qy    201 TrpValThrSerLysProLeuProGluTyrLeuLeu--LysLysIleThrAsnAsnCys 219
            DNA Sequencing by: Agencourt Bioscience Corporation                              ||||||:::||
            Clone distribution: MGC clone distribution information can be          Db    693 TGGGTGACGTCCAAGCCCCTCCCGGAGTACCCTGGGAAAGAGAATTGGCAACACTGC 752
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov                                                  Qy    220 ValPheIleValIleHisArgSerThrThrSerGlnThrThrLysValSerAlaAspAsp 239
            Plate: LLAM13289 row: h column: 14                                               |:::||
            High quality sequence stop: 632.                                       Db    753 ------------CATCTTTCATCCGTCATTCACCGGCAGCACCCACC 788
FEATURES             Location/Qualifiers
     source          1..852                                                        Qy    240 ThrProGlyThrIleLeuGlnSerPhe 248
                     /organism="Homo sapiens"                                                ::::|||
                     /mol_type="mRNA"                                              Db    789 AGGCCAGGAACCATTTAAAGGCTTTC 815
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6045373"                                         Search completed: February 15, 2004, 06:38:04
                     /tissue_type="embryonal carcinoma, cell line"                  Job time : 5305 secs
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_92"
                     /note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI;
                      Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                      Average insert size 2.5 kb. Library enriched for
                      full-length clones and constructed by Life Technologies.
                      Note: this is a NIH_MGC Library."
BASE COUNT   185 a    271 c    250 g    146 t
ORIGIN

Alignment Scores:
Pred. No.:              1.8e-109           Length:         852
Score:                  1036.50            Matches:        204
Percent Similarity:     85.54%             Conservative:   9
Best Local Similarity:  81.93%             Mismatches:     27
Query Match:            17.90%             Indels:         9
DB:                     13                 Gaps:           2

US-09-974-573-1 (1-1102) x BQ232683 (1-852)

Qy     1 MetGluLeuGluAsnTyrGluGlnProValValLeuArgGluAspAsnArgArgArgArg 20
         ||||||||||||||||:::::||||||||||||||||||||||||
Db    93 ATGGAGCTGGAGAACTATAAACAGCCCGTGGTGCTGAGAGAGGACAACTGCCGAGGCGC 152

Qy    21 ArgArgMetLysProArgSerThrAlaAlaSerLeuSerMetGluLeuProIle 40
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   153 CGGAGGATGAAGCCCCGAGTGCTGCGCCAGCCTGTCCTCATGGAGCTCATCCCCATC 212

Qy    41 GluPheValLeuProThrSerGlnAsnArgAsnThrLysThrProGluThrAlaLeuLeuHis 60
         ||||||||||||||||||:::||||||||||||
Db   213 GAGTTCGTGCTGCCCACCAGCCAGAATCGCAAATGCAAGAGCCCCGAAAGCGGCTGCTGCAC 272

Qy    61 ValAlaGlyHisGlyAsnValGluGlnMetLysAlaGluLeuArgLeuArgAlaLeuGlu 80
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